

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
31 October 2002 (31.10.2002)

PCT

(10) International Publication Number
WO 02/086443 A2

- (51) International Patent Classification⁷: **G01N**
- (21) International Application Number: PCT/US02/12476
- (22) International Filing Date: 18 April 2002 (18.04.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- | | | |
|------------|-------------------------------|----|
| 60/284,770 | 18 April 2001 (18.04.2001) | US |
| 60/290,492 | 10 May 2001 (10.05.2001) | US |
| 60/339,245 | 9 November 2001 (09.11.2001) | US |
| 60/350,666 | 13 November 2001 (13.11.2001) | US |
| 60/334,370 | 29 November 2001 (29.11.2001) | US |
| 60/372,246 | 12 April 2002 (12.04.2002) | US |
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- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Declaration under Rule 4.17:**
— of inventorship (Rule 4.17(iv)) for US only
- Published:**
— without international search report and to be republished upon receipt of that report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

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METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences of genes that are up- and down-regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include early detection of lung cancers, monitoring and early detection of relapse following treatment of lung cancers, monitoring response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous lesions of the lung. Examples of benign or precancerous lesions include: atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBF-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

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In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

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very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be “substantially identical.” This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat’l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents

used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

5 The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two
10 or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type
15 promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers
20 to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or
25 synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding,
30 duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary “moderately stringent hybridization conditions” include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

“Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

5 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is
10 characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.
15 Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

 The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-
20 regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine
25 the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,
30 which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

 Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

 A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

 For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

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Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S.

Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and Ouellette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and
5 software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at
10 least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample
15 source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic
20 bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern
25 encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in
30 or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux,
5 SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices
10 linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

15 The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

20 In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

25 Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary
30 memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of lung cancer-associated proteins

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains.

Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding
10 linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in
15 accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two
30 organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Khuyveromyces fragilis and *K. lactis*, *Pichia guillermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are

prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

- 5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue,
10 although variants can also be selected which have modified characteristics as will be more fully outlined below.

- While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be
15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

- 20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

- Substitutions, deletions, insertions or any combination thereof may be used to arrive
25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

- 30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, croton, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to

many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable
5 label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological
10 imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from
15 blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune
20 response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the
25 skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids,
30 modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

5

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening
10 assays or by evaluating the effect of drug candidates on a “gene expression profile” or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

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In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or
20 by evaluating the effect of drug candidates on a “gene expression profile”. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

25

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. “Modulation” thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman
Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems
typically automate procedures, including sample and reagent pipetting, liquid dispensing,
timed incubations, and final readings of the microplate in detector(s) appropriate for the
assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide
detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides
technical bulletins describing screening systems for detecting the modulation of gene
transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or
random or directed digests of proteinaceous cellular extracts, may be used. In this way
libraries of proteins may be made for screening in the methods of the invention. Particularly
preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins,
with the latter being preferred, and human proteins being especially preferred. Particularly
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g.,
substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30
amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to
about 15 being particularly preferred. The peptides may be digests of naturally occurring
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical
equivalents herein is meant that the nucleic acid or peptide consists of essentially random
sequences of nucleotides and amino acids, respectively. Since these random peptides (or
nucleic acids, discussed below) are often chemically synthesized, they may incorporate a
nucleotide or amino acid at any position. The synthetic process can be designed to generate
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible
combinations over the length of the sequence, thus forming a library of randomized candidate
bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are
5 randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription
20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as,
25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin
30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer

phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

 Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a
25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a
30 normal phenotype and become contact inhibited and would grow to a lower density.

 In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

5 Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g.,
15 Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.).

Various techniques which measure the release of these factors are described in
20 Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and
30 invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of, or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

30 **Methods of identifying variant lung cancer-associated sequences**

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

- 5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

10 The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

- 15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

- 25 In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In:
30 Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

5 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

 The present invention also provides for kits for screening for modulators of lung
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

5 Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAccn	UnigenelD	Unigene Title	70% chron/90% NL	70% SQUAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		***Immunoglobulin Heavy Chain, VdJrc Reg	2.68	3.28
	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
10	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitter)	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta receptor	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
15	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a1	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
20	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
25	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
	103280	X79981	Hs.76205	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; l	1.86	1
	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
30	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
	104865	AA045136	Hs.22575	ESTs	1.23	0.49
35	104989	AA102098	Hs.118615	ESTs	0.63	0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
40	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
	106797	AA478962	Hs.169943	ESTs	1.18	0.32
45	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidyl)	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
	107994	AA036811	Hs.165030	ESTs	0.7	0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
55	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
	108435	AA078787	Hs.194101	ESTs	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
60	109613	F03031	Hs.27519	ESTs	1.01	0.29
	109837	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
65	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
	111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
70	113195	T57112		***yc20g11.s1 Stratagene lung (#937210)	1.22	0.35
	113238	T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
	113695	T96965	Hs.17948	ESTs	1.54	0.28
75	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
80	115279	AA279760	Hs.63671	ESTs	1.79	0.91
	115566	AA398083	Hs.43977	ESTs	0.86	0.2
	115965	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16

	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
5	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		***yr30g11.s1 Soares fetal liver spleen	1.32	0.53
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
	119861	W80715		ESTs; Moderately similar to !!!! ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
15	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
	123978	C20653	Hs.170278	ESTs	1.52	0.32
	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		***yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
20	125167	W45560	Hs.102541	ESTs	1.46	0.69
	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AI417667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		***HUM145B09B Clontech human fetal brain	0.94	0.36
25	127002	R35380	Hs.24979	ESTs	3.02	4.06
	127307	AA369367	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AI302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.33
30	128624	AA479209	Hs.102647	ESTs	1.45	0.58
	128789	AA486567	Hs.105695	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
35	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
	129402	T63781		***yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
40	129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!! ALU SUBFAM	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
45	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23630	Hs.258675	EST	1.86	2.09
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
55	132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57056	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
60	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
65	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50683	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H88354	Hs.8861	ESTs	1.35	0.33
	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
75	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
80	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calitonin/alpha-CGRP, alt. transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, alt. transcript 12	0.85	1.9
85	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45

	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
5	101124	L10343	Hs.112341	*Protease inhibitor 3, skin-derived (SKA	0.62	2.67
	101175	L18920	Hs.36980	*Melanoma antigen, family A, 2"	1	1
	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (comifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
10	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		*Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
15	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	*Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
20	101809	M86849		*Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
	101845	M93426	Hs.78867	*Protein tyrosine phosphatase, receptor-	1	1
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	*Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	*Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
25	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
30	102623	U66083	Hs.37110	*Melanoma antigen, family A, 9 (MAGE-9)"	1	1
	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
35	102913	X07696	Hs.80342	keratin 15	0.7	4.72
	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin	1.15	3.35
	102963	X15943	Hs.37058	*Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	*Integrin, beta 4"	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloproteinase 1 (interstitial c	1	14.93
40	103058	X57348	Hs.184510	Stratiferin	1.25	4.17
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
	103119	X63629	Hs.2877	*Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	*Alcohol dehydrogenase 7 (class IV), mu	1	1
45	103312	X82693	Hs.3185	*Lymphocyte antigen 6 complex, locus D;	0.92	1.28
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	5T4 Oncofetal antigen	1	3.93
50	103594	Z31560	Hs.816	*SRY (sex determining region Y)-box 2, p	0.71	7.23
	103768	AA089997		*ESTs, Highly similar to integral membra	0.99	1.8
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
55	104733	AA019498	Hs.23071	ESTs	1.18	1.88
	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!! ALU SUBFAMI	1.64	2.89
	105012	AA116036	Hs.9329	*Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
60	105263	AA227926	Hs.6682	ESTs	0.95	2.87
	105298	AA233459	Hs.26369	ESTs	1	1.13
	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
65	106012	AA411621	Hs.8895	ESTs; same as BFH67	0.94	2.04
	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
70	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
75	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61460	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
80	108857	AA133250	Hs.62180	ESTs	1	1
	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
85	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
	109970	H09281	Hs.13234	ESTs	1.13	2.16

	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
5	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kD)*	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
	113970	W86748	Hs.8109	ESTs	1.17	1.73
15	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
20	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density l	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
	115522	AA331393	Hs.47378	ESTs	0.5	3.29
25	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
30	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456968	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
35	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
45	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
50	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983	AA398209	Hs.97587	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
55	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
60	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R05041	Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
70	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
	126645	AI167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
	127221	AI354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	AI204246		KIAA1085 protein	1.8	3.16
75	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
80	129404	AA172056	Hs.111128	ESTs	1	1
	129466	L42583		*Genbank Homo sapiens keralin 6 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keralin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
	130080	X14850	Hs.147097	*H2A histone family, member X*	0.98	1.96
85	130385	AA126474	Hs.155223	stanniocalcin 2	1	1

	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	"Doublecortin; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
15	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	"laminin gamma2 chain gene (LINC2), exon	1	1
20	132659	Z75190	Hs.54481	"Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69611	Hs.64311	"A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.286145	"SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564i1922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	***collagen, type XI, alpha 1***	0.76	2.86
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	"Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
50	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206	AA262491	Hs.186572	ESTs	1	1
	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102456	survival of motor neuron protein interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
70	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		***Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		***Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
	100398	D84557	Hs.155462	minichromosome maintenance deficient (ml	1.08	1.9
85	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Gila-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Epican, Alt. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutral)	1.35	2.73
	101181	L19686	Hs.73798	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-6) alpha t	0.69	2.78
	101342	L76191	Hs.182018	interleukin-1 receptor-associated kinase	1.04	1.84
20	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
30	101853	M94362	Hs.76084	lamin B2	0.84	1.19
	101977	S83364		***putative Rab5-interacting protein (cl	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201957	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		***Homo sapiens enterocyte differentiati	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76538	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activa	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78565	Hs.204133	hexabrachion (tenascin C; cytotoxicin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
75	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
80	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA155532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
85	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to pIL2 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.s.a	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscul	0.59	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777O23 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.57
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finger	0.96	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.67987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
	120242	Z98443	Hs.86366	ESTs	0.83	2.01

	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
5	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST	1.93	2.33
	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ [H.sapiens]	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
15	123398	AA521265	Hs.105514	ESTs	1	1.93
	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
20	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
30	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinaio	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
	128733	AA328993	Hs.104558	ESTs	1.34	1.94
40	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
45	129703	AA401348	Hs.179999	ESTs	0.97	1.63
	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosylt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
55	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepli	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.66	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3593	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.06	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
5	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
10	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
15	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45
	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DPI; DPL)	0.7	6.21
20	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-URNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
25	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
30	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
	134193	F09570	Hs.7980	ESTs	0.98	1.48
35	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
	134498	M63180	Hs.84131	threonyl-URNA synthetase	1.2	2.64
40	134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
45	134693	N70361	Hs.8854	ESTs	1.09	1.82
	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
	134914	U29615	Hs.91093	chitinase 1 (chilotriosidase)	1.16	1.29
50	134953	L10678	Hs.91747	profilin 2	0.95	1.76
	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
	135051	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

55 Table 1B shows the accession numbers for those pkeys in Table 1A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

60 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
65	100661 23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655
	100667 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29066 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342696 H50700 70 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
75	100668 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29066 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342696 H50700 80 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
85	101332 25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 A1471482 A1970337 AA737616 A1827444 AW003286 A1742333 A1344044 A1765634

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100780 458_127

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100830 4002_1

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100906 4312_1

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100930 16865_1

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102221 3861_1

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101809 32963_1

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102590 15932_1

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101977 29073_1

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AI948838 AW235336 AW172827 AA095289 BE046383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA468838 AA806983
AA625873 W78031 BE206307 AA550803 AI743147 AI990075 AA948274 AA129533 AI635399 AA605313 AI624669 AW594319 AI221834 AI337434
AI307706 BE550282 AI760467 AI630636 AI221521 AW674314 AW078889 AI933732 AI686989 AI186928 AW074595 AI127486 AL079644
AI910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977
AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113
R04438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AI375913 BE384156 W24652 AA746288 AA568232 BE090591
H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594 AA583483 AW873194 AW575166 AI128799
AI803319 AL042776 AW074313 AI887722 AI032284 AA447521 AI123885 N29334 AI354911 AW090687 AA232763 AA435535 AI2236910
AA047124 AA236734 AW514610 H93467 AA962007 AI446783 AA127259 AI613495 AI686720 AI587374 AA936731 AA702453 AI859757
AA216786 AI251819 AI469227 AA806022 AI092324 N71868 AA958782 AA236919 AA809450 AA227220 AA765284 AI192007 AW768810
AA805794 AA729280 AA806238 AW768817 N71879 AI050685 AA505822 AA668974 AI688160 BE045915 AW466315 AA731314 AA649568
AA834316 AW591901 AW063876 AW294770 AI300266 AI336094 AI560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675
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BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AI359165
AI638794 AI151283 AI863925 AW444977 AI207392 AA931263 AA443112 R40138 AW068538 AA351008 AA676972 R62503 AA916492 AW001865
H42334 H38280 AA121497 AA114137 AI750938 M17783 AA383786 BE274462 AI753182 C05975 AA347404 AW069298 AI754351 AI754044
AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560
R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591
BE389677 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803
NM_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085
AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356
AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221
AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597
N22401
N22401
M55998
M57293
AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425
AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
 R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
 R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
 R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
5	100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
10	100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
15	100138	U83508	Hs.2463	angiotensinogen 1			2.30					
20	100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
25	100306	U86749	Hs.80598	transcription elongation factor A (SII); KIAA0275 gene product						3.06		
30	100447	NM_014767	Hs.74583	Vpre-B								3.16
35	100458	S74019	Hs.247979	Hepatocyte Growth Factor Receptor	42.40					4.13		
40	100862	AA005247	Hs.285754	actin; alpha; cardiac muscle				125.60				
45	100959	AA359129	Hs.118127	phosphoglycerate mutase 2 (muscle)	36.40							
50	101032	BE206854	Hs.46039	amyloid beta (A4) precursor protein-binding				34.60				
55	101081	AF047347	Hs.4880	solute carrier family 6 (neurotransmitter)				193.20				
60	101088	X70697	Hs.553	transmembrane 4 superfamily member 2						3.10		
65	101125	AJ250562	Hs.82749	interleukin 8 receptor; beta				54.86				
70	101180	U11874	Hs.846	"Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
75	101308	L41390		enhancer of filamentation 1 (cas-like do				36.40				
80	101330	L43821	Hs.80261	Calcitonin receptor-like			2.29					
85	101345	NM_005795	Hs.152175	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
90	101346	AI738616	Hs.77348	lipoprotein lipase								3.54
95	101397	M26380	Hs.180878	complement component 8; beta polypeptide							3.81	
100	101414	NM_000066	Hs.38069	actin; alpha 1; skeletal muscle				34.60				
105	101435	NM_001100	Hs.1288	interleukin 1 receptor; type I				37.60				
110	101507	X16896	Hs.82112	cytochrome P450; subfamily IIB (phenobar								4.25
115	101530	M29874	Hs.1360	zinc finger protein; Y-linked			2.54					
120	101537	AI469059	Hs.184915	cytochrome P450; subfamily XVII (steroid		5.50						
125	101542	NM_000102	Hs.1363	EDG1; endothelial differentiation, sphin	39.40							
130	101545	BE246154	Hs.154210	thyroid stimulating hormone receptor		13.00						
135	101554	BE207611	Hs.123078	Intercellular adhesion molecule 2, exon								3.38
140	101560	AW958272	Hs.83733	protein kinase; cAMP-dependent; catalyti						4.37		
145	101574	M34182	Hs.158029	troponin C; slow								3.80
150	101605	M37984	Hs.118845	guanylate binding protein 1; interferon-	30.20						2.75	
155	101621	BE391804	Hs.62661	Sjogren syndrome antigen A1 (52kD; ribon								
160	101680	AA299330	Hs.1042	solute carrier family 8 (sodium/calcium						3.37		
165	101829	AW452398	Hs.129763	mannose receptor; C type 1				38.20				
170	101842	M93221	Hs.75182	"Hs-TBX2=T-box gene (T-box region) [huma			2.32					6.85
175	101961	AW004056	Hs.168357	uteroglobin								6.75
180	101994	T92248	Hs.2240	transcription factor CP2			2.45					
185	102020	AU077315	Hs.154970	aldehyde dehydrogenase 7								3.98
190	102091	BE280901	Hs.83155	forkhead box F1	54.60							3.62
195	102112	AW025430	Hs.155591	folate receptor 1 (adult)								
200	102190	AA723157	Hs.73769	fructose-bisphosphatase 1								
205	102202	NM_000507	Hs.574	Multimerin			2.32					
210	102241	NM_007351	Hs.268107	Accession not listed in Genbank		7.00						
215	102310	U33839		"Human sodium cotransporter RKST1 mRNA,	29.40							
220	102397	U41898		"Homo sapiens skeletal muscle LIM-protei								3.75
225	102571	U60115	Hs.239069	Human clone W2-6 mRNA from chromosome X						3.07		
230	102620	AA976427	Hs.121513	"Human ataxia-telangiectasia locus prote			2.40					
235	102636	U67092		solute carrier family 21 (prostaglandin			3.15					
240	102667	U70867	Hs.83974	"Human B-cell receptor associated protei						3.56		
245	102675	U72512	Hs.7771	progastrin (pepsinogen C)								4.51
250	102698	M18667	Hs.1867	opioid-binding protein/cell adhesion mol					12.00			
255	102727	U79251	Hs.99902	corticotropin releasing hormone	37.40							
260	102852	V00571	Hs.75294	thyroid and eye muscle autoantigen D1 (6					13.00			
265	103026	X54162	Hs.79386	pregnancy-zone protein	28.80							
270	103028	X54380	Hs.74094	Human mRNA for T cell receptor; clone IG					10.00			
275	103098	M86361		parvalbumin		6.00						
280	103117	X63578	Hs.295449	H.sapiens MAL gene exon 4			2.47					
285	103241	X76223		Cadherin 5, VE-cadherin (vascular epithe			2.69					
290	103280	U84722	Hs.76206	keratin; hair; acidic; 5							2.16	
295	103360	Y16791	Hs.73082									

	103496	Y09267	Hs.132821	flavin containing monooxygenase 2					3.27	5.97
	103508	Y10141		*H.sapiens DAT1 gene, partial, VNTR*						
	103561	NM_001843	Hs.143434	contactin 1	2.40					
	103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.99					
5	103575	Z26256		*H.sapiens isoform 1 gene for L-type cal					4.18	
	103627	Z48513		H.sapiens XG mRNA (clone PEP6)					3.44	
	103767	BE244667	Hs.296155	CGI-100 protein				2.25		
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR		46.55				
10	104078	AA402801	Hs.303276	ESTs					3.05	
	104326	AW732858	Hs.143067	ESTs					3.54	
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl					3.16	
	104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80					
	104473	AI904823	Hs.31297	ESTs						3.38
	104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC		2.47				
15	104495	AW975687	Hs.292979	ESTs	28.60				3.42	
	104595	AI799603	Hs.271568	ESTs						
	104597	AI364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein [6.00				
	104659	AW969769	Hs.105201	ESTs	34.00					
20	104686	AA010539	Hs.18912	ESTs		11.00				
	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80					
	104764	AI039243	Hs.278585	ESTs			60.40			
	104776	AA026349		ESTs	34.20					
	104825	AA035613	Hs.141883	ESTs		3.03				
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C	41.20					
25	104942	NM_016348	Hs.10235	ESTs						3.27
	104989	R65998	Hs.285243	ESTs			40.00			
	105062	AW954355	Hs.36529	ESTs						3.20
	105101	H63202	Hs.38163	ESTs	34.20					
30	105173	U54617	Hs.8364	ESTs						4.17
	105194	R06780	Hs.19800	ESTs		16.00				
	105226	R58958	Hs.26608	ESTs			2.34			
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr			2.72			
	105394	BE245812	Hs.8941	ESTs			2.61			
	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60					
35	105789	AF105941	Hs.18142	arrestin; beta 2						3.59
	105817	AA397825		synaptopodin				4.46		
	105847	AW964490	Hs.32241	ESTs			35.40			
	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi		3.43				
40	105999	BE268786	Hs.21543	ESTs	7.00		42.60			
	106075	AA045290	Hs.25930	ESTs						
	106178	AL049935	Hs.301763	KIAA0554 protein	34.80					
	106381	AB040916	Hs.24106	ESTs			12.00			
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2				3.69		
45	106536	AA329648	Hs.23804	ESTs			96.40			
	106569	R20909	Hs.300741	sorcin			47.20			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			220.40			
	106842	AF124251	Hs.26054	novel SH2-containing protein 3		2.55				
	106844	AA485055	Hs.158213	sperm associated antigen 6	39.20					
50	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl		2.28				
	106943	AW888222	Hs.9973	ESTs						4.28
	106954	AF128847	Hs.204038	ESTs						4.32
	107106	AA862496	Hs.28482	ESTs			10.45			
	107163	AF233588	Hs.27018	ESTs		2.57				
55	107201	D20378	Hs.30731	EST				3.84		
	107238	D59362	Hs.330777	EST		8.00				
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospho		10.67				
	107530	Y13622	Hs.85087	latent transforming growth factor beta b		2.32				
	107688	AW082221	Hs.60536	ESTs			34.60			
60	107706	AA015579	Hs.29276	ESTs	28.40					
	107723	AA015967		EST				3.29		
	107727	AA149707	Hs.173091	DKFZP434K151 protein			80.80			
	107750	AA017291	Hs.60781	ESTs			51.40			
	107751	AA017301	Hs.235390	ESTs				3.14		
65	107873	AK000520	Hs.143811	ESTs		9.00				
	107899	BE019261	Hs.83869	ESTs; Weakly similar to !!! ALU SUBFAM1				3.65		
	107994	AA036811	Hs.48469	ESTs			44.60			
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c			32.00			
	108041	AW204712	Hs.61957	ESTs			30.80			
70	108048	AI797341	Hs.165195	ESTs				4.75		
	108338	AA070773		*zm53g11.s1 Stratagene fibroblast (#9372		2.33			2.92	
	108434	AA078899		*zm94b1.s1 Stratagene colon HT29 (#93722						
	108447	AA079126		*zm92a11.s1 Stratagene ovarian cancer (#						
	108480	AL133092	Hs.68055	ESTs			34.00			
75	108499	AA083103		*zn1b12.s1 Stratagene hNT neuron (#93723						3.36
	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence			19.00			
	108550	AA084867		*zn11f6.s1 Stratagene hNT neuron (#93723			12.00			
	108604	AA934589	Hs.49696	ESTs		2.33				
	108625	AW972330	Hs.283022	ESTs						5.82
80	108629	AA102425		*zn24c6.s1 Stratagene neuroepithelium NT				3.42		
	108655	AA099960		*zm65c6.s1 Stratagene fibroblast (#93721		7.00				
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05				
	108864	AI733852	Hs.199957	ESTs	28.80					
	108895	AL138272	Hs.62713	ESTs	32.80					
	108921	AI568801	Hs.71721	ESTs			57.80			
85	108967	AA142989	Hs.71730	ESTs	28.80					

	109001	AJ056548	Hs.72116	ESTs; Moderately similar to hedgehog-int	2.57				
	109003	AA147497	Hs.71825	ESTs				2.11	
	109004	AA156235	Hs.139077	EST	5.60				
5	109065	AA161125	Hs.252739	EST			10.00		
	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA				3.44	
	109490	AA233416	Hs.139202	ESTs				2.92	
	109510	AJ798863	Hs.87191	ESTs		2.40			
	109578	F02208	Hs.27214	ESTs	10.00				
10	109601	F02695	Hs.311662	EST			40.80		
	109613	H47315	Hs.27519	ESTs			54.40		
	109650	R31770	Hs.23540	ESTs	31.20				
	109682	H18017	Hs.22869	ESTs		8.40			
	109724	D59899	Hs.127842	ESTs			29.40		
15	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene			8.00		
	109833	R79864	Hs.29889	ESTs		10.00			
	109837	H00656	Hs.29792	ESTs		6.49			
	109977	T64183	Hs.282982	ESTs				2.75	
	109984	AI796320	Hs.10299	ESTs			107.00		
20	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B				2.22	
	110271	H28985	Hs.31330	ESTs				3.48	
	110280	AW874263	Hs.32468	ESTs	44.20				
	110420	R93141	Hs.184261	ESTs			32.00		
	110578	T62507	Hs.11038	ESTs	28.40				
	110634	R98905	Hs.35992	ESTs			20.00		
25	110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-					4.15
	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H.			56.80		
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfam		3.13			
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic		5.33			
30	110971	AI760098	Hs.21411	ESTs			44.60		
	111023	AV655386	Hs.7645	ESTs	32.40				
	111057	T79639	Hs.14629	ESTs			17.14		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f				4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein					3.42
	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap					3.91
35	111442	AW449573	Hs.181003	ESTs			33.20		
	111737	H04607	Hs.9218	ESTs			53.00		
	111747	AI741471	Hs.23666	ESTs	46.20				
	111807	R33508	Hs.18827	ESTs		16.00			
40	111862	R37472	Hs.21559	EST				3.91	
	112045	AI372588	Hs.8022	TU3A protein					2.74
	112057	R43713	Hs.22945	EST					4.92
	112214	AW148652	Hs.167398	ESTs			13.00		
	112263	R52393	Hs.25917	ESTs		2.43			
45	112314	AW206093	Hs.748	ESTs		9.00			
	112324	R55965	Hs.26479	limbic system-associated membrane protei			14.00		
	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H		2.49			
	112380	H63010	Hs.5740	ESTs		2.34			
	112425	AA324998	Hs.321677	ESTs; Weakly similar to !!!! ALU SUBFAM		8.00			
50	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9				4.53	
	112492	N51620	Hs.28694	ESTs			29.80		
	112541	AF038392	Hs.116674	ESTs				3.62	
	112620	R80552	Hs.29040	ESTs		2.37			
	112623	AW373104	Hs.25094	ESTs		2.26			
55	112867	T03254	Hs.167393	ESTs			12.00		
	112894	T08188	Hs.3770	ESTs		6.50			
	112954	AA928953	Hs.6655	ESTs		7.00			
	113029	AW081710	Hs.7369	ESTs; Weakly similar to !!!! ALU SUBFAM					4.39
	113086	AA346839	Hs.209100	DKFZP434C171 protein					4.47
60	113140	T50405	Hs.175967	ESTs			10.00		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		14.00			
	113257	AI821378	Hs.159367	ESTs				3.72	
	113394	T81473	Hs.177894	ESTs				3.60	
	113437	T85349	Hs.15923	EST	35.00				
65	113454	AI022166	Hs.16188	ESTs		6.00			
	113502	T89130		ESTs	39.60				
	113552	AI654223	Hs.16026	ESTs					3.88
	113645	T95358	Hs.333181	ESTs				2.58	
	113691	T96935	Hs.17932	EST			38.20		
70	113706	AA004693	Hs.269192	ESTs				3.09	
	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro		2.31			
	113924	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				
	114035	W92798	Hs.269181	ESTs			13.00		
	114058	AK002016	Hs.114727	ESTs					5.00
75	114084	AA708035	Hs.12248	ESTs			40.60		
	114121	H05785	Hs.25425	ESTs		2.31			
	114124	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)		7.00			
	114275	AW515443	Hs.306117	interleukin 13 receptor; alpha 1		6.00			
	114297	AA149707	Hs.173091	DKFZP434K151 protein			48.80		
80	114427	AA017176	Hs.33532	ESTs; Highly similar to Miz-1 protein [H				3.45	
	114449	AA020736		*ze63b11.s1 Soares retina N2b4HR Homo sa			10.00		
	114452	AI369275	Hs.243010	ESTs; Moderately similar to RTCO_HUMAN G		14.00			
	114609	AA079505		*zm97a5.s1 Stratagene colon HT29 (#93722				3.13	
	114648	AA101056		*zn25b3.s1 Stratagene neuroepithelium NT			35.40		
85	114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy					3.42
	114762	AA146979	Hs.288464	ESTs	33.00				

	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00			
	115302	AL109719	Hs.47578	ESTs			12.00		
	115365	AW976252	Hs.268391	ESTs				3.32	
	115559	AL079707	Hs.207443	ESTs			48.00		
	115566	AI142336	Hs.43977	ESTs			56.20		
10	115683	AF255910	Hs.54650	ESTs, Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.s			33.60		
	115819	AA486620	Hs.41135	Endomucin 2			74.40		
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs			388.80		
	116035	AA621405	Hs.184664	ESTs			33.20		
15	116049	AA454033	Hs.41644	ESTs			45.80		
	116081	AI190071	Hs.55278	ESTs				3.57	
	116082	AB029495	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tuftelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti			30.00		
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20				
25	116835	N39230	Hs.38218	ESTs			41.20		
	116970	AB023179	Hs.9059	KIAA0962 protein			91.00	11.00	
	117023	AW070211	Hs.102415	ESTs					
	117027	AW085208	Hs.130093	ESTs	49.40				
	117036	H88908	Hs.41192	EST			32.60		
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs			30.60		
	117325	N23599	Hs.43396	ESTs				9.29	
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
35	117543	BE219453	Hs.42722	ESTs		16.00			
	117567	AW444761	Hs.44565	ESTs				12.00	
	117570	N48649	Hs.44583	ESTs				11.00	
	117600	N34963	Hs.44676	EST					3.74
	117730	N45513	Hs.46608	ESTs		6.00			
40	117791	N48325	Hs.93956	EST		9.00			
	117929	N51075	Hs.47191	ESTs			29.20		
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109667	Hs.124154	Homo sapiens mRNA full length insert cDN			2.40		
	118446	N66361	Hs.269121	ESTs			2.28		
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs					3.10
	118549	N68163	Hs.322954	EST					3.41
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs					3.58
	118935	AI979247	Hs.247043	KIAA0525 protein			33.00		
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAM1				11.43	
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi			52.60		
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank					3.50
	119824	W74536	Hs.184	advanced glycosylation end product-speci		2.75			
60	119831	AL117664	Hs.58419	DKFZP586L2024 protein					3.21
	119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB			33.80		
	119889	W84346	Hs.58671	ESTs			30.03		
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs					3.80
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)			36.60		
	120378	AA223249	Hs.285728	ESTs		12.00			
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40				
	120504	AA256837		ESTs			8.00		
	120512	N55761	Hs.194718	ESTs	33.00				
70	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa					4.18
	120777	AA287702	Hs.10031	KIAA0955 protein			46.60		
	121082	AA398722		ESTs			39.00		
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST					5.08
75	121363	AI287280	Hs.97933	ESTs			12.00		
	121366	AI743515		ESTs			20.00		
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev					3.32
	121518	AA412155		ESTs			30.20		
	121545	AA412442	Hs.98132	ESTs		2.29			
80	121622	AA416931	Hs.126065	ESTs		9.00			
	121665	AA416556	Hs.98234	ESTs			34.80		
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs	38.80				
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs					3.61

	121835	AB033030	Hs.300670	ESTs	2.34				
	121841	AA427794	Hs.104864	ESTs	2.61				
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
5	121938	AA428659	Hs.98610	ESTs		46.80			
	121950	AA429515	EST			31.40			
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98746	EST				3.58	
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
	122247	AA436676	Hs.98890	EST		39.80			
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro	9.00				
	122266	AA436840	Hs.98907	EST				3.60	
	122285	AA436981	Hs.121602	EST				3.14	
15	122409	AA446830	Hs.99081	ESTs	30.80				
	122485	AA524547	Hs.160318	phospholemmann		2.65			
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	15.00				
	122772	AW117452	Hs.99489	ESTs	6.67				
20	122831	AI857570	Hs.5120	ESTs				3.37	
	122913	AI638774	Hs.105328	ESTs		32.20			
	123049	BE047680	Hs.211869	ESTs		41.80			
	123076	AI345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs				2.58	
25	123309	N52937	Hs.102679	ESTs		19.00			
	123455	AA353113	Hs.112497	ESTs		82.80			
	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST	35.40				
	123802	AA620448	Homo sapiens clone 24760 mRNA sequence	58.00					
30	123837	AI807243	Hs.112893	ESTs		32.40			
	123844	AA938905	Hs.120017	olfactory receptor, family 7; subfamily		2.63			
	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR		70.60			
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
35	124160	R40290	Hs.124685	ESTs		13.00			
	124205	H77570	Hs.108135	ESTs				4.74	
	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270952	ESTs		29.40			
	124348	AI796320	Hs.10299	ESTs	17.00				
40	124358	AW070211	Hs.102415	*yw35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AI814166	Hs.107197	ESTs				3.14	
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate		2.48			
	124468	N51413	Hs.109284	ESTs		30.80			
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph				6.03	
45	124519	AI670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO		2.50			
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
	124866	AI768289	Hs.304389	ESTs	8.00				
	124874	BE550182	Hs.127826	ESTs		37.60			
	125097	AW576389	Hs.335774	ESTs		10.00			
50	125179	AW206468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs				2.79	
	125299	T32982	Hs.102720	ESTs		34.20			
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
	125810	H00083	aryl hydrocarbon receptor-interacting pr	32.20					
55	126176	BE242256	Hs.2441	KIAA0022 gene product	12.00				
	126303	D78841	HUM525A05B Human placenta polyA+ (TFuji			33.60			
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu		29.80			
	126773	AA648284	Hs.187584	ESTs	39.60				
60	127307	AW962712	Hs.126712	ESTs; Weakly similar to pL2 hypotheticala	28.80				
	127462	AA760776	Hs.293977	aa59b04.s1 NCL_CGAP_GCB1 Homo sapiens c		34.40			
	127486	AW002846	Hs.105468	ESTs	9.00				
	127572	AA594027	Hs.191788	ESTs	2.36				
	127609	X80031	Hs.530	ESTs		29.40			
65	127832	AW976035	Hs.292396	ESTs		37.20			
	127898	AA774725	Hs.128970	ESTs				4.42	
	128073	AW340720	Hs.125983	ESTs		38.40			
	128101	AA905730	Hs.128254	ESTs	7.33				
	128149	NM_012214	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-				2.58	
70	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)	3.09				
	128333	W68800	Hs.12126	ESTs; Weakly similar to LR8 [H.sapiens]		34.40			
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT	10.00				
	128426	AI265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
75	128634	AA464918	ESTs; Moderately similar to !!!! ALU SUB			41.60			
	128687	AW271273	Hs.23767	ESTs		87.00			
	128726	AI311238	Hs.104476	ESTs				4.02	
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp		9.00			
	128833	W26667	Hs.184581	ESTs				3.76	
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor	2.66				
	128878	R25513	Hs.10683	ESTs				3.10	
	128885	AF134803	Hs.180141	cofilin 2 (muscle)		11.00			
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi					3.68
85	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
	129098	AW580945	Hs.330466	ESTs	34.60				

	129210	AL039940	Hs.202949	KIAA1102 protein					4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29				
	129262	BE222198	Hs.109843	ESTs			3.30		
5	129301	AF182277	Hs.330780	Human cytochrome P450-IIB (hIIB3) mRNA;					4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93				
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80			
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD			10.00		
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1				3.40	
	129782	AW016932	Hs.104105	EST	9.00				
	129950	F07783	Hs.1369	decay accelerating factor for complement		87.80			
	129958	R27496	Hs.1378	annexin A3		44.60			
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque	2.72				
15	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr		42.20			
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	2.54				
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr		51.60			
	130312	AF056195	Hs.15430	DKFZP586G1219 protein				3.16	
	130436	NM_001928	Hs.155597	D component of complement (adipsin)					4.11
20	130523	AA999702	Hs.214507	ESTs				4.77	
	130799	AB028945	Hs.12696	ESTs	6.00				
	130885	NM_005883	Hs.20912	adenomatous polyposis coli like				3.54	
	131002	AL050295	Hs.22039	KIAA0758 protein					3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00				
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20				
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40			
	131066	AW169287	Hs.22588	ESTs		29.60			
	131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot			9.00		
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding					3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfam				3.14	
	131179	AA171368	Hs.184482	DKFZP586D0624 protein				3.80	
	131182	AI824144	Hs.23912	ESTs					3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98				
	131277	AA131466	Hs.23767	ESTs	3.15				
35	131281	AA251716	Hs.25227	ESTs		32.20			
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma					3.44
	131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev				6.40	
	131355	R52804	Hs.25956	DKFZP564D206 protein	8.00				
	131391	AW085781	Hs.26270	ESTs	10.00				
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80				
	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f					4.03
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin VIa [39.00				
	131545	AL137432	Hs.28564	ESTs			11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity			10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47				
	131675	H15205	Hs.30509	ESTs				3.06	
	131676	AI126821	Hs.30514	ESTs	45.80				
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	2.28				
	131717	X94630	Hs.3107	CD97 antigen					3.78
50	131756	AA443966	Hs.31595	ESTs		40.60			
	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi					3.67
	131821	AA017247	Hs.164577	ESTs	2.87				
	131839	AB014533	Hs.33010	KIAA0633 protein					3.48
55	131861	AL096858	Hs.184245	KIAA0929 protein Mx2 interacting nuclea	54.00				
	132015	AI418006	Hs.3731	ESTs		49.20			
	132070	BE622641	Hs.38489	ESTs		34.80			
	132242	AA332697	Hs.42721	ESTs	2.68				
	132334	AW080704	Hs.45033	lacrima proline rich protein	4.66				
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20				
60	132490	NM_001290	Hs.4980	LIM binding domain 2	2.66				
	132533	AI922988	Hs.172510	ESTs	13.00				
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60			
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin high				4.02	
	132652	N41739	Hs.61260	ESTs				3.18	
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1			11.43		
	133028	R51604	Hs.300842	ESTs	2.37				
	133071	BE384932	Hs.64313	ESTs	2.27				
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63				
	133129	AA428580	Hs.65551	ESTs					5.49
70	133147	AA026533	Hs.66	interleukin 1 receptor-like 1	6.20				
	133151	NM_014051	Hs.94896	ESTs				3.69	
	133213	AA903424	Hs.6786	ESTs		31.40			
	133276	AW978439	Hs.69504	ESTs			9.00		
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20				
75	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20				
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)				3.72	
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr					3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65				
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80			
80	133779	T58486	Hs.222566	ESTs				3.05	
	133978	AF035718	Hs.78061	transcription factor 21	2.92				
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec					3.45
	134000	AW175787	Hs.334841	selenium binding protein 1					4.05
	134111	AI372588	Hs.8022	TU3A protein	4.49				
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f				3.27	
	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [40.80			

	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept				3.76
	134677	AA251363	Hs.177711	ESTs		32.20		
	134745	NM_000685	Hs.89472	angiotensin receptor 1B	15.00			
5	134749	T28499	Hs.89485	carbonic anhydrase IV		3.05		
	134786	T29618	Hs.89640	angiotensin 1 receptor; TEK tyrosine ki			57.80	
	134825	U33749	Hs.197764	thyroid transcription factor 1				3.73
	134978	AI829008	Hs.333383	ficolin (collagen/fibrinogen domain-cont		2.52		
	135010	N50465	Hs.92927	ESTs		31.60		
10	135053	AW796190	Hs.93678	ESTs			3.21	
	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80			
	135091	AA493650	Hs.94367	ESTs				4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate	8.00			
	135203	C15737	Hs.269386	ESTs			4.31	
15	135236	AI636208	Hs.96901	ESTs	43.00			
	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd			6.42	
	135346	NM_000928	Hs.992	phospholipase A2; group I3 (pancreas)		3.82		
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-		4.15		
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20			
20	135388	W27965	Hs.99865	EST	38.80			
	135402	L12398	Hs.99922	dopamine receptor D4			4.21	

TABLE 2B shows the accession numbers for those primekeys lacking unigenelD's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	108447	43452_7 AA079126
	108550	120073_1 AA084867 AA084996
	108655	127522_1 AA099960 AA113013
	102397	44371_1 U41898
	126303	1525933_1 D78841 D78880
40	125810	1554054_1 H00083 R81062
	103627	2615_2 Z48513 Z48512
	121366	280401_1 AI743515 AA405617 AW276706
	114609	116777_1 AA079505 AA079537
	115272	172113_1 AW015947 AA211890 AA279425
45	108338	112186_1 AA070773 AA070774
	108434	114012_1 AA078899 AA078782 AA075788
	123802	genbank_AA620448 AA620448
	102310	NOT_FOUND_entrez_U33839 U33839
	102636	entrez_U67092 U67092
50	104776	genbank_AA026349 AA026349
	120504	genbank_AA256837 AA256837
	113502	genbank_T89130T89130
	108499	genbank_AA083103 AA083103
	101308	entrez_L41390 L41390
55	108629	genbank_AA102425 AA102425
	103098	Z21_215 M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223
	103508	entrez_Y10141 Y10141
	103575	entrez_Z26256 Z26256
60	119514	NOT_FOUND_entrez_W37937 W37937
	121082	genbank_AA398722 AA398722
	128634	AA464918_at AA464918
	105817	genbank_AA397825 AA397825
	121518	genbank_AA412155 AA412155
65	114449	genbank_AA020736 AA020736
	114648	genbank_AA101056 AA101056
	121950	genbank_AA429515 AA429515
	107723	genbank_AA015967 AA015967

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
10	R1:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.				
	R2:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas				
	R3:	70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples				
15						
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2 R3
20	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40	
	135378	AW961818	Hs.24379	MUM2 protein		2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)		
	135235	AW298244	Hs.293507	ESTs	12.40	
	135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67	
25	134951	BE305081	Hs.169358	hypothetical protein		8.00
	134799	M36821	Hs.89690	GRO3 oncogene		8.20
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous		
	134772	NM_000829	Hs.163697	glutamate receptor, ionotropic, AMPA 4	29.80	
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase		1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV		2.07
30	134696	BE326276	Hs.8861	ESTs		
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60	
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase		1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciogeni		1.92
35	134570	U66615	Hs.172280	SW/SNF related, matrix associated, acti	13.20	
	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h		1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp87)		6.20
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci		
	134343	D50683	Hs.82028	transforming growth factor, beta recepto		
40	134323	BE170651	Hs.8700	deleted in liver cancer 1		
	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1		
	134299	AW580939	Hs.97199	complement component C1q receptor		
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60	
	134182	D52059	Hs.7972	KIAA0871 protein	12.20	
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec		
	133978	AF035718	Hs.78061	transcription factor 21		
	133835	AI677897	Hs.76640	RGC32 protein		
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2		
	133633	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	15.20	
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A		
	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAIL		1.77
	133488	AA335295	Hs.74120	adipose specific 2		
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein		2.08
	133337	AF085983	Hs.293676	ESTs		9.60
55	133200	AB037715	Hs.183639	hypothetical protein FLJ10210		1.77
	133153	AF070592	Hs.66170	HSKM-B protein	30.60	
	133130	AI128606	Hs.6557	zinc finger protein 161	22.60	
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein		
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80	
60	132836	AB023177	Hs.29900	KIAA0960 protein		
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60	
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40	
	132548	X12830	Hs.193400	interleukin 6 receptor		7.20
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76
65	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524		1.88
	132240	AB018324	Hs.42676	KIAA0781 protein	21.20	
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2		1.99
	132199	AL041299	Hs.165084	ESTs	15.20	
	131751	T96555	Hs.31562	ESTs		1.76
70	131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-li	27.80	
	131694	NM_000246	Hs.3076	MHC class II transactivator		4.00
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2		
	131676	AI126821	Hs.30514	ESTs		6.20
	131629	Z45794	Hs.238809	ESTs	21.40	
75	131589	C18825	Hs.29191	epithelial membrane protein 2		
	131536	AA019201	Hs.269210	ESTs		9.40
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59
	131355	R52804	Hs.25956	DKFZP564D206 protein		4.48
	131253	R71802	Hs.24853	ESTs	15.00	
80	131207	AF104266	Hs.24212	latrophilin		1.75
	131156	AI472209	Hs.323117	ESTs		1.84
	131066	AW169287	Hs.22588	ESTs		
	131051	N64328	Hs.268744	KIAA1796 protein	3.54	
	131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr		1.93
85	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60	
	130762	D84371	Hs.1898	paraoxonase 1	12.00	

	130657	AW337575	Hs.201591	ESTs		
	130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)		
	130589	AL110226	Hs.16441	DKFZP434H204 protein		2.08
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled)		1.91
	130555	R69743	Hs.116774	integrin, alpha 1	9.60	
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	6.60	
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator		1.91
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20	
	129958	R27496	Hs.1378	annexin A3	5.05	
	129898	AI672731	Hs.13256	ESTs		
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60	
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase		
	129626	F13272	Hs.111334	feritin, light polypeptide		
15	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63	
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f		
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		2.53
	129527	AA769221	Hs.270847	delta-tubulin	39.20	
	129402	W72062	Hs.11112	ESTs		2.11
20	129385	AA172106	Hs.110950	Rag C protein	15.20	
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40	
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83	
	129240	AA361258	Hs.237868	interleukin 7 receptor		1.95
	129210	AL039940	Hs.202949	KIAA1102 protein		
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	4.20	
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2		
30	128789	AW368576	Hs.139851	caveolin 2		2.24
	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20	
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40	
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm		1.78
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH		2.51
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00	
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00
	128458	H55864	Hs.56340	ESTs		
	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20	
40	127968	AA830201	Hs.124347	ESTs	21.30	
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60	
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40	
	127896	AI669586	Hs.222194	ESTs	7.00	
45	127859	AA761802	Hs.291559	ESTs	14.00	
	127817	AA836641	Hs.163085	ESTs	14.00	
	127742	AW293496	Hs.180138	ESTs	11.00	
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		
50	127582	AA908954	Hs.130844	ESTs	19.60	
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40	
	127535	AA568424	Hs.164450	ESTs	17.50	
	127404	AI379920	Hs.270224	ESTs	14.60	
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40	
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60	
	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00	
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80	
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 I E2IG5		
	127242	AW390395	Hs.181301	cathepsin S	22.60	
60	127167	AA625690	Hs.190272	ESTs	21.40	
	127046	AA321948	Hs.293968	ESTs	41.20	
	126928	AA480902	Hs.137401	ESTs	11.00	
	126900	AF137386	Hs.12701	plasmolipin		1.78
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60	
65	126816	AA248234		gb:csq2228.seq.F Human fetal heart, Lamb	12.20	
	126812	AB037860	Hs.173933	nuclear factor I/A	17.19	
	126666	AA648886	Hs.151999	ESTs	13.57	
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.40	
	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	4.67	
70	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00	
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77	
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60	
	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	3.50	
	126182	AA721331	Hs.293771	ESTs	13.40	
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20	
	126142	H86261	Hs.40568	ESTs	14.00	
	126077	M78772	Hs.210836	ESTs	16.59	
	125994	AI990529	Hs.270799	ESTs	17.40	
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00	
80	125847	AW161885	Hs.249034	ESTs	49.57	
	125831	H04043		gb:yy45c03.r1 Soares_placenta Nb2HP Homo		
	125731	R61771	Hs.26912	ESTs	13.20	
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20	
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S		
	125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60	
85	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40	

	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AI422996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl		10.60
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
10	124578	N68321	Hs.231500	EST	21.43	
	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:yyw37g07.s1 Morton Fetal Cochlea Homo	14.64	
15	124306	AW973078	Hs.293039	ESTs		4.00
	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
20	123961	AL050184	Hs.21610	DKFZP434B203 protein		1.79
	123936	NM_004673	Hs.241519	angiotensin-like 1	15.80	
	123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602964		gb:nc97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	
25	123596	AA421130	Hs.112640	EST	10.93	
	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
30	123073	AA485061	Hs.105652	ESTs	31.20	
	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg		
35	122553	AA451884	Hs.190121	ESTs	40.00	
	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap		1.89
	121992	AI860775	Hs.98506	ESTs	3.60	
	121989	W55487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193767	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:z174e03.r1 Soares_testis_NHT Homo sap	14.80	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20	
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00	
	120484	AA253170	Hs.96473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST	7.20	
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
65	119824	W74536	Hs.184	advanced glycosylation end product-speci		
	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	tryptase beta 1		
	119126	R45175	Hs.117183	ESTs	12.60	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis		10.00
	118901	AW292577	Hs.94445	ESTs		3.96
	118661	AL137554	Hs.49927	protein kinase NYD-SP15		9.60
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to		1.90
	118416	N66028	Hs.49105	FKBP-associated protein	16.20	
	118379	N64491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s		3.80
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113		1.86
	118032	N52802	Hs.47544	EST		5.00
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence		4.00
85	117404	N39725	Hs.15220	zinc finger protein 106		1.90
	117314	N32498	Hs.42829	ESTs	14.20	

	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	20.20	2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen			
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
	116766	AI608657	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhms2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			
	116166	AL039940	Hs.202949	KIAA1102 protein		2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106		1.75	
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
15	115965	AA001732	Hs.173233	hypothetical protein FLJ10970		2.36	
	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		
	115844	AI373062	Hs.332938	hypothetical protein MGCS370	18.57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	11.82		
20	115672	AI889110	Hs.73251	ESTs	10.60		
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1		1.76	
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
	114999	BE246481	Hs.87856	ESTs	19.20		
	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
30	114769	AA149060	Hs.296100	ESTs	11.00		
	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
	114736	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
	114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5		2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs		2.00	
40	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL		1.82	
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN !!!!			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.15	
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
	113560	T91015	Hs.268626	ESTs	32.00		
	113552	AI654223	Hs.16026	hypothetical protein FLJ23191			
	113540	AW152618	Hs.16757	ESTs			
	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
50	113288	AI076838	Hs.12967	ESTs	12.40		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom		1.92	
55	113089	T40707	Hs.270862	ESTs	14.33		
	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheli		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yq74b08.s1 Soares fetal liver spleen	26.60		
	112691	R88708	Hs.220647	ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
	111998	R42379	Hs.138283	ESTs	11.00		
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A		1.77	
	111737	H04607	Hs.9218	ESTs		1.86	
70	111605	T91081	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr		1.88	
	111280	AA373527	Hs.19385	CGI-58 protein	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			
75	111232	AI247763	Hs.16928	ESTs	27.60		
	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein		2.18	
	110824	AI767183	Hs.26942	ESTs	12.20		
80	110776	AB032417	Hs.19545	frizzled (Drosophila) homolog 4		1.75	
	110576	H60869	Hs.37889	ESTs	13.00		
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs		2.31	
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			
85	109958	AA001266	Hs.133521	ESTs	11.25		
	109893	AA884208	Hs.30484	ESTs		2.68	

	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothe		3.91	
	109796	AI800515	Hs.12024	ESTs		17.20	
5	109688	R41900	Hs.22245	ESTs		9.60	
	109648	H17800	Hs.7154	ESTs	22.80		
	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs		1.89	
10	109472	AK001989	Hs.91165	hypothetical protein		6.00	
	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128654		gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothe	11.00		
15	108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)	26.00		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			
	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str		1.83	
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
20	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
25	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
30	107230	AI034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
35	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase		1.76	
	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
40	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL		2.05	
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60		
45	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106667	AW360847	Hs.16578	ESTs			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		2.40	
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5		1.78	
	106562	AL031846	Hs.152151	plakophilin 4		1.76	
50	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot		2.19	
	106533	AL134708	Hs.145998	ESTs	23.20		
	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
55	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
	105894	AI904740	Hs.25691	receptor (calcitonin) activity modifying		1.94	
	105847	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-		1.75	
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm		2.47	
60	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
65	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1		1.92	
	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
70	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
	104825	AA035613	Hs.141883	ESTs		1.87	
	104781	AA099904	Hs.21610	DKFZP434B203 protein		1.93	
	104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
75	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein		1.91	
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
80	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD		1.80	
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
85	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)		1.76
5	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t		2.15
	102698	M18667	Hs.1867	progastricsin (pepsinogen C)		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
10	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
15	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M93221	Hs.75182	mannose receptor, C type 1		
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		
	101764	A198550	Hs.81256	S100 calcium-binding protein A4 (calcium		1.78
	101716	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80	
20	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I		2.22
	101447	M21305		gb:Human alpha satellite and satellite 3	504.80	
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co		31.00
	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N		1.75
	101345	NM_005795	Hs.152175	calcitonin receptor-like		
25	101338	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h		2.24
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5		2.01
30	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte		7.52
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		1.91
	100893	BE245294	Hs.180789	S164 protein	15.40	
35	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80	
	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri		4.00
40	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		4.24
	100351	D64158				6.20
	100299	D49493	Hs.2171	growth differentiation factor 10		21.20
	100134	AA305746	Hs.49	macrophage scavenger receptor 1		
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2		1.79
45	100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible		5.40
	100066				11.29	

TABLE 3B shows the accession numbers for those primekeys lacking unigenelD's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
125831	1522905_1	H04043 D60988 D60337
126816	122973_1	AA248234 AA090985
126852	136135_1	AA399961 AA128347
121059	273450_1	AA393283 AA398628
120637	200885_1	AA811804 AA809404 AA286907 AW977624
122011	7617_-2	AA431082
120934	177521_1	AA226198 AA226513 AA383773
123802	genbank_AA620448	AA620448
116814	genbank_H50834	H50834
118329	genbank_N63520	N63520
104404	H58762_at	H58762
104776	genbank_AA026349	AA026349
113502	genbank_T89130T89130	
101262	entrez_L35854	L35854
108573	genbank_AA086005	AA086005
101447	entrez_M21305	M21305
124357	genbank_N22401	N22401
108781	genbank_AA128654	AA128654
112794	genbank_R97018	R97018
100351	entrez_D64158	D64158
100555	tigr_HT2245	M69181 M81105 U51039

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
100210	D26361	Hs.3104	KIAA0042 gene product	20.40
100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
100877	X80821	Hs.27973	KIAA0874 protein	35.56
100893	BE245294	Hs.180789	S164 protein	43.40
101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
101447	M21305		gb:Human alpha satellite and satellite 3	193.60
101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
102391	AA296874	Hs.77494	deoxyguanosine Kinase	13.90
102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
102829	NM_006183	Hs.80962	neurotensin	116.80
103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
104896	AW015318	Hs.23165	ESTs	29.40
105038	AW503733	Hs.9414	KIAA1488 protein	21.50
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60
106533	AL134708	Hs.145998	ESTs	59.80
106575	AW970602	Hs.105421	ESTs	43.40
106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
106851	A1458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
106995	AB023139	Hs.37892	KIAA0922 protein	20.88
107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
108609	BE409857	Hs.69499	hypothetical protein	19.67
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	59.20
109260	AW978515	Hs.131915	KIAA0863 protein	28.60
109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
109292	AW975746	Hs.188662	KIAA1702 protein	
109384	AA219172	Hs.86849	ESTs	21.00
109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
109445	AA232103	Hs.189915	ESTs	24.20
109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
109633	AW003785	Hs.170267	ESTs	20.40
109786	A1989482	Hs.146286	kinesin family member 13A	19.60
109958	AA001266	Hs.133521	ESTs	24.00
110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
111084	H44186	Hs.15456	PDZ domain containing 1	61.20
111132	AB037807	Hs.83293	hypothetical protein	24.60
111229	AW389845	Hs.110855	ESTs	27.20
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
112897	AW206453	Hs.3782	ESTs	22.00
112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40

	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFp434E082 (fr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
15	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI591147	Hs.61232	ESTs	20.80
20	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yy16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.67987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
40	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	28.80
	124006	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20
50	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.54
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AI022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
	129785	H19006	Hs.184780	ESTs	72.20
85	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
5	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	A1879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0648 protein	21.00
15	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
20	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothe	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
35	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	69.33
	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
45	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primekeys lacking unigenes/D's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325605 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigenelD:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
20	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5
	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
40	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
45	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
	100906	AU076916	Hs.5398	guanine monophosphate synthetase					5.16
55	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
	101045	J05614		gb:Human proliferating cell nuclear anti					4.69
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (5.69
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	opioid receptor, mu 1			6.40		
	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
65	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
	101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
70	101369	NM_000892	Hs.1901	kalikrein B, plasma (Fletcher factor) 1				12.80	
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small protine-rich protein 1B (cornifin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
75	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetratri				12.00	
	101502	M26958		gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
80	101535	X57152	Hs.99853	fibrillarlin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

5	101695	M69136	Hs.135626	chymase 1, mast cell	4.79			
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21			
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	55.50			
	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino			4.10	
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant			18.57	
10	101804	M86699	Hs.169840	TTK protein kinase	4.50			
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00			
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56			
	101842	M93221	Hs.75182	mannose receptor, C type 1			12.80	
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor			5.88	
15	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80			
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			4.35	
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)		7.40		
	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4			5.12	
	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,			12.00	
20	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20			
	102154	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.62			
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85			
	102217	AA829978	Hs.301613	JTV1 gene			6.18	
	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu			4.49	
25	102234	AW163390	Hs.278554	heterochromatin-like protein 1			5.80	
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50			
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)			5.15	
	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta			4.17	
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro			9.33	
30	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87			
	102368	U39817	Hs.36820	Bloom syndrome	15.91			
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma		19.20		
	102404	NM_005429	Hs.79141	vascular endothelial growth factor C			14.00	
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family			12.00	
35	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2			4.57	
	102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like			3.98	
	102610	U65011	Hs.30743	preferentially expressed antigen in mela	77.50			
	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50			
	102642	AA205847	Hs.23016	G protein-coupled receptor		22.00		
40	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein			12.80	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50			
	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50			
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C			9.24	
45	102696	BE540274	Hs.239	forkhead box M1			5.54	
	102768	U82321		gb:Homo sapiens clone 14.9B mRNA sequenc	6.60			
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e			3.78	
	102784	U85658	Hs.61795	transcription factor AP-2 gamma (activat			4.26	
	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H		14.40		
50	102829	NM_006183	Hs.80962	neurotensin	8.00			
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1			5.50	
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin		6.70		
	102913	NM_002275	Hs.80342	keratin 15	4.64			
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93			
55	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol			11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)			7.26	
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01			
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90			
	103038	AA926960	Hs.334883	CDC28 protein kinase 1			8.79	
60	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin			4.27	
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro		9.80		
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05			
	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07			
	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm			5.62	
65	103192	M22440	Hs.170009	transforming growth factor, alpha		7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			4.70	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		100.00		
	103316	X83301	Hs.324728	SMA5			9.80	
	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71			
70	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00			
	103385	NM_007069	Hs.37189	similar to rat HREV107			11.00	
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93			
	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,			5.15	
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr			3.98	
75	103446	X98834	Hs.79971	sal (Drosophila)-like 2			21.40	
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive		13.00		
	103477	AJ011812	Hs.119018	transcription factor NRF		6.40		
	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02			
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50			
80	103558	BE616547	Hs.2785	keratin 17	6.41			
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp			3.84	
	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	78.50			
	103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51			
	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50			
85	103768	AF086009		gb:Homo sapiens full length insert cDNA			4.48	
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468	8.00			
	103847	AF219946	Hs.102237	tubby super-family protein	10.40			
	103913	AW967500	Hs.133543	ESTs			15.60	
	104094	AA418187	Hs.330515	ESTs		6.60		

	104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034			26.00	
	104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80			
	104261	AW248364	Hs.5409	RNA polymerase I subunit				3.98
	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80			
5	104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	10.29			
	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21			
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m			15.79	
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H			17.40	
	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40			
10	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr				6.55
	104754	AI206234	Hs.155924	cAMP responsive element modulator			10.00	
	104758	BE560269	Hs.7010	NPD002 protein				4.47
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87			
	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83			
15	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86			
	105026	AA809485	Hs.124219	hypothetical protein FLJ12934		11.00		
	105076	AI598252	Hs.37810	hypothetical protein MGC14833				5.01
	105132	AA148164	Hs.247280	HBV associated factor				3.99
	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti		11.00		
20	105158	AW976357	Hs.234545	hypothetical protein NUF2R		16.00		
	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32			
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00			
	105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi			10.00	
25	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69			
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8			9.20	
	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,		7.80		
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12			
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82			
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro			27.00	
30	105848	AW954064	Hs.24951	ESTs			7.60	
	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha				4.14
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome			16.80	
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip			23.40	
35	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50			
	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00			
	106159	AK001301	Hs.3487	hypothetical protein FLJ10439				3.95
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36				6.04
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		13.20		
40	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso				5.02
	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 [6.60			
	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa				5.04
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced				7.25
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		13.80		
45	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75			
	106586	AA243837	Hs.57787	ESTs			10.84	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			45.60	
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00			
	106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00			
50	106813	C05766	Hs.181022	CGI-07 protein			11.40	
	106895	AK001826	Hs.25245	hypothetical protein FLJ11269		6.00		
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	6.56			
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S				4.27
	107054	AI076459	Hs.15978	KIAA1272 protein			34.80	
55	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71			
	107098	AI823593	Hs.27688	ESTs			24.80	
	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)				7.05
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60			
	107198	AV657225	Hs.9846	KIAA1040 protein		19.20		
60	107203	D20426	Hs.41639	programmed cell death 2		7.60		
	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50			
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71			
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence		8.71		
	107516	X57152	Hs.99853	fibrillarin				4.33
65	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)				4.00
	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80			
	107851	AA022953	Hs.61172	EST		8.00		
	107901	L42612	Hs.335952	keratin 6B	3.40			
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88			
70	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50			
	108015	AW298357	Hs.49927	protein kinase NYD-SP15			23.40	
	108056	AA043675	Hs.62633	ESTs			12.80	
	108075	AI867370	Hs.139709	hypothetical protein FLJ12572			12.80	
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00			
75	108296	N31256	Hs.161623	ESTs	6.60			
	108305	AA071391		gb:zm61e06.r1 Stratagene fibroblast (937			11.80	
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer			11.80	
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			20.80	
	108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937	6.40			
80	108573	AA086005		gb:zi84c04.s1 Stratagene colon (937204)			25.40	
	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	9.60			
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285			14.60	
	108695	AB029000	Hs.70823	KIAA1077 protein	3.00			
	108699	AA121514	Hs.70832	ESTs			10.00	
85	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		11.00		
	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21			

	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
5	108860	AA133334	Hs.129911	ESTs	6.09			
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00			
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines	10.58			
10	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
	109418	AJ866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-li		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
15	109543	AA564994	Hs.222851	ESTs	12.67			
	109548	H17800	Hs.71154	ESTs			10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gb:HSC33H092 normalized infant brain cDN			16.00	
	109704	AJ743880	Hs.12876	ESTs		11.00		
20	109792	R49625		gb:yg61f03.s1 Soares infant brain 1N1B H			12.60	
	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00			
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
25	110500	AA907723	Hs.36962	ESTs	4.50			
	110551	AW450381	Hs.14529	ESTs		8.60		
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
30	110916	BE178102	Hs.24349	ESTs		6.80		
	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
	111337	AA837396	Hs.263925	LIS1-Interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AJ476429	Hs.19238	ESTs			10.40	
35	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
	111597	R11499	Hs.189716	ESTs			9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6.80		
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
	112054	R43590		gb:yc85g02.s1 Soares infant brain 1N1B H		10.80		
40	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
	112382	R59904		gb:yh07g12.s1 Soares infant brain 1N1B H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00			
	112539	R70318	Hs.339730	ESTs			37.20	
45	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin			4.83	
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
50	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00		
55	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0563 gene product			9.40	
	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE			13.91	
	113984	R96696	Hs.35598	ESTs		7.80		
60	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20		
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42			
	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
65	114313	H18456	Hs.27946	ESTs			10.00	
	114339	AA782845	Hs.22790	ESTs		7.80		
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f			4.14	
	114560	AI452469	Hs.165221	ESTs			9.80	
	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60		
70	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720		6.00		
	114833	AI417215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31	
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3			4.03	
75	115097	AA256213	Hs.72010	ESTs			35.40	
	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m			4.19	
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
80	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
85	115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H		6.00		

	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81			
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14			
	115793	AA424883	Hs.70333	hypothetical protein MGC10753			11.80	
	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL			9.71	
5	115892	AA291377	Hs.50831	ESTs		27.40		
	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53			
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82			
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970			34.29	
	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g				8.23
10	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00			
	116090	AI591147	Hs.61232	ESTs	5.17			
	116096	AA682382	Hs.59982	ESTs		8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60		
	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17				5.82
15	116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypotheti				4.08
	116278	NM_003686	Hs.47504	exonuclease 1	9.50			
	116335	AK001100	Hs.41690	desmocollin 3	3.67			
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00		
	116503	AI925316	Hs.212617	ESTs			12.60	
20	116674	AI768015	Hs.92127	ESTs		32.00		
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp		7.60		
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F		9.80		
	116993	AI417023	Hs.40478	ESTs				10.20
25	117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo				15.20
	117317	AI263517	Hs.43322	ESTs				13.40
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,				20.60
	117396	W20128	Hs.296039	ESTs				10.60
	117412	N32536	Hs.42645	ESTs				16.00
	117519	N32528	Hs.146286	kinesin family member 13A				9.11
30	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42				4.01
	117721	N46100	Hs.93939	EST				19.80
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71			
	117903	AA768283	Hs.47111	ESTs				17.80
	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f				4.17
35	118013	AI674126	Hs.94031	ESTs				10.60
	118017	AI813444	Hs.42197	ESTs		8.82		
	118186	N22886	Hs.42380	ESTs		7.00		
	118325	AI868065	Hs.166184	intersectin 2				13.80
40	118367	N64269	Hs.48946	EST		6.14		
	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14			
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3		12.40		
	118709	AA232970	Hs.293774	ESTs				12.20
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50			
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22			
	119052	R10889		gb:ylf38d02.s1 Soares fetal liver spleen		9.60		
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome		6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa				9.44
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot				11.80
	119499	AI918906	Hs.55080	ESTs		14.80		
	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00			
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50			
55	119941	AA699485	Hs.58896	ESTs		8.00		
	119994	AA642402	Hs.59142	ESTs	7.73			
	120102	W67353	Hs.170218	KIAA0251 protein		39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91			
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par		8.20		
60	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73			
	120599	AA804448	Hs.104463	ESTs		7.00		
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos				10.00
	120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GCB1 Homo sapiens		9.40		
	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein				13.80
65	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00		
	120880	AA360240	Hs.97019	EST		15.60		
	120983	AA398209	Hs.97587	EST			27.66	
	121034	AL389951	Hs.271623	nucleoporin 50kD			20.80	
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80		
70	121313	AA402713	Hs.97872	ESTs				10.00
	121369	AW450737	Hs.128791	CGI-09 protein	25.71			
	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte				5.42
	121476	AA412311	Hs.97903	ESTs		8.30		
	121509	AA868939	Hs.97888	ESTs		8.59		
75	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50			
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00			
	121838	AA425680	Hs.98441	ESTs				10.40
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00			
	121991	AA430058	Hs.98649	EST				12.20
80	122089	AW016543	Hs.98682	hypothetical protein FKSG32		8.60		
	122105	AW241685	Hs.98699	ESTs		6.14		
	122163	AA435702	Hs.98829	EST				10.40
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap				18.20
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50			
	122338	AA443311	Hs.98998	ESTs	4.80			
85	122414	AI313473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00		

	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.40	
	122702	AI220089	Hs.99439	ESTs	9.20		
5	122852	AI580056	Hs.98992	ESTs		10.40	
	122925	AW268962	Hs.111335	ESTs	6.80		
	123005	AW369771	Hs.52620	integrin, beta 8	12.60		
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro		5.35	
	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti	6.06		
10	123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H	12.40		
	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po	11.80		
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein	13.00		
	123519	AW015887	Hs.112574	ESTs	12.20		
15	123614	AK000492	Hs.98806	hypothetical protein	7.80		
	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L		10.60	
	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490	7.00		
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma	9.80		
20	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
	123900	AA621223	Hs.112953	EST		12.80	
	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.02		
	124069	AF134160	Hs.7327	claudin 1	27.80		
25	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha		35.80	
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f		11.00	
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo		16.00	
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)		6.08	
30	124874	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog		21.00	
	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
	124969	AI650360	Hs.100256	ESTs		10.80	
	125000	T58615	Hs.110640	ESTs		9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypotheti	7.60		
35	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
	125299	T32982	Hs.102720	ESTs		9.57	
	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC		14.00	
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p	8.20		
	125418	AA777690	Hs.188501	ESTs		13.20	
40	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.96		
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225		11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5		4.31	
45	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass		15.60	
	125769	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	3.20		
	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1NIB H	7.40		
50	125924	BE272506	Hs.82109	syndecan 1		4.23	
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein		3.98	
	126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen		10.60	
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen	6.67		
55	126435	AW614529	Hs.285847	CGI-19 protein		10.60	
	126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino		4.38	
	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi		14.80	
60	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g		4.01	
	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_		11.60	
	126627	AA497044	Hs.20887	hypothetical protein FLJ10392		14.60	
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
65	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
	126892	AF121856	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs		22.83	
	126979	AA210954		gb:zq89h10.r1 Stratagene hNT neuron (937		11.80	
70	126986	AI279892	Hs.46801	sorting nexin 14		11.60	
	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s		20.80	
	127066	R25066		gb:yq42c07.r1 Soares infant brain 1NIB H		27.60	
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens		21.60	
	127139	AA830233	Hs.293585	ESTs		11.20	
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
	127225	AA315933	Hs.120879	ESTs		16.80	
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,		13.60	
80	127500	AW971353	Hs.162115	ESTs	11.20		
	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	7.80		
	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs		13.80	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		28.00	
85	127662	W80755	Hs.8294	KIAA0196 gene product		19.80	
	127668	AI343257	Hs.139993	ESTs		11.20	

	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836641	Hs.163085	ESTs			24.60
5	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
	127969	F06458	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
10	128077	AI310330	Hs.128720	ESTs			9.60
	128166	NM_006147	Hs.11801	interferon regulatory factor 6			9.24
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954968	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
15	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
	128539	R46163	Hs.258618	ESTs	12.60		
	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9			10.00
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	16.80		
20	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
	128796	AJ000152	Hs.105924	defensin, beta 2	8.12		
	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plakophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
25	129008	AL079648	Hs.301088	ESTs	8.80		
	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein	8.00		
30	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00		
	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
35	129466	L42583	Hs.334309	keratin 6A	12.94		
	129494	AI148976	Hs.112062	ESTs			11.00
	129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129641	AI911527	Hs.11805	ESTs			12.00
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
40	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA156214	Hs.12152	APMCF1 protein			5.71
	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.56		
45	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein			4.03
	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34		7.00	
	130026	T40480	Hs.332112	EST	6.40		
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
50	130149	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	2.74		
	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (tRNA-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein			9.60
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
55	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
	130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
65	130869	J03626	Hs.2057	uridine monophosphate synthetase (orotat			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein			9.60
	130994	W17044	Hs.327337	ESTs	12.40		
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21		
	131031	NM_001650	Hs.288650	aquaporin 4			9.80
70	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
75	131185	BE280074	Hs.23960	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
80	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00		
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium ion		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
85	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11

	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00		
	131885	BE502341	Hs.3402	ESTs	6.48		
	131921	AA456093	Hs.34720	ESTs		8.40	
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00		
	131958	NM_014062	Hs.3566	ART-4 protein			3.82
	131965	W79283	Hs.35962	ESTs	3.03		
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.60	
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30		
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00		
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40	
	132162	AA315805	Hs.94560	desmoglein 2			12.25
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70		
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71		
15	132181	AW961231	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	3.83		
	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50		
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50		
	132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe			9.20
20	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80
	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60	
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40	
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38		
	132544	L19778	Hs.51011	H2A histone family, member P		7.00	
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64		
	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60	
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95		
	132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20	
30	132653	Z15008	Hs.54451	laminin, gamma 2 (necin (100kD), kallini	4.38		
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	4.60		
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71		
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83
	132892	AW834050	Hs.9973	tensin			12.00
	132906	BE613337	Hs.234896	germinin	3.09		
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87
	132962	AA576635	Hs.6153	CGI-48 protein	3.50		
40	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18		
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19		
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96		
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55		
	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96
45	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28
	133155	M58583	Hs.662	cerebellin 1 precursor			10.80
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00		
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50	
	133421	AF134160	Hs.7327	claudin 1	2.85		
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p			4.66
	133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80	
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14		
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11	
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07		
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1			4.60
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr			13.00
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56		
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20	
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00		
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara		24.60	
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40	
	134272	X76040	Hs.278614	protease, serine, 15	4.50		
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00	
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.80		
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68		
	134423	H53497	Hs.83006	CGI-139 protein			3.84
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60	
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70
	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio			4.63
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00		

	134724	AF045239	Hs.321576	ring finger protein 22		12.00	
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00		
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20	
5	134806	AD001528	Hs.89718	spermine synthase			4.58
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle			4.79
	134859	D26488	Hs.90315	KIAA0007 protein		6.20	
	134891	R51083	Hs.90787	ESTs		7.40	
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00		
10	134993	BE409809	Hs.301005	purine-rich element binding protein B			4.48
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50		
	135080	AI761180	Hs.94211	rd1 (required for cell differentiation,	5.00		
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00	
	135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin			4.01
15	135184	U13222	Hs.96028	forkhead box D1		7.00	
	135242	AI583187	Hs.9700	cyclin E1	13.50		
	135286	AW023482	Hs.97849	ESTs	6.46		
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80	
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00		
20	135371	NM_008025	Hs.997	protease, serine, 22	8.00		
	135393	L11244	Hs.99886	complement component 4-binding protein,		14.60	

TABLE 5B shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	117079	1621717_1 H92325 T97125
	124305	242183_1 AW963221 AA344870 AA344871 H93331
	101502	18202_6 M26958
	109792	754958_1 R49625 F10674
	126034	1598157_1 H60340 N91637
40	102768	44641_1 U82321 H66077
	126345	1653833_1 N49713 N49819 W03810
	127066	1703458_1 R25066 R20144 R20145 Z43845
	127099	244301_1 AA347668 AW956810 Z44271 F07065 F07064 R13506
	119243	1774795_1 T12603 T12604
45	125875	1566433_1 H14480 N98295
	112054	1538292_1 R43590 F10439
	126979	171411_1 AA210954 AA211007
	126992	880655_1 AI809521 H12174 Z42556
	122318	292419_1 AA429743 AA442754
50	114699	135322_1 AA127386 R15644 AA127404
	114793	150742_1 AA158245 AA158235
	108305	111550_1 AA071391 AA069892 AA069891
	108393	113411_1 AA075211 AA075245 AA075126 AA074946
	100867	tigr_HT4586 U14622
55	123731	genbank_AA609839 AA609839
	109700	genbank_F09609 F09609
	120715	genbank_AA292700 AA292700
	113702	genbank_T97307 T97307
	115113	genbank_AA256460 AA256460
60	101045	entrez_J05614 J05614
	108554	genbank_AA084948 AA084948
	108573	genbank_AA086005 AA086005
	119052	149538_1 R10889 R10888
	126522	416020_1 W31912 AI167491
65	126605	439280_1 AA676910 AA778853 AA778865 W86800
	103768	46922_1 W42667 AI580740 AI690440 AI561350 AW467906 AW151450 AI825927 AL041716 AI885600 AI742213 AW248624 AI955498 AA033947
		AA845593 AI623711 N68583 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
		AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
70		AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
		H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881
		AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214
		AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375
		AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
		AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881
75		AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
		AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515
		AI866186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492
		AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169
		AA219425 AA629558 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339
80		AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255
		AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788
		AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967
		W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009549 C03892 AW149464 AA310963 AA219693
		AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409
85		AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
		W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972535 AW298594 AA375893 T12139 W28186 AW243849
 AI288629 AA843996 W15260 AI188286 AW248079 R15836

119599 genbank_W45552 W45552
 112382 genbank_R59904 R59904
 105264 genbank_AA227934 AA227934
 100071 entrez_A28102 A28102
 123315 714071_1 AA496369 AA496646

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)		2.68
101972	S82472		gb:beta-pol-DNA polymerase beta (exon a		2.11
102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
102832	U92015		gb:Human clone 143789 defective mariner	13.50	
103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
103439	X98266		gb:H.sapiens mRNA for ligase like protei		2.50
103563	L02911	Hs.150402	activin A receptor, type I	9.00	
103857	AI076795	Hs.45033	lacrimal proline rich protein		3.94
104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
106131	BE514788	Hs.296244	SNARE protein		2.17
106672	H47233	Hs.30643	ESTs	7.00	
106872	T56887	Hs.18282	KIAA1134 protein	11.50	
106960	AA156238	Hs.32501	ESTs		2.38
106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protei		2.95
108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
108599	AB018549	Hs.69328	MD-2 protein	13.00	
108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothei		2.40
109247	AA314907	Hs.85950	ESTs	7.00	
109630	R44607	Hs.22672	ESTs		5.00
110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
110234	H24458	Hs.32085	EST	16.50	
110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
111057	T79639	Hs.14629	ESTs	16.50	
111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
112291	R53972	Hs.26026	ESTs		3.00
112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
113009	T23699	Hs.7246	ESTs		4.50
113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
113121	T48011	Hs.8764	EST		2.21
113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
113757	AA703095	Hs.18631	ESTs		2.65
113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
113884	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
114987	AA251016	Hs.87808	EST		6.00
115460	AW958439	Hs.38613	ESTs		2.27
115722	W91892	Hs.59609	ESTs		9.00
116261	AA481788	Hs.190150	ESTs	9.50	
116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
117178	H98675	Hs.269034	ESTs		2.68
117757	AF088019	Hs.46732	EST	7.50	
118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
118657	AI822106	Hs.49902	ESTs		2.39
120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi		3.50
120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
120524	AA261852	Hs.192905	ESTs	6.00	
120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

	121558	AA412497	gb:z195g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146 ESTs	10.00	
	121936	AI024600	Hs.98612 ESTs	15.00	
5	121938	AA428659	Hs.98610 ESTs	14.00	
	122177	AA435789	Hs.98833 EST	8.93	
	123442	AA299652	Hs.111496 Homo sapiens cDNA FLJ11643 fis, clone HE	13.04	
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50	
	123756	AA609971	Hs.112795 EST	11.00	
10	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
	124371	N24924	Hs.188601 ESTs	6.50	
	127477	BE328720	Hs.280651 ESTs		4.33
	127591	AI190540	Hs.131092 ESTs		3.02
	128252	AA455924	Hs.192228 ESTs	7.00	
15	128426	AI265784	Hs.145197 ESTs		2.08
	128925	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT		2.11
	128945	AI990506	Hs.8077 Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00	
	129105	AI769160	Hs.108681 Homo sapiens brain tumor associated prot	15.50	
	129235	AW977238	Hs.126084 KIAA1055 protein		4.25
20	129506	AB020684	Hs.11217 KIAA0877 protein	6.50	
	129595	U09550	Hs.1154 oviductal glycoprotein 1, 120kD (mucin 9		10.00
	130160	AA305688	Hs.267695 UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	
	130340	D82326	Hs.239106 solute carrier family 3 (cystine, dibasi	11.50	
	131220	AB023194	Hs.300855 KIAA0977 protein	17.50	
	131430	AI879148	Hs.26770 fatty acid binding protein 7, brain	6.10	
25	132114	NM_006152	Hs.40202 lymphoid-restricted membrane protein		6.15
	132458	AA935315	Hs.48965 Homo sapiens cDNA: FLJ21693 fis, clone C		5.58
	132647	NM_006927	Hs.54432 sialyltransferase 4B (beta-galactosidase	7.50	
	132655	D49372	Hs.54460 small inducible cytokine subfamily A (Cy		2.53
30	132682	AI077500	Hs.54900 serologically defined colon cancer antig		2.50
	132747	AA345241	Hs.55950 ESTs, Weakly similar to KIAA1330 protein		2.83
	132812	R50333	Hs.92186 Leman coiled-coil protein		3.82
	133337	AF085983	Hs.293676 ESTs		5.00
	133876	AL134906	Hs.771 phosphorylase, glycogen; liver (Hers dis		3.00
35	134119	AW157837	Hs.79226 fasciculation and elongation protein zet		2.06
	134464	AA302983	Hs.239720 CCR4-NOT transcription complex, subunit		2.27
	134542	M14156	Hs.85112 insulin-like growth factor 1 (somatomedi		11.50
	135002	AA448542	Hs.251677 G antigen 7B	87.00	
40	135305	AA203555	Hs.98288 Homo sapiens cDNA FLJ14903 fis, clone PL		6.50

TABLE 6B show the accession numbers for those primekeys lacking unigeneID's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
55	108562	36375_1 AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
	103439	35330_1 X98266 N41124
	123551	genbank_AA608837 AA608837
	123861	genbank_AA620840 AA620840
	102832	entrez_U92015 U92015
60	101972	entrez_S82472 S82472
	121558	genbank_AA412497 AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.				
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.				
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3		164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein		77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
	101046	K01160		(NONE)	672.00	
20	101056	AW970254	Hs.889	Charot-Layden crystal protein	66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2		77.20
	101497	W05150	Hs.37034	homeo box A5	62.80	
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20	
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08	
	101941	S77583		gb:HERV10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	sialyltransferase		103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (lazarol	67.00	
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha		69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2		65.70
	102796	AL079646	Hs.107019	sympleskin; Huntingtin interacting protei		58.80
	102829	NM_006183	Hs.80962	neurotensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		212.10
	103260	X78416	Hs.3155	casein, alpha		130.70
	103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60	
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
	105024	AA126311	Hs.9879	ESTs	68.20	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		71.10
45	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
	106999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
50	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
	108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
	109597	AA989362	Hs.293780	ESTs	85.00	
	109691	T65568	Hs.12860	ESTs		58.70
55	109704	AI743880	Hs.12876	ESTs		60.60
	110942	R63503	Hs.28419	ESTs	76.40	
	111722	R23924	Hs.23596	EST	74.60	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	64.80	
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70
	113073	N39342	Hs.103042	microtubule-associated protein 1B		120.20
	114251	H15261	Hs.21948	ESTs	127.20	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
	115815	AW905328	Hs.180842	ribosomal protein L13	66.40	
65	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH		226.60
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	
	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	
70	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo		63.50
	120484	AA253170	Hs.96473	EST	81.60	
	120983	AA398209	Hs.97587	EST		81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
	121423	AW973352	Hs.290585	ESTs	64.40	
75	122553	AA451884	Hs.190121	ESTs		60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60	
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H		80.20
	124472	N52517	Hs.102670	EST	71.00	
	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 antino aci		104.90
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs		69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	
	126020	H79863	Hs.114243	ESTs		62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3		62.80
85	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		60.10

	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
5	127987	AI022103	Hs.124511	ESTs	96.60	
	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
10	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
15	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
	131775	AB014548	Hs.31921	KIAA0648 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
20	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30
	133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 protein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
25	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primekeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
40	103207	30635_4	X72790
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
45	116571	genbank_D45652	D45652
	118466	genbank_N66741	N66741
	101046	entrez_K01160 K01160	
	101941	entrez_S77583 S77583	
	103351	entrez_X89211 X89211	
50	123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung
 R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
15	300097	AI916973	Hs.213603	ESTs	5.46	4.69
	300117	AW189787	Hs.147474	ESTs	0.58	0.56
	300197	AI686661	Hs.218286	ESTs	4.26	5.44
	300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
	300225	AI989963	Hs.197505	ESTs	1.68	1.75
20	300247	AW274682	Hs.161394	ESTs	1.08	2.28
	300256	AI469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
	300337	AI707881	Hs.202090	ESTs	5.80	9.09
	300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
	300374	AI859947	Hs.314158	ESTs	2.99	4.38
25	300387	AW270150	Hs.254516	ESTs	1.50	2.53
	300440	AI421541	Hs.146164	ESTs	3.98	5.25
	300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
	300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
30	300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75
	300627	W27363		gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
	300630	AW118822	Hs.128757	ESTs	2.91	5.86
	300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
	300738	AI623332	Hs.130541	KIAA1542 protein	1.82	1.71
35	300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
	300790	AI492471	Hs.188270	ESTs	1.29	1.18
	300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
	300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
	300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
40	300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
	300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
	300926	AA504860		gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
	300960	AI041019	Hs.152454	ESTs	2.74	4.46
	300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
45	300962	AA593373	Hs.293744	ESTs	1.46	1.51
	300967	AA565209	Hs.269439	ESTs	0.39	1.30
	300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
	300988	AI927208	Hs.208952	ESTs	0.16	0.37
	301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.23	1.94
50	301098	AA677570	Hs.185918	ESTs	6.76	14.28
	301157	AA729905	Hs.231916	ESTs	3.16	8.85
	301162	AI142118	Hs.129004	ESTs	1.68	7.18
	301170	AA737594	Hs.247606	ESTs	4.40	6.42
	301192	AI808751	Hs.121188	ESTs	6.38	11.59
55	301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35	7.78
	301267	AW297762	Hs.255690	ESTs	1.56	1.61
	301281	AA843986	Hs.190586	ESTs	2.19	1.78
	301341	AI819198	Hs.208229	ESTs	0.76	0.76
	301382	AA912839	Hs.163369	ESTs	1.00	1.81
60	301407	AW450466	Hs.126830	ESTs	1.48	1.51
	301452	AA975688	Hs.159955	ESTs	0.51	1.46
	301483	AW272467	Hs.254655	Untitled	2.40	5.02
	301494	AI678034	Hs.131099	ESTs	2.79	3.41
	301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
65	301531	AI077462	Hs.134084	ESTs	2.52	3.76
	301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
	301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
70	301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04
	301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
	301822	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36
	301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
	301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88	5.49
75	301882	T78054		gb:yc97g09.r1 Soares infant brain 1N18 H	2.28	3.80
	301905	AI991127	Hs.117202	ESTs	1.00	1.00
	301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
	301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
	302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
80	302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
	302041	NM_001501	Hs.129715	gonadotropin-releasing hormone 2	0.71	0.99
	302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
	302094	AI286176	Hs.6786	ESTs	0.52	1.20
	302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
85	302148	AW269618	Hs.23244	ESTs	3.04	3.87

	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfam1	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsilon	5.82	9.34
	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
15	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:alpha-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
20	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
30	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged Ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothi	0.53	0.67
50	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gb:Homo sapiens clone 2A1 scFV antibody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	0.72	0.76
55	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224652	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
	303978	AW513315		gb:xx043c12.x1 NCI_CGAP_Ut1 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xxu71a11.x1 NCI_CGAP_Kd8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xtf68f05.x1 NCI_CGAP_Ut2 Homo sapiens	2.20	9.35
	303999	AW516611		gb:xxp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
85	304006	AW517947		gb:xtf68h02.x1 NCI_CGAP_Ut2 Homo sapiens	3.21	4.07

	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB2187 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1NIB H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
15	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
	304234	W81608		gb:zd68h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304956	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nl01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCI_CGAP_GCB1 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GCB0 Homo sapiens	4.49	8.71
	305690	AA813477		gb:ai67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA864374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s	1.56	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, poly	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.20	2.70
	306242	AA932805		gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:oi53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA966650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:oo35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67	7.44
	306446	AA977348		gb:oo72e12.s1 NCI_CGAP_Kid6 Homo sapiens	3.92	6.27

	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
5	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
	306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
10	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
15	306751	AI032589		gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
20	306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnan uterus_NbH	3.55	6.44
25	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
30	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307426	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:ql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
35	307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
	307608	AI290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:lb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
40	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
	307730	AI336092		gb:ql43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:ql27f07.x1 Soares_pregnan uterus_NbH	1.00	1.00
	307764	AI342731		gb:qp26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
45	307783	AI347274		gb:lc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:ql18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
	307807	AI351799		gb:ql09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:ql09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:ql94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
50	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
	307902	AI380462		gb:lg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
55	308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
60	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:lj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2.38		8.72
	308122	AI480123	Hs.309411	EST	2.70	3.86
	308154	AI500600		gb:ln93d08.x1 NCI_CGAP_Ut2 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
65	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (K1-1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
70	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
	308413	AI636253	Hs.196511	ESTs	3.16	4.82
	308450	AI660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
75	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
80	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
85	308875	AI832332		gb:al48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AI833240		gb:al76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	308898	AI858845		gb:wl32d10.x1 NCI_CGAP_U11 Homo sapiens	2.45	3.44
5	308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
	308966	AI870704		gb:wl47h01.x1 NCI_CGAP_U11 Homo sapiens	1.00	1.00
	308979	AI873111		gb:wl52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15	11.10
	309045	AI910902		gb:tlq39f01.x1 NCI_CGAP_U11 Homo sapiens	0.61	0.59
	309051	AI911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
10	309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
	309083	AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AI928178		gb:wo95a11.x1 NCI_CGAP_Kid11 Homo saplen	1.00	2.92
	309128	AI928816	Hs.180842	ribosomal protein L13	1.38	5.55
15	309164	AI937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
	309177	AI951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
	309288	AI991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wxq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
20	309411	AW085201	Hs.244144	EST	4.30	7.14
	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_U14 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
25	309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
	309532	AW151119		gb:xg33e10.x1 NCI_CGAP_U11 Homo sapiens	1.18	4.40
	309526	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
30	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.90
35	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
40	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_U12 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
45	310002	AI439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	AI203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310115	AI611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310146	AI206614	Hs.197422	ESTs	9.50	15.31
	310193	AI627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261	AI240483	Hs.201217	ESTs	3.28	4.40
	310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AI242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103	ESTs	2.19	3.12
60	310333	AI253200	Hs.145402	ESTs	1.17	1.91
	310346	AI261340	Hs.145517	ESTs	4.81	9.95
	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
65	310446	AI275715	Hs.145926	ESTs	2.18	3.85
	310468	AI984074	Hs.196398	ESTs	3.39	5.19
	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AI681145	Hs.160724	ESTs	3.30	7.33
70	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AI302654	Hs.208024	ESTs	3.26	3.46
	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	AI962234	Hs.196102	ESTs	5.60	6.49
	310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
	310648	AI347863	Hs.156672	ESTs	0.17	0.69
	310694	AI654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	AI472124	Hs.157757	ESTs	4.82	6.27
	310714	AI418446	Hs.157882	ESTs	1.76	3.51
80	310722	AI989803	Hs.157289	ESTs	1.14	6.85
	310756	AI916560	Hs.158707	ESTs	8.46	13.01
	310764	AI376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AI421677	Hs.161332	ESTs	6.37	7.94
	310858	AI871000	Hs.161330	ESTs	6.07	9.84

	310864	AJ924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
5	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AJ560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AJ521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AJ564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	AJ990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	perixin	0.65	0.95
	311187	AJ638374	Hs.224189	ESTs	2.46	2.78
	311220	AJ56040	Hs.196532	ESTs	1.10	2.52
15	311230	AJ989808	Hs.197663	ESTs	1.41	1.75
	311236	AJ653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AJ671221	Hs.199887	ESTs	1.00	1.41
	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
20	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AJ682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
25	311405	AW290961	Hs.201815	ESTs	3.80	11.66
	311409	AJ698839	gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94	
	311420	AJ936291	Hs.209867	ESTs	5.30	12.56
	311443	AJ791521	Hs.192206	ESTs	4.39	6.09
	311467	AJ934909	Hs.175377	ESTs	1.00	1.04
30	311479	AJ933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	arfaplin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
35	311537	AJ805121	Hs.211828	ESTs	3.69	5.85
	311543	AJ681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AJ819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AJ922143	Hs.211334	ESTs	2.39	3.32
	311586	AJ827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450675	Hs.212709	ESTs	1.00	1.00
	311621	AJ924307	Hs.213464	ESTs	4.16	6.74
45	311635	AJ928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AJ682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AJ056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AJ089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
60	311896	AW206447	gb:UH-BI1-afg-g-02-D-UI.s1 NCI_CGAP_Su	1.66	1.13	
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AJ597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
65	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AJ382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78	4.92
70	312046	AJ580018	Hs.268591	ESTs	4.11	7.32
	312056	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
75	312094	Z78390	gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48	
	312097	AJ352096	Hs.112180	zinc finger protein 148 (pH2-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AJ052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AJ052572	Hs.269864	ESTs	2.41	3.32
	312201	AJ928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613	gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13	
85	312252	AJ128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gb:tz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.37	3.98
	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.146924	ESTs	1.11	1.00
	312507	AI168177	Hs.143653	ESTs	5.89	8.24
15	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
	312599	AI865073	Hs.125720	ESTs	3.75	5.29
20	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
	312925	N90868	Hs.271695	ESTs	2.50	4.25
30	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
	312984	N25871	Hs.177337	ESTs	2.03	2.13
35	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
	313056	AI651930	Hs.135684	ESTs	1.51	2.04
40	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
	313136	N59284	Hs.288010	ESTs	0.49	1.36
45	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
	313255	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74	2.06
50	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
	313325	AI420611	Hs.127832	ESTs	1.20	2.27
55	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
	313417	AA741151	Hs.137323	ESTs	0.63	3.01
60	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
65	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
	313672	AW468891	Hs.122948	ESTs	3.46	5.80
70	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stralagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
	313774	AW136836	Hs.144583	ESTs	1.38	1.19
75	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
	313835	AI538438	Hs.159087	ESTs	5.74	8.88
80	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
	313883	AI949384		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.90	10.91
85	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00

	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
	314128	AA935633	Hs.194628	ESTs	2.90	6.35
15	314151	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo1.42		1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AI754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179556	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	fidgulin-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473		gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
85	315526	AI193048	Hs.128685	ESTs	1.67	1.78

	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
5	315562	AA737415	Hs.152826	ESTs	2.66	2.48
	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.56
10	315634	AA837085	Hs.220585	ESTs	0.50	1.40
	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
15	315730	H25899	Hs.201591	ESTs	0.11	0.60
	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gbz115a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	AI652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTs	1.48	1.60
	316275	AI671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	AI028478	Hs.157447	ESTs	3.51	6.69
	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs	4.70	6.04
	316519	AI929097		gbxod10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
50	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
60	316891	AW298119	Hs.202536	ESTs	1.64	2.97
	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
70	317137	AW341567	Hs.125710	ESTs	2.82	5.12
	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
75	317266	AA906289	Hs.203614	ESTs	1.00	1.00
	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs	3.58	8.13
	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126860	ESTs	1.88	4.15
85	317521	AI824338	Hs.126891	ESTs	3.12	4.55
	317529	AI916517	Hs.126865	ESTs	2.73	3.34

	317570	AI733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
5	317627	AI346110	Hs.132553	ESTs	1.50	1.39
	317650	AI733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	AI307659	Hs.174794	ESTs	5.33	9.59
	317701	AI674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	AI733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AI498273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
20	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865	AI298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	AI915599	Hs.129225	ESTs	4.68	7.48
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
30	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	AI024540	Hs.131574	ESTs	1.21	1.27
	318117	AI208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!!	5.90	6.98
35	318223	AI077540	Hs.134090	ESTs	1.05	0.90
	318240	AI085377	Hs.143610	ESTs	3.10	2.40
	318255	AI082692	Hs.134662	ESTs	0.02	1.05
	318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	AI493501	Hs.170974	ESTs	2.46	5.62
	318428	AI949409	Hs.194591	ESTs	0.77	0.45
	318458	AI149783	Hs.158438	ESTs	3.54	4.92
	318467	AI151395	Hs.144834	ESTs	4.56	5.62
	318473	AI939339	Hs.146883	ESTs	2.08	4.05
45	318476	AI693927	Hs.265165	ESTs	4.22	8.07
	318487	AI167877	Hs.143716	ESTs	1.47	1.05
	318488	AI217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTHI188 HTCCL1 Homo sapiens cDNA 5/3	2.58	5.20
50	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
55	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596	AI470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
65	318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AI962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865	H10818		gb:ym04f10.r1 Soares infant brain 1NIB H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
75	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AI219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.269622	ESTs	5.84	9.79
80	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13678	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12839	ESTs	5.87	7.26

	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ12927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279	T65094	Hs.12677	CGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
15	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	AI809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	AI382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
25	319523	T69499	Hs.191184	ESTs	1.55	3.25
	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:ylf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1NIB H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HT0	2.51	3.55
35	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
	319708	R15372	Hs.22664	ESTs	1.00	1.22
40	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
55	320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	AI699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
60	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
65	320188	AW419200	Hs.172318	ESTs	1.26	1.00
	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	teklin 2 (testicular)	0.18	1.09
	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	AI167978	Hs.139851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
80	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320388	H16065	Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
85	320436	AA253352	Hs.293663	ESTs	2.22	3.49
	320438	W24548	Hs.5669	ESTs	3.53	8.14

	320448	AI240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folistatin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83	5.83
	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AI445591		gb:yr04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
25	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
30	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AJ473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uropod 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
35	320927	AI205786	Hs.213923	ESTs	0.18	1.46
	320957	AJ878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
	321130	H43750	Hs.125494	ESTs	1.00	3.14
45	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
50	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF068654		gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
	321270	R83560		gb:yy76c06.s1 Soares fetal liver spleen	3.80	5.26
55	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
	321356	R93443	Hs.271770	ESTs	3.10	4.66
60	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
	321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
65	321468	AA514198	Hs.38540	ESTs	2.46	6.50
	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
70	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108551	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06	7.19
	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
	321581	AA019964	Hs.28803	ESTs	4.88	6.73
75	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
	321642	AW085917	Hs.247084	ESTs	1.52	1.38
80	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
	321700	N55160	Hs.167260	ESTs	4.57	7.46
85	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
5	321777	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
20	322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341937		gb:ql10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
	322091	AI819863	Hs.106243	ESTs	1.59	1.75
25	322125	R93901		gb:yy16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52567		gb:yl85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gb:yl88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:yl94c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
	322212	AF087995	Hs.134877	ESTs	3.42	4.84
35	322221	AI890619	Hs.179662	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	AI792140	Hs.49265	ESTs	0.66	2.76
40	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
	322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AI394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	IRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AI916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AI110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AI608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	AI962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AI377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
80	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	AI365585	Hs.146246	ESTs	0.30	1.14
	322968	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
85	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AJ733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	AJ700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
15	323232	AA148722	Hs.224680	ESTs	0.45	1.35
	323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	AJ697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	AJ336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
	323359	AA234172	Hs.137418	ESTs	0.34	1.18
25	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	AJ672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD (H.sapien	0.43	0.80
30	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AJ652287		gb:EST382593 MAGE resequences, MAGK Homo2.21		3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	AJ185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	AJ814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
40	323678	AL042121	Hs.20880	ESTs	3.33	5.10
	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
45	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	AJ869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AJ472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	AJ381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
	324275	AA429088	Hs.98523	ESTs	3.62	5.38
65	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	AJ198841	Hs.128173	ESTs	4.08	5.91
	324325	AL138153	Hs.300410	ESTs	5.88	8.25
70	324338	AL138357	Hs.145078	regulator of differentiation (in S. pomb	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	AJ924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	AJ148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
5	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.07	0.95
10	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
	324886	AA806794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
15	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
20	325114	D83901	Hs.315562	ESTs	2.73	3.17
	325146	AI064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653682	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
25	325235				2.64	4.12
	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
30	325389				0.88	1.05
	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
35	325559				7.48	21.40
	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
40	325597				2.98	13.40
	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
45	325739				0.59	0.88
	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
50	325895				7.78	15.98
	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
55	325971				4.88	7.42
	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
60	326163				3.27	5.70
	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
65	326274				1.00	8.09
	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
70	326589				9.20	13.49
	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
80	326964				0.41	1.70
	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
85	327053				3.55	6.31
	327075				1.59	1.40

	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
5	327220	1.28	1.54
	327224	6.56	12.91
	327288	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
10	327361	2.69	4.41
	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
15	327467	6.58	18.01
	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
20	327606	2.06	3.61
	327611	5.90	14.26
	327642	4.05	8.74
	327654	1.05	2.08
	327734	1.00	1.00
25	327775	1.46	11.79
	327796	3.47	5.65
	327840	3.26	6.64
	327940	5.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.59
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
	328113	0.72	0.91
35	328157	5.58	5.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
40	328299	2.20	3.06
	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328806	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329067	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	6.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00

	329764			5.78	15.50	
	329816			2.09	5.44	
	329860			3.13	10.77	
	329993			7.83	14.21	
5	330020			5.58	13.12	
	330036			3.32	5.57	
	330052			4.31	7.97	
	330085			1.34	1.76	
	330088			4.70	12.46	
10	330093			0.44	1.06	
	330100			3.47	4.83	
	330106			2.14	3.61	
	330107			3.17	6.87	
	330120			5.61	11.89	
15	330123			4.50	12.74	
	330208			1.55	7.62	
	330263			13.10	23.38	
	330300			2.81	4.98	
	330313			3.00	4.41	
20	330366			0.67	0.76	
	330372			4.76	11.82	
	330385	AA449749	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14	2.15
	330397	D14659	Hs.154387	KIAA0103 gene product	0.40	1.15
	330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
	330478	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
	330568	U56244		(NONE)	2.83	4.79
35	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
40	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AA017045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
50	330740	AA297746	Hs.22654	Homo sapiens voltage-gated sodium channe	0.27	2.04
	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
	330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
55	330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
60	330844	AA063037	Hs.66803	ESTs	0.93	1.16
	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
65	330968	H16568	Hs.23748	ESTs	0.48	0.96
	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
	331046	N66563	Hs.191358	ESTs	0.99	8.56
	331060	N75081	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
70	331108	R41408	Hs.21983	ESTs	1.00	2.75
	331131	R54797		gb:yg87b07.s1 Soares infant brain 1NIB H	6.04	10.68
	331135	R61398	Hs.4197	ESTs	0.80	0.96
	331170	T23461	Hs.159293	ESTs	2.63	4.29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
75	331183	T40769	Hs.8469	ESTs	1.00	3.01
	331203	T82310		(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
80	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
	331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
	331402	AA505135	Hs.44037	ESTs	1.80	3.93
85	331422	F10802	Hs.163528	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:cd74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.249989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member l	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
	331718	AA191404	Hs.104072	ESTs	6.80	11.77
15	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
30	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
35	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	necln 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
45	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.11112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	trypsin beta 1	0.51	1.00
50	332504	AA053917	Hs.15106	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52

	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
5	333260	0.75	1.01
	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
	333628	1.90	1.90
15	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.96
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
35	333966	8.10	14.30
	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934	4.01	7.43
	334945	1.04	2.96
	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
65	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.96	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17

	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
5	335814	1.13	1.48
	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
10	335868	2.98	6.43
	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
15	335995	0.37	1.17
	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336066	0.54	1.63
20	336107	0.95	0.70
	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
25	336419	0.65	0.79
	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
30	336636	2.13	1.83
	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
35	336675	0.31	1.18
	336684	1.50	1.14
	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
40	336900	6.14	12.73
	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
45	337054	2.78	7.35
	337128	7.20	16.14
	337162	3.45	5.34
	337183	5.72	11.41
	337184	3.72	5.90
50	337192	1.27	1.06
	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
55	337325	2.76	3.72
	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
60	337549	1.66	2.31
	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
65	337786	5.07	9.73
	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12
	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
75	338145	1.70	1.97
	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
80	338182	3.32	4.63
	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66

	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.67
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
	338937	6.55	12.26
25	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.36	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
	187363_1	AW340926 AA249063 N86075
50	44320_1	AI341937 AW003063 U34725 AA904742
	42705_1	X57414 X57415
	43034_1	X13075 X13076
	46779_1	R93901 AF075073 R93902
	46861_1	H69434 AF085958 H69846
55	46873_1	H52567 H52557 AF085970 H52164
	46882_1	H56535 AF085980 H56712
	46885_1	H92891 AF085982 H92777
	1615102_1	H84849 H84252 H84260 H86664 H85320
	1615333_1	H95531 H95521 H84529
60	111953_1	AA070412 AA102346 AA081885
	627492_1	H22544 H46842 AI204929
	47271_1	W69304 AF086283 W69200
	218439_1	AA625149 AA313030 AA313052 H97463
	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
65	47422_1	W79150 AF086419
	814584_1	AI668646 AJ734214 W17348
	293660_1	AW979268 AA878419 AA431342 AA431628
	682222_1	AI308300 AI308296
	25196_2	AI093967
70	979809_1	AL120701 AL135041 AL121524
	38927_1	AF147359 T58511 T58560
	473768_2	W88919 W89125
	1574395_1	Z42308 H23514
	82296_1	AA005129 AA679084 AA694399
75	85042_1	AA011522 AA702841 AA011691 AA330797
	380580_1	AI239464 AI239473 AA625812 AI208703
	37372_1	AF074666 AI110759 AF090902
	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
	697809_1	AI347274 AW844024
80	269032_1	AA381722 AA381829 AW963906 AW963902 AA381242
	221345_1	AA488472 W27363 AA317053 BE082689 AW967036 BE079872
	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
	403558_1	AA678177 AA677034
	233842_1	AL118754 AA333202 H38001
85	442885_1	AA847835 AA768376
	333127_1	AA504860 AA504911

	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	L08442 D51348
	302742	458_39	L12061
	318499	364430_1	T25451 AA585296 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909260 AI909259
	312094	797889_1	Z78390 T97427
15	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
	312389	902067_1	AI863140 W80703 R43474
25	319611	1566863_1	H14957 R56522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
30	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
	306442	AA976899	
40	306446	AA977348	
	306458	AA978186	
	306510	AA988546	
	306557	AA994530	
	306572	AA995686	
45	306582	AA996248	
	306656	AI004024	
	306686	AI015615	
	306751	AI032589	
	308011	AI439473	
50	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	306956	AI125111	
	306958	AI125152	
55	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
	308599	AI719893	
60	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
	308808	AI818289	
65	308875	AI832332	
	308886	AI833240	
	308898	AI858845	
	308966	AI870704	
	308979	AI873111	
70	303011	41689_1	AF090405 AF090407 AF090406
	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072	AA641012	
	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
80	303998	AW516449	
	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413	AA724659	
	305447	AA737856	
85	321244	29327_1	AF068654 AF068656 AF068655

	305614	AA782866	
	305637	AA806124	
	305639	AA806138	
5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243	
	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
15	307415	AI242118	
	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307561	AI282207	
20	307608	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
25	307796	AI350556	
	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
30	307820	AI355761	
	307852	AI365541	
	309122	AI928178	
	309164	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
	302679	311853_1	H65022 AA186889
45	309923	AW340684	
	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
	302705	31765_1	U09060 U09061
50	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
	304114	R78946	
60	304155	H68696	
	304203	N56929	
	304234	W81608	
	304348	AA179868	
	304430	AA347682	
65	304456	AA411240	
	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
70	304760	AA580401	
	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
75	306109	AA911861	
	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
	330568	NOT_FOUND_entrez	U56244
80	330599	15323_-12	U90437
	331131	genbank_R54797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	467396_1	AA828597 N54811
85	332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, I. et.al.	Plus	73381-73768
	332816	Dunham, I. et.al.	Plus	359844-360030
15	332906	Dunham, I. et.al.	Plus	1923101-1923205
	332911	Dunham, I. et.al.	Plus	1961767-1961858
	332912	Dunham, I. et.al.	Plus	1962120-1962246
	332922	Dunham, I. et.al.	Plus	2009620-2009738
20	332956	Dunham, I. et.al.	Plus	2510528-2510658
	332959	Dunham, I. et.al.	Plus	2518145-2518213
	333138	Dunham, I. et.al.	Plus	3369205-3369323
	333139	Dunham, I. et.al.	Plus	3369495-3369571
	333221	Dunham, I. et.al.	Plus	3978070-3978187
25	333380	Dunham, I. et.al.	Plus	4904775-4904846
	333387	Dunham, I. et.al.	Plus	4910935-4910997
	333512	Dunham, I. et.al.	Plus	5560510-5560564
	333524	Dunham, I. et.al.	Plus	5612620-5612780
	333585	Dunham, I. et.al.	Plus	6234778-6234894
30	333618	Dunham, I. et.al.	Plus	6562391-6562566
	333627	Dunham, I. et.al.	Plus	6620584-6620903
	333628	Dunham, I. et.al.	Plus	6629004-6629233
	333650	Dunham, I. et.al.	Plus	6796852-6797128
	333678	Dunham, I. et.al.	Plus	7068223-7068288
35	333750	Dunham, I. et.al.	Plus	7608165-7608234
	333763	Dunham, I. et.al.	Plus	7692491-7692630
	333767	Dunham, I. et.al.	Plus	7694407-7694623
	333768	Dunham, I. et.al.	Plus	7695440-7695697
	333769	Dunham, I. et.al.	Plus	7696625-7696707
40	333772	Dunham, I. et.al.	Plus	7706773-7706902
	333777	Dunham, I. et.al.	Plus	7746805-7746916
	333846	Dunham, I. et.al.	Plus	8008623-8008757
	333884	Dunham, I. et.al.	Plus	8153960-8154161
	333887	Dunham, I. et.al.	Plus	8154882-8155025
45	333891	Dunham, I. et.al.	Plus	8156437-8156709
	333892	Dunham, I. et.al.	Plus	8156825-8157001
	333948	Dunham, I. et.al.	Plus	8583497-8583627
	333954	Dunham, I. et.al.	Plus	8563186-8563335
	333966	Dunham, I. et.al.	Plus	8655643-8655826
50	333968	Dunham, I. et.al.	Plus	8681004-8681241
	334061	Dunham, I. et.al.	Plus	9686941-9687077
	334094	Dunham, I. et.al.	Plus	9889953-9890105
	334113	Dunham, I. et.al.	Plus	10282459-10282597
	334161	Dunham, I. et.al.	Plus	10599033-10599180
55	334219	Dunham, I. et.al.	Plus	12716160-12716384
	334239	Dunham, I. et.al.	Plus	13056569-13056693
	334333	Dunham, I. et.al.	Plus	13603544-13603657
	334378	Dunham, I. et.al.	Plus	13907239-13907370
	334382	Dunham, I. et.al.	Plus	13915866-13916036
60	334562	Dunham, I. et.al.	Plus	14987847-14987940
	334588	Dunham, I. et.al.	Plus	15032740-15032817
	334616	Dunham, I. et.al.	Plus	15176123-15176470
	334633	Dunham, I. et.al.	Plus	15333206-15333305
	334866	Dunham, I. et.al.	Plus	18872214-18872317
65	334891	Dunham, I. et.al.	Plus	19299770-19299944
	334934	Dunham, I. et.al.	Plus	20103970-20104058
	335015	Dunham, I. et.al.	Plus	20682792-20682945
	335120	Dunham, I. et.al.	Plus	21436286-21436384
	335125	Dunham, I. et.al.	Plus	21441390-21441471
70	335179	Dunham, I. et.al.	Plus	21634405-21634526
	335188	Dunham, I. et.al.	Plus	21669118-21669328
	335211	Dunham, I. et.al.	Plus	21774611-21774680
	335361	Dunham, I. et.al.	Plus	22807292-22807445
	335379	Dunham, I. et.al.	Plus	22899306-22899420
75	335414	Dunham, I. et.al.	Plus	23235546-23235684
	335416	Dunham, I. et.al.	Plus	23237354-23237465
	335496	Dunham, I. et.al.	Plus	24164386-24164545
	335497	Dunham, I. et.al.	Plus	24167666-24167869
	335558	Dunham, I. et.al.	Plus	24740167-24740347
80	335586	Dunham, I. et.al.	Plus	24990333-24990497
	335586	Dunham, I. et.al.	Plus	25439839-25439920
	335784	Dunham, I. et.al.	Plus	25942710-25942792
	335823	Dunham, I. et.al.	Plus	26365925-26366004
	335983	Dunham, I. et.al.	Plus	27938968-27939070
85	335995	Dunham, I. et.al.	Plus	28009044-28009184
	336021	Dunham, I. et.al.	Plus	28686482-28686559

	336034	Dunham, I. et.al.	Plus	29014404-29014590
	336038	Dunham, I. et.al.	Plus	29022963-29023165
	336107	Dunham, I. et.al.	Plus	29987731-29987869
5	336632	Dunham, I. et.al.	Plus	983890-985529
	336633	Dunham, I. et.al.	Plus	985591-986221
	336634	Dunham, I. et.al.	Plus	986296-986670
	336635	Dunham, I. et.al.	Plus	987908-988364
	336636	Dunham, I. et.al.	Plus	988418-989185
10	336637	Dunham, I. et.al.	Plus	989276-990813
	336638	Dunham, I. et.al.	Plus	991906-993240
	336659	Dunham, I. et.al.	Plus	1896402-1896478
	336694	Dunham, I. et.al.	Plus	2420546-2420616
	336721	Dunham, I. et.al.	Plus	3371522-3371586
	336900	Dunham, I. et.al.	Plus	10236423-10236523
15	336948	Dunham, I. et.al.	Plus	12692290-12692381
	337028	Dunham, I. et.al.	Plus	16644817-16644942
	337054	Dunham, I. et.al.	Plus	17821742-17821922
	337162	Dunham, I. et.al.	Plus	23478943-23479145
	337183	Dunham, I. et.al.	Plus	23943606-23943696
20	337184	Dunham, I. et.al.	Plus	23973949-23974016
	337268	Dunham, I. et.al.	Plus	28011979-28012034
	337299	Dunham, I. et.al.	Plus	29022656-29022775
	337389	Dunham, I. et.al.	Plus	31401509-31401579
	337493	Dunham, I. et.al.	Plus	33330760-33330981
25	337549	Dunham, I. et.al.	Plus	34474472-34474531
	337755	Dunham, I. et.al.	Plus	3971764-3971900
	337809	Dunham, I. et.al.	Plus	4449059-4449193
	337871	Dunham, I. et.al.	Plus	5443027-5443101
30	337958	Dunham, I. et.al.	Plus	6969162-6969270
	338008	Dunham, I. et.al.	Plus	7697068-7697236
	338033	Dunham, I. et.al.	Plus	8092128-8092271
	338110	Dunham, I. et.al.	Plus	10384481-10384621
	338112	Dunham, I. et.al.	Plus	10391398-10391600
	338145	Dunham, I. et.al.	Plus	11386629-11386692
35	338148	Dunham, I. et.al.	Plus	11448985-11449085
	338179	Dunham, I. et.al.	Plus	12808775-12808833
	338197	Dunham, I. et.al.	Plus	13638107-13638181
	338279	Dunham, I. et.al.	Plus	16168944-16169091
	338316	Dunham, I. et.al.	Plus	17089711-17089988
40	338322	Dunham, I. et.al.	Plus	17132477-17132547
	338357	Dunham, I. et.al.	Plus	18062184-18062402
	338359	Dunham, I. et.al.	Plus	18074402-18074501
	338366	Dunham, I. et.al.	Plus	18252026-18252189
	338374	Dunham, I. et.al.	Plus	18371200-18371282
45	338414	Dunham, I. et.al.	Plus	19345573-19345660
	338418	Dunham, I. et.al.	Plus	19435506-19435596
	338501	Dunham, I. et.al.	Plus	21244713-21244828
	338506	Dunham, I. et.al.	Plus	21221871-21221953
50	338523	Dunham, I. et.al.	Plus	21509763-21509864
	338662	Dunham, I. et.al.	Plus	24404720-24404899
	338804	Dunham, I. et.al.	Plus	27236005-27236108
	338836	Dunham, I. et.al.	Plus	27792166-27792272
	338879	Dunham, I. et.al.	Plus	28410653-28410734
55	338937	Dunham, I. et.al.	Plus	29160655-29160725
	338993	Dunham, I. et.al.	Plus	30077787-30078184
	339047	Dunham, I. et.al.	Plus	30760793-30760968
	339100	Dunham, I. et.al.	Plus	31141580-31141765
	339114	Dunham, I. et.al.	Plus	31456454-31456519
	339121	Dunham, I. et.al.	Plus	31583467-31583536
60	339170	Dunham, I. et.al.	Plus	32216399-32216527
	339293	Dunham, I. et.al.	Plus	33223671-33223819
	332858	Dunham, I. et.al.	Minus	1339607-1339397
	332982	Dunham, I. et.al.	Minus	2628296-2628109
	332984	Dunham, I. et.al.	Minus	2632606-2632457
65	332998	Dunham, I. et.al.	Minus	2711704-2711565
	333058	Dunham, I. et.al.	Minus	3028925-3028811
	333097	Dunham, I. et.al.	Minus	3204124-3204036
	333121	Dunham, I. et.al.	Minus	3308446-3308358
70	333122	Dunham, I. et.al.	Minus	3309596-3309531
	333123	Dunham, I. et.al.	Minus	3310817-3310749
	333140	Dunham, I. et.al.	Minus	3377220-3376309
	333260	Dunham, I. et.al.	Minus	4308400-4308304
	333603	Dunham, I. et.al.	Minus	6466335-6465727
75	333604	Dunham, I. et.al.	Minus	6467090-6466768
	333904	Dunham, I. et.al.	Minus	8217374-8217261
	333906	Dunham, I. et.al.	Minus	8218238-8218063
	334183	Dunham, I. et.al.	Minus	11832582-11832508
	334187	Dunham, I. et.al.	Minus	11921456-11921205
80	334222	Dunham, I. et.al.	Minus	12732417-12732289
	334223	Dunham, I. et.al.	Minus	12734365-12734269
	334255	Dunham, I. et.al.	Minus	13200776-13200692
	334492	Dunham, I. et.al.	Minus	14478333-14478172
	334648	Dunham, I. et.al.	Minus	15363301-15363222
	334787	Dunham, I. et.al.	Minus	16299093-16298937
85	334933	Dunham, I. et.al.	Minus	20078117-20077991

	334945	Dunham, I. et al.	Minus	20138885-20138637
	334967	Dunham, I. et al.	Minus	20173311-20173218
	334990	Dunham, I. et al.	Minus	20341159-20341087
5	335093	Dunham, I. et al.	Minus	21297367-21297214
	335288	Dunham, I. et al.	Minus	22304275-22303770
	335289	Dunham, I. et al.	Minus	22305950-22305708
	335548	Dunham, I. et al.	Minus	24662773-24662673
	335551	Dunham, I. et al.	Minus	24679828-24678961
10	335619	Dunham, I. et al.	Minus	25082677-25082498
	335620	Dunham, I. et al.	Minus	25092561-25092434
	335621	Dunham, I. et al.	Minus	25098878-25098767
	335682	Dunham, I. et al.	Minus	25421215-25421093
	335755	Dunham, I. et al.	Minus	25763806-25763747
	335814	Dunham, I. et al.	Minus	26320043-26319845
15	335815	Dunham, I. et al.	Minus	26320518-26320421
	335835	Dunham, I. et al.	Minus	26393311-26393245
	335851	Dunham, I. et al.	Minus	26604863-26604742
	335868	Dunham, I. et al.	Minus	26711437-26711300
20	335896	Dunham, I. et al.	Minus	26977639-26977558
	335936	Dunham, I. et al.	Minus	27360474-27360400
	335948	Dunham, I. et al.	Minus	27555924-27555788
	336066	Dunham, I. et al.	Minus	29241080-29240842
	336205	Dunham, I. et al.	Minus	30477456-30477311
25	336275	Dunham, I. et al.	Minus	32086675-32086536
	336292	Dunham, I. et al.	Minus	32818035-32817927
	336331	Dunham, I. et al.	Minus	33594527-33594371
	336419	Dunham, I. et al.	Minus	34052568-34052445
	336675	Dunham, I. et al.	Minus	2020758-2020664
30	336684	Dunham, I. et al.	Minus	2158060-2157993
	336716	Dunham, I. et al.	Minus	3259952-3259862
	336798	Dunham, I. et al.	Minus	5888954-5888757
	337043	Dunham, I. et al.	Minus	17407330-17407251
	337046	Dunham, I. et al.	Minus	17610892-17610821
35	337128	Dunham, I. et al.	Minus	22215251-22215034
	337192	Dunham, I. et al.	Minus	24591853-24591771
	337194	Dunham, I. et al.	Minus	24610510-24610359
	337229	Dunham, I. et al.	Minus	26716579-26716481
	337325	Dunham, I. et al.	Minus	30015948-30015800
40	337497	Dunham, I. et al.	Minus	33371317-33371258
	337500	Dunham, I. et al.	Minus	33376212-33376158
	337603	Dunham, I. et al.	Minus	1299296-1299194
	337605	Dunham, I. et al.	Minus	1346555-1346397
	337671	Dunham, I. et al.	Minus	3260634-3260547
45	337786	Dunham, I. et al.	Minus	4133203-4133081
	337862	Dunham, I. et al.	Minus	5347658-5347550
	338083	Dunham, I. et al.	Minus	9318438-9318301
	338158	Dunham, I. et al.	Minus	11794465-11794343
	338161	Dunham, I. et al.	Minus	12124716-12124658
50	338182	Dunham, I. et al.	Minus	12824919-12824827
	338189	Dunham, I. et al.	Minus	12878594-12878478
	338199	Dunham, I. et al.	Minus	13760865-13760780
	338215	Dunham, I. et al.	Minus	14055447-14055355
	338469	Dunham, I. et al.	Minus	20520387-20520242
55	338549	Dunham, I. et al.	Minus	22049171-22049081
	338561	Dunham, I. et al.	Minus	22311966-22311856
	338671	Dunham, I. et al.	Minus	24508421-24508346
	338676	Dunham, I. et al.	Minus	24637427-24637369
	338726	Dunham, I. et al.	Minus	25926206-25925618
50	338779	Dunham, I. et al.	Minus	27030151-27029795
	338871	Dunham, I. et al.	Minus	28301708-28301611
	338872	Dunham, I. et al.	Minus	28300921-28300790
	338966	Dunham, I. et al.	Minus	29614876-29614749
	339229	Dunham, I. et al.	Minus	32722330-32722199
55	339264	Dunham, I. et al.	Minus	32975145-32975053
	325228	6381940	Plus	2630-2694
	325235	6381943	Minus	162154-162264
	329588	3962484	Plus	1169-1619
	329560	3962491	Plus	2095-2990
70	329541	3983503	Minus	2765-3059
	325328	5866875	Plus	86780-86854
	325340	6017033	Minus	166656-166819
	325373	5866920	Minus	1136686-1136777
	325367	5866920	Minus	922881-922958
75	325389	5866921	Plus	239672-239759
	325436	5866939	Minus	29778-29907
	325498	5866967	Plus	173372-173930
	325471	6017034	Minus	289268-289342
	325557	6056302	Plus	50921-51050
30	325559	6249595	Minus	118590-119172
	325560	6249595	Minus	133794-133981
	325569	6249599	Plus	79927-80217
	325587	6682462	Plus	126724-126967
	325585	6682462	Plus	73476-73574
35	325597	5866992	Plus	1065020-1065089
	325639	5867002	Plus	253525-253608

	325739	5867038	Minus	205138-205269
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735	6552447	Minus	269122-269190
	325685	6682468	Plus	117397-117483
	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
	329643	6448539	Plus	53403-53537
	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895	5867097	Plus	358317-358476
	325925	5867124	Plus	115749-115962
	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
40	326515	5867439	Plus	36683-36809
	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	95187-95248
50	326605	5867637	Plus	24656-24749
	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
55	326693	6682502	Minus	335002-335095
	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	75340-75456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
65	327130	6531976	Plus	20247-22343
	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
70	327224	5867534	Plus	188468-188544
	327321	6249562	Minus	99745-99836
	327361	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611	5867868	Minus	175053-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97564-97710
	327734	5867940	Minus	31003-31583

	327775	5867964	Minus	130791-130871
	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
5	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
15	327984	5868216	Plus	66611-66677
	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905862	Minus	3246-3302
20	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38889-40010
	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
	328666	5868254	Minus	778-901
25	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
30	328743	5868289	Plus	274638-274726
	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
35	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335406
	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
	328934	5868500	Plus	846342-846448
45	328949	6456765	Minus	43552-43619
	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
50	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
	329037	5868562	Minus	32466-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
60	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigenelD's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586*:gi 6330167 dbj BAA86477.1 (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457*:gi 7512178 pir T30337 polypr	1.00	400.00
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397*:gi 7499898 pir T33295 hypo	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823*:gi 10432400 emb CAC10290.1 (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397*:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463*:Homo sapiens myxovirus (infl	1.37	1.43
403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813*:gi 12737279 ref XP_012163.1 k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020*:Homo sapiens CGI-75 protein (14.29	91.00
404101			C8000950:gi 423560 pir A47318 RNA-bind	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP00000244562:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00

404287			C6001909:gi704441 dbj BAA18909.1 [D298	29.71	42.00
404298			C6001238*:gi121715 sp P26697 GTA3_CHICK	1.30	1.00
404347			Target Exon	1.00	1.00
404440			NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
404721			NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
404794	NM_000078		cholesteryl ester transfer protein, plas	1.07	1.38
404854			Target Exon	1.61	2.01
404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
404927			Target Exon	1.00	1.00
404996			Target Exon	1.00	1.00
405449			CY000047*:gi11427234 ref XP_009399.1 z	1.00	1.00
405568			NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
405572			Target Exon	0.76	1.14
405646			C12000200:gi14557225 ref NP_000005.1 al	1.01	1.28
405676	BE336714		cytochrome c-1	1.13	2.89
405770			NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
405932			C15000305:gi13806122 gb AAC69198.1 (AF0	1.99	1.99
406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
406360			Target Exon	1.00	35.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406467			Target Exon	1.00	1.00
406621	X57809	Hs.181125	immunoglobulin lambda locus	1.41	1.74
406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
406663	U24683	Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
406673	M34996	Hs.198253	major histocompatibility complex, class	0.98	3.09
406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged im,	1.30	1.53
406678	U77534		gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
406685	M18728		gb:Human nonspecific crossreacting antig	1.46	2.85
406687	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
406698	X03058	Hs.73931	major histocompatibility complex, class	1.01	2.52
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
406851	AA609784		major histocompatibility complex, class	0.75	1.91
406964	M21305		gb:Human alpha satellite and satellite 3	38.15	1114.00
406967	M24349		gb:Human parathyroid hormone-like protei	1.00	1.00
406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
407128	R83312	Hs.237260	EST	1.00	1.00
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
407168	R45175	Hs.117183	ESTs	2.16	18.00
407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.10	1.57
407242	M18728		gb:Human nonspecific crossreacting antig	1.12	2.85
407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
407366	AF026942	Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	1.00	26.00
407430	AF169351		gb:Homo sapiens protein tyrosine phospho	1.00	25.00
407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
407710	AW022727	Hs.23616	ESTs	1.00	28.00
407720	AB037776	Hs.38002	KIAA1355 protein	1.89	1.31
407746	AK001962		hypothetical protein FLJ11100	1.00	1.00
407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.51	5.00
407758	D50915	Hs.38365	KIAA0125 gene product	1.00	28.00
407782	AA608956	Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	7.88	3.83
407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
407944	R34008	Hs.239727	desmocollin 2	111.30	70.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
408063	BE086548	Hs.42346	calcineurin-binding protein calcarsin-1	195.78	231.00
408070	AW148852		gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00	1.00
408101	AW968504	Hs.123073	CDC2-related protein kinase 7	37.84	61.00
408122	AI432652	Hs.42824	hypothetical protein FLJ10718	0.85	1.71
408212	AA297567	Hs.43728	hypothetical protein	5.88	7.91
408243	Y00787	Hs.624	interleukin 8	4.27	9.98
408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
408354	AI382803	Hs.159235	ESTs	1.00	73.00
408369	R38438	Hs.182575	solute carrier family 15 (H7??) transport	1.41	16.50
408380	AF123050	Hs.44532	diubiquitin	15.19	37.22
408482	NM_000676	Hs.45743	adenosine A2b receptor	1.65	1.19
408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
408536	AW381532	Hs.135188	ESTs	1.55	1.50
408545	AW235405	Hs.253690	ESTs	1.00	1.00
408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
408633	AW963372	Hs.46677	PRO2000 protein	107.16	56.00
408660	AA525775		ESTs, Moderately similar to PC4259 ferri	1.00	1.00
408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	52.24	141.00
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00

	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, del	1.00	89.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
15	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
	409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.90	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI561173	Hs.67688	ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibit	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
45	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.08	1.90
75	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adiclan	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	23.34	34.00
80	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
85	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
5	412811	H06382		ESTs	1.00	11.00
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22	1.88
	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
15	413223	A1732182	Hs.191866	ESTs	5.73	27.00
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516	fidgetin-like 1	1.00	1.00
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.45
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
	413573	A1733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
30	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
40	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
45	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AJ434699	Hs.77356	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
75	415227	AW821113	Hs.72402	ESTs	1.87	49.00
	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
80	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypothesi	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415989	AI267700		ESTs	78.89	1.00

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
5	416177	AA174069	Hs.187607	ESTs	1.00	9.00
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
20	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	mel proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
25	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
30	417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
35	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	56.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	calhepsin K (pseudodysostosis)	3.96	5.16
60	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgulin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
80	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
	418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor I	1.10	1.14
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256105	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
15	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
20	419474	AW968619	Hs.155849	ESTs	13.63	62.00
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.66	3.63
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AI793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
30	419729	AA586442	Hs.21411	gb:nc53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419936	AI792788		gb:cl91d05.y5 NCI_CGAP_Kid5 Homo sapiens	1.00	1.00
	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	AI623693	Hs.323494	ESTs	45.04	54.00
45	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
50	420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to 138022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
80	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
85	421773	W69233	Hs.112457	ESTs	1.12	1.14
	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptid	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
15	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
	422424	AJ186431	Hs.296638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
30	422656	AJ870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	53.00
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
	422963	AA401369	Hs.190721	ESTs	171.41	17.00
40	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidemolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
55	423551	AA327598	Hs.233785	ESTs	3.54	4.33
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
65	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151064		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
80	424120	T80579	Hs.290270	ESTs	1.00	1.00
	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
85	424340	AA339036	Hs.7033	ESTs	0.88	1.15

	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Cnk2	95.55	92.00
5	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
	424420	BE614743	Hs.146588	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424503	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVI, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
15	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
	424867	AJ024860	Hs.153591	Nol56 (D. melanogaster)-like protein	1.23	1.05
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	1.00	53.00
30	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	AJ751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
35	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	AJ923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	AJ077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	AJ949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orolat	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
75	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	AJ493134		sclerostin	1.00	1.00
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
85	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:ae70b06.s1 Stralagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
5	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361552	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
15	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
	427562	R56424	Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
20	427666	AJ791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
25	427719	AJ393122	Hs.134726	ESTs	7.03	4.52
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfami	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
30	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
35	428129	AJ244311	Hs.26912	ESTs	1.00	42.00
	428169	AJ928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
	428434	AJ909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratifin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
50	428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
55	428801	AW277121	Hs.254881	ESTs	1.67	6.15
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
60	428969	AF120274	Hs.194689	artemin	1.36	1.24
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	AJ753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
	429164	AI688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs	1.00	7.00
	429228	AI553633	Hs.326447	ESTs	39.47	29.25
70	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
75	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
80	429551	AW450624	Hs.220931	ESTs	2.89	65.00
	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
85	429616	AI982722	Hs.120845	ESTs	1.00	1.00
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
5	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
10	430114	AA847744	Hs.99640	ESTs	1.00	1.00
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00	51.00
	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
15	430300	U60805	Hs.238648	oncosterin M receptor	1.00	35.00
	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
20	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
25	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
30	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I7885 serine/th	0.94	1.28
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	AI332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
45	431322	AW970822		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
50	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
	431548	AI834273	Hs.9711	novel protein	5.66	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	67.12	91.00
55	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
60	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	1.00	1.00
65	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12.r1 Stralagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
75	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
80	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
	432867	AW016936	Hs.233364	ESTs	1.00	1.00
85	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
15	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
20	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
25	434217	AW014795	Hs.23349	ESTs	14.11	57.00
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.48	1.56
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
30	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
35	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	lg superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
40	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00	1.00
	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
	435509	AI458679	Hs.181915	ESTs	1.00	1.00
	435525	AI831297	Hs.123310	ESTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
55	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
60	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
65	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV integration site fami	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
70	436443	AW138211	Hs.128746	ESTs	1.12	9.26
	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
80	436839	AA401369	Hs.190721	ESTs	1.00	17.00
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.05	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
85	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.35	1.78
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
5	437259	AI377755	Hs.120695	ESTs	1.00	205.00
	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AI125859	Hs.112607	ESTs	1.35	1.75
10	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	AI306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	AI954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
20	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	74.05	35.00
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942	AI888256	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
25	438113	AI467908	Hs.8882	ESTs	1.80	2.39
	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	AI918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
30	438494	AA908678	Hs.130183	ESTs	2.05	80.00
	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
35	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AI886558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
40	438915	AA280174	Hs.285881	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96696	Hs.35598	ESTs	1.00	28.00
45	439128	AI949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
50	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
60	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig)	2.36	1.88
65	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
70	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
75	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
80	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440994	AI160011	Hs.272068	ESTs	1.29	1.14
85	441020	AA401369	Hs.190721	ESTs	142.99	17.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	441128	AA570256	ESTs, Weakly similar to T23273 hypotheti	4.13	3.50
	441290	W27501	Hs.89605 cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	Hs.23044 RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
5	441377	BE218239	Hs.202656 ESTs	22.03	1.00
	441390	AI692560	Hs.131175 ESTs	3.65	7.70
	441497	R51064	Hs.23172 ESTs	1.00	1.00
	441525	AW241867	Hs.127728 ESTs	1.53	1.42
	441553	AA281219	Hs.121296 ESTs	1.89	1.57
10	441607	NM_005010	Hs.7912 neuronal cell adhesion molecule	1.47	2.11
	441633	AW958544	Hs.112242 normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Hs.7921 Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	Hs.7957 adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721 ESTs	44.15	17.00
	441801	AW242799	Hs.86366 ESTs	1.00	1.00
15	441919	AI553802	Hs.128121 ESTs	1.00	122.00
	441937	R41782	Hs.22279 ESTs	0.86	1.37
	441954	AI744935	Hs.8047 Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810 CDA11 protein	1.00	46.00
20	442029	AW956698	Hs.14456 neural precursor cell expressed, develop	9.92	45.00
	442072	AI740832	Hs.12311 Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	Hs.166314 ESTs	3.61	3.14
	442117	AW664964	Hs.128899 ESTs	3.00	5.49
	442137	AA977235	Hs.128830 ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
25	442159	AW163390	Hs.278554 heterochromatin-like protein 1	1.92	1.66
	442179	AA983842	Hs.333555 chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	Hs.150614 ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178 hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Hs.176508 Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
	442547	AA306997	Hs.217484 ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
30	442556	AL137761	Hs.8379 Homo sapiens mRNA; cDNA DKFZp566L2424 (f	1.00	53.00
	442619	AA447492	Hs.20183 ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	Hs.23210 ESTs	1.00	19.00
	442717	R88362	Hs.180591 ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
35	442875	BE623003	Hs.23625 Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
	442914	AW188551	Hs.99519 hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	Hs.8858 bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	Hs.131562 ESTs	8.45	64.00
	443068	AI188710	ESTs	1.00	27.00
40	443204	AW205878	Hs.29643 Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	Hs.143655 ESTs	12.42	2.00
	443247	BE614387	Hs.333893 c-Myc target JPO1	128.84	96.00
	443324	R44013	Hs.164225 ESTs	0.02	4.59
	443383	AI792453	Hs.166507 ESTs	1.00	47.00
45	443400	R28424	Hs.250648 ESTs	18.52	61.00
	443426	AF098158	Hs.9329 chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	Hs.9605 cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	Hs.269636 ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645 fibrinogen, B beta polypeptide	1.00	16.00
50	443633	AL031290	Hs.9654 similar to pregnancy-associated plasma p	1.00	39.00
	443648	AI085377	Hs.143610 ESTs	39.81	70.00
	443715	AI583187	Hs.9700 cyclin E1	48.74	7.00
	443723	AI144442	Hs.157144 syntaxin 6	1.29	1.30
	443802	AW504924	Hs.9805 KIAA1291 protein	1.75	1.61
55	443859	NM_013409	Hs.9914 follistatin	1.35	1.13
	443892	AA401369	Hs.190721 ESTs	1.00	17.00
	443947	W24187	gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082 potassium intermediate/small conductance	5.71	6.87
60	444006	BE395085	Hs.10086 type I transmembrane protein Fn14	1.47	1.92
	444009	AI380792	Hs.135104 ESTs	1.00	77.00
	444017	U04840	Hs.214 neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	Hs.13281 ESTs	1.00	29.00
	444129	AW294292	Hs.256212 ESTs	1.00	1.00
	444279	U62432	Hs.89605 cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	Hs.239 forkhead box M1	2.91	1.14
	444378	R41339	Hs.12569 ESTs	1.00	1.00
	444381	BE387335	Hs.283713 ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
	444461	R53734	Hs.25978 ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217 KIAA0877 protein	24.91	90.00
70	444489	AI151010	Hs.157774 ESTs	1.00	111.00
	444619	BE538082	Hs.8172 ESTs, Moderately similar to A46010 X-fin	1.00	70.00
	444665	BE613126	Hs.47783 B aggressive lymphoma gene	30.56	139.00
	444707	AI188613	Hs.41690 desmocollin 3	1.00	1.00
	444735	BE019923	Hs.243122 hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	Hs.11950 GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	Hs.62180 anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	Hs.12457 hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	Hs.147613 ESTs	1.00	73.00
	445413	AA151342	Hs.12677 CGI-147 protein	28.14	50.00
80	445417	AK001058	Hs.12680 Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	Hs.322971 ESTs	1.00	1.00
	445462	AA378776	Hs.288649 hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830 hypothetical protein	1.87	70.00
	445537	AJ245671	Hs.12844 EGF-like-domain, multiple 6	1.71	2.72
85	445580	AF167572	Hs.12912 skb1 (S. pombe) homolog	1.52	1.34
	445654	X91247	Hs.13046 thioredoxin reductase 1	1.51	1.52

	445669	AJ570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-	49.42	54.00
5	445885	AJ734009	Hs.127699	KIAA1603 protein	1.00	132.00
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AJ347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
10	446078	AJ339982	Hs.156061	ESTs	1.00	42.00
	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
	446293	AJ420213	Hs.149722	ESTs	1.00	2.00
15	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AJ377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
	446574	AJ310135	Hs.335933	ESTs	3.89	72.00
20	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
25	446856	AJ814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AJ811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
	446989	AK001898	Hs.16740	hypothetical protein FLJ11035	2.82	3.12
30	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AJ357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
35	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AJ878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AJ199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AJ375572	Hs.172634	ESTs	1.00	12.00
	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
45	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AJ963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19236	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AJ817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AJ538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AI955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AJ366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
75	448826	AJ580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AJ581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AJ471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AI625777	Hs.344766	ESTs	8.33	44.00
85	449054	AF148848	Hs.22934	myoneurin	73.85	104.00
	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	AI638293		gb:tt09b07.x1 NCI_CGAP_GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86
	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
15	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementation	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	51.26	93.00
	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protein	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	15.02	124.00
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-related	1.00	143.00
	451253	H48299	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	AI805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	AI821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
50	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodomain	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTs	1.39	1.32
	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.245005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell granule	1.55	1.00
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252766	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
	453103	AI301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
85	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00

5	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
	453331	AI240665	Hs.8850	ESTs	199.42	340.00		
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17		
	453459	BE047032	Hs.257789	ESTs	2.84	5.58		
10	453563	AW608906.comp		Hs.181163	hypothetical protein MGC5629	4.58	90.00	
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
15	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00		
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964	AI961486	Hs.12744	ESTs	1.00	1.00		
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
25	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	stathmin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
30	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
	456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
40	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15		
45	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
50	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00	1.00		
	458247	R14439	Hs.209194	ESTs	7.00	9.85		
55	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
	459670	F01020	Hs.172004	titin	1.00	1.00		
60	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 9B

65	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
70	Pkey	CAT Number
	407746	10125_1
		AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461
		AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320
		D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1
	408660	107294_1
75	409522	113735_1
	409866	1156522_1
	410032	1170435_1
	411089	123172_1
		AA525775 AA056342 AI538978 AW975281 AA664986
		AA075382 AA075431
		AW502152 H41202 H29772
		BE065985 BE065944 BE066008 BE066083 BE066093
		AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386
		AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
80	411152	1234028_1
		BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202
		AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
	412537	1304_1
		AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024
		T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AL044113 AA382556
		AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865

		AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598589 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99530 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA456370 N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI925845 AW945895 Z42183 T31621 T97478 D62703 AA242966 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T7755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H483077 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW407774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344008 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T69245 T74380 T67862 T74474 T56068 AI792788 BE142230 AA252019 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AW881145 AA490718 M85637 AA304575 T06067 AA331991 AL119930 AA320696 AW752565 AL031985 AL137241 AI792386 AI733664 AI857654 AI049911 AA337221 AA336756 AW966196 AW953120 R56325 AA349562 AI493134 AI498691 AW771508 AI498457 AI768408 AI783524 AI383985 AI580267 D79813 AA393768 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA663848 AA400100 AA401424 AI038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA93675 AA837380 BE006554 BE006473 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140589 AI242544 AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341 AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI308821 AI919424 AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C0618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115 AL133551 AL041090 AI117481 AL122069 AW439292 AI968826 AW072916 AI184913 AA489195 AW469994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937 BE041395 AA491826 AA621946 AA715980 AA666102 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AW89376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AA628980 AI126603 BE504035
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438091 44964_1 AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400
AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571
AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI555133 N94964 AI268939
AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207
AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994
AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
AW979121 AA847986 AA829098
439000 467716_1 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
439285 47065_1 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
439780 47673_1 AL109688 R23665 R26578
441128 51021_2 AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171
AI359627 AI005068 AI356567 AA232991 AW016855 AA908902 AA233101 AA127550 BE512923
443068 558874_1 AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
443947 586160_1 W24187 W24194 R17789
447636 7301_1 Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649
AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883
AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659
AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
AA096002 N83992
448993 79225_1 AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265
AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245
AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417
AA911497 BE537702
449305 804424_1 AI638293 AW813561
451105 859083_1 AI761324 AW880941 AW880937
451320 86576_1 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
451807 8865_1 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291
AW450652 AW449519 AA93634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756
452410 9163_1 AL133619 AA468118 AA383064 AI476447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732
AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747
R74039 N35031 AI804128 AW513621 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI125754 AI200813
AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316
AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
454241 1067807_1 BE144666 BE184942 AW238414 BE184946
455175 1257335_1 AW993247 AW861464
456237 168730_1 AA203682 R11958
458098 47395_1 BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393
AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395
AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407
BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400512	9796593	Minus	1439-1615
400517	9796686	Minus	49996-50346
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400665	8118496	Plus	16879-17023
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
400763	8131616	Minus	35537-35784
401027	7230983	Minus	70407-70554,71060-71160
401093	8516137	Minus	22335-23166
401203	9743387	Minus	172961-173056,173868-173928
401212	9858408	Plus	87839-88028
401411	7799787	Minus	144144-144329
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
401714	6715702	Plus	96484-96681
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401797	6730720	Plus	6973-7118
401961	4581193	Minus	124054-124209
401985	2580474	Plus	61542-61750
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402265	3287673	Plus	21059-21168
402297	6598824	Plus	35279-35405,35573-35659
402408	9796239	Minus	110326-110491

	402420	9796339	Plus	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
5	402994	2996643	Minus	4727-4969
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	116458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
	404076	9931752	Minus	3848-3967
15	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
20	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
	404440	7528051	Plus	80430-81581
25	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
30	404927	7342002	Plus	68690-69563
	404966	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405676	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
	406137	9166422	Minus	30487-31058
40	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease

Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59580 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
65	404394			ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
	404916			Target Exon	1.00	159.00
	405257			Target Exon	1.00	422.00
70	407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
	407568	AA740964	Hs.62699	ESTs	1.00	123.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	tol-like receptor 2	39.65	149.00
75	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL040178	Hs.142003	ESTs	0.10	11.90
80	414154	AW205314	Hs.323060	ESTs	0.62	2.09
	414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
85	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.29	2.64
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
10	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrophin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
15	420656	AA279098	Hs.187636	ESTs	1.65	8.07
	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
	422426	W79117	Hs.58559	ESTs	0.03	7.44
20	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
25	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
30	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
35	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429496	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	angiopoietin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
40	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
45	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
	436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
	437119	AI379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312789	Hs.283689	activator of CREM in testis	0.67	122.67
50	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	AI669586	Hs.222194	ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23.32	370.00
55	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
60	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
65	447357	AI375922	Hs.159367	ESTs	0.46	2.64
	448106	AI800470	Hs.171941	ESTs	18.05	296.00
	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449275	AW450848	Hs.205457	periastin	0.56	1.38
	450400	AI694722	Hs.279744	ESTs	0.88	4.33
70	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
	458332	AI000341	Hs.220491	ESTs	1.00	192.00
75	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control	0.40	2.40
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
80	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
5	425438	T62216	Hs.270840	ESTs	0.23	9.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	0.46	2.43
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
15	443709	AI082692	Hs.134662	ESTs	0.00	3.02
	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
20	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883*:gij[6753278]ref[NP_033938.1] c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptide transpor	0.89	1.39
25	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
	402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:gij[9955960]ref[NP_063957.1] AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
30	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106			C11001637*:gij[5032241]ref[NP_005732.1] z	1.00	235.00
35	405381			Target Exon	1.00	93.00
	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
45	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AI049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
65	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N64464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
80	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
85	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
	417673	T87281	Hs.16355	ESTs	0.15	15.54

	418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
5	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
	420256	U84722	Hs.76205	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
	421470	R27496	Hs.1378	annexin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00	129.00
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
25	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
30	423696	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
35	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	tol1-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	AJ478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
45	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Prl Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
50	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AI734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
60	432596	AJ224741	Hs.278461	matrilin 3	0.04	5.79
	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
65	434445	AI349306	Hs.11782	ESTs	0.60	1.84
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
75	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene fami	1.00	77.00
	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
80	442200	AW590572	Hs.235768	ESTs	0.78	5.83
	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
85	443951	F13272	Hs.111334	ferritin, light polypeptide	0.55	2.09
	444330	AI597655	Hs.49265	ESTs	1.00	90.00

	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AI741471	Hs.23666	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69
	446917	AI347863	Hs.156672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheli	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
15	450693	AW450461	Hs.203965	ESTs	1.00	91.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
25	453390	AA862496	Hs.28482	ESTs	1.00	72.00
	453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	455579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 A1872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AI797007 R73390 AA961010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758 AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896
423696	23112_1	Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
430212	314437_1	AA469153 AI718503 AA469225
436532	421802_1	AA721522 AW975443 T93070
453531	97026_1	AA417940 AA036735 T07025
454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400754	7331445	Plus	144559-144684
401045	8117619	Plus	90044-90184,91111-91345
401083	3242744	Plus	33192-33360
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
403021	7547270	Plus	120799-120966
403421	9665041	Minus	126609-126773,139986-140205
403438	9719679	Plus	90792-90938
403687	7387384	Plus	9009-9534
403764	7717105	Minus	118692-118853
404277	1834458	Minus	91665-91946
404288	2769644	Plus	3512-3691
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
404518	8151988	Plus	84494-84603
404916	7341826	Plus	91057-91188
405106	8079395	Minus	80877-81418
405257	7329310	Plus	73121-73273
405381	6006920	Minus	7636-8054

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigenelD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigenel Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122: Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
407869	AI827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	1.00	3.00
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	AI015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	AI834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
441377	BE218239	Hs.202656	ESTs	22.03	1.00
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
444931	AV652066	Hs.75113	general transcription factor IIIA	1.00	54.00
446102	AW168067	Hs.317694	ESTs	1.00	1.00
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	1.00	11.00
447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
448844	AI581519	Hs.177164	ESTs	1.00	31.00
449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
452689	F33868	Hs.284176	transferrin	1.54	1.44
453392	U23762	Hs.32964	SRV (sex determining region Y)-box 11	1.00	16.00
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872836 BE298825 BE299889 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE117131 AA722407 AA293803 AI468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M54982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343080 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA505787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D02160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756

TABLE 11C

Pkey: Unique number corresponding to an Eos probeset.
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 N1_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	N1_position
403329	8516120	Plus	96450-96598
406399	9256288	Minus	63448-63554

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

5	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
	450832	AW970602	Hs.105421	ESTs	25.17	36.00
	452240	AI591147	Hs.61232	ESTs	13.42	1.00
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27
10	453830	AA534296	Hs.20953	ESTs	24.92	25.00
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00

TABLE 12B

15 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

20 Pkey CAT Number Accession
 439285 47065_1 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 30 Nl_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nl_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
35 401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
40 404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix HuQ3 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccon	UnigenelD	Unigenel Title	R1	R2
408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
436532	AA721522		gb:uv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 Pref.Utility: Preferred Utility
 Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigenelD	Unigenel Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X56839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
412719	AW016610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	periostin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
15	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
25	428969	AF120274	Hs.194689	artemin	diag	extracellular
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AF538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
	436481	AA379597	Hs.5199	HSPC150 protein similar to ublquitin-con	s.m.	
40	437016	AU076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AF581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF-1	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664984	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folistatin	diag	extracellular
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
55	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
	447033	AF357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AF199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AF581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450375	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
70	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	plasma membrane
75	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AF693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

414883 15024_1 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150
AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667
R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045
AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239
AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789
AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
15 450375 83327_1 AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probaset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
25 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Seq ID No: Sequence ID number
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title

Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines
Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor
Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs
Seq ID No: 49	311034	BE567130	Hs.311369	ESTs, Highly similar to NKGD_HUMAN NKG2-
Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,
Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
Seq ID No: 106 & 107	417542	J04129	Hs.82269	progestagen-associated endometrial prote
Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifer
Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monophosphate synthetase
Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

	Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100668	L05424	Hs.169610	CD44 antigen (homing function and Indian
5	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
15	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
20	Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
25	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
30	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
35	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaeta-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
40	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin; lissencephaly, X-linked (d
45	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 7B
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
50	Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
	Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
55	Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
	Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTERa2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
65	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
70	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
75	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
	Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
80	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
	Seq ID No: 282	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen
	Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
	Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
85	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 297 & 298	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
5	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342-Homo sapiens kinesin protein 9
10	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
15	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327	403329			unnamed protein product (Homo sapiens)
	Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
20	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
25	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
30	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
35	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
40	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
45	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb-Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,
	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
50	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
55	Seq ID No: 400 & 401	423961	D13666	Hs.136348	perlestin (OSF-2os)
	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
60	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adican
	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
65	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
70	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
75	Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 442 & 443	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
80	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist

	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s]
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
	Seq ID No: 486 & 487	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
15	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
25	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80952	neurotensin
30	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
45	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progesterone-associated endometrial prola
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
50	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
55	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
70	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting antig
	Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting antig
	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting antig
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type I transmembrane protein Fn14

Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrophin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose inducible
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cyt)
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precursor
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin)
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic)
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophosphatidylcholine
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kallikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H ⁺ transport)
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeobox 5

TABLE 15B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
		AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
		AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
		AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
		AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 125672-126076
403329	8516120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

	1	11	21	31	41	51	
10	GCCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTCACCACG	AGAGGAGGAT	CCACCCGGAG	AGGAGGATCT	ACCTGGAGAG	300
	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
15	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCACG	420
	AATAATGCCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
	CGCCCTGGC	CCCGGGTGTG	CCAGCCCTGC	GCGGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCCAGC	TCGCGCGCTT	CTGCGCGGCC	CTGCGCCCCC	TGGAACCTCT	GGGCTTCCAG	600
	CTCCCGCCGC	TCCAGAACT	GCGCCTGCGC	AACAATGGCC	ACAGTGTGCA	ACTGACCCCTG	660
20	CCTCCTGGGC	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGCTCT	GCAGCTGCAT	720
	CTGCACTGGG	GGGCTGCAGG	TCGTCCGGGC	TCGGAGCACA	CTGTGGAAGG	CCACCGTTTC	780
	CCTGCGCAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCTTG	840
	GGGCGCCGGC	GAGGCTGGC	CGTGTGGGCC	GCCTTTCTGG	AGGAGGGCCC	GGAGAAAAC	900
	AGTGCCTATG	AGCAGTTGCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
25	CAGGTCCAG	GACTGGACAT	ATCTGCACTC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACGCCCTGT	GCCCAGGGTG	TCATCTGGAC	TGTGTTTAACT	1080
	CAGACAGTGA	TGCTGAGTGC	TAAGCAGCTC	CACACCTCT	CTGACACCCT	GTGGGGACCT	1140
	GGTGAATCTC	GGCTACAGCT	GAATCTCCGA	GCGACGCAGC	CTTTGAATGG	GCGAGTGATT	1200
	GAGGCTCTCT	TCCCTGCTGG	AGTGGACAGC	AGTCTCTGGG	CTGCTGAGCC	AGTCCAGCTG	1260
30	AATTCCTGCC	TGGCTGCTGG	TGACATCCTA	GCCCTGTTTT	TGGCCTCCT	TTTTGCTGTC	1320
	ACCAGCGTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CAAAAGGGGT	1380
	GTGAGCTACC	GCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGAGGAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGCTA	ACTGTCTCTG	CCTGCTCATT	1500
35	ATGCCACTTC	CTTTTAACTG	CCAAGAAATT	TTTTAAATA	AATATTATA	AT	

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

	1	11	21	31	41	51	
40	MAPLCPSPWL	PLLIPAPAPG	LTVQLLSLL	LLMPVHPQRL	PRMQEDSPLG	GGSSGEDDPL	60
	GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPVVKP	KSEEGSLKL	EDLPTVEAPG	120
	DPQEPQNNAH	RDKEGDDQSH	WRYGGDPWP	RVSPACAGRF	QSPVDIRPQL	AAPCFALRPL	180
	ELLGQLPPL	PELRLRNNGH	SVQTLPPGL	EMALGPGRY	RALQLHLHWG	AAGRPGSEHT	240
45	VEGHRFPABI	HVVHLSTAF	RVDEALGRPG	GLAVLAAFL	EGPEENSAYE	QLLSRLERIA	300
	EEGSETQVPG	LDISALLPSD	FSRYFYEGS	LTPPPCAQGV	IWTFVNTQVM	LSAKQLHTLS	360
	DTLWGPGRSR	LQLNFRATQP	LNGRVIEASF	PAGVDSSPRA	AEPVQLNSCL	AAGDILALVF	420
	GLLFAVTSVA	FLVQMRRQHR	RGTKGVSYR	PAEVAETGA			

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

	1	11	21	31	41	51	
55	AGCGGGGTG	TCTATTAAC	TGTTCAAAA	GTATCAGGAG	TTGTCAAGGC	AGAGAAGAGA	60
	GTGTTTGCAA	AAGGGGGAAA	GATGTTTGCT	GCCTCTTTAA	GACTAGGACT	GAGAGAAAGA	120
	AGAGGAGAGA	GAAAGAAAGG	GAGAGAAATT	TGAGCCCCAG	GCTTAAGCCT	TTCCAAAAAA	180
	TAATAATAAC	AATCATCGGC	GGCGGCAGGA	TCGGCCAGAG	GAGGAGGGAA	GCGCTTTTTT	240
60	TGATCCTGAT	TCCAGTTTGC	CTCTCTCTTT	TTTTCCCCCA	AATTATTTCT	CGCCTGATTT	300
	TCTCTCGGGA	GCCCTGCGCT	CCCGACACCC	CCGCCCCGCT	CCCTCTCTCC	TCTCCCCCGG	360
	CCCGCGGGCC	CCCAAGATC	CCGCGCGGCC	CGAGGTCGG	CGGCGCGCG	CGGGCGGGC	420
	COGCGCACAG	CGCCCGCATG	TACAACATGA	TGGAGACGGA	GCTGAAGCCG	CGGGCCCGC	480
	AGCAAACTTC	GGGGGGCGGC	GGCGGCAACT	CCACCGCGGC	GGCGGCGGC	GGCAACACGA	540
65	AAAAACAGCC	GGACCGCTC	AAGCGGCCA	TGAATGCCTT	CATGGTGTGG	TCCCGCGGGC	600
	AGCGGCGCAA	GATGGCCAG	GAGAAACCCA	AGATGCACAA	CTCGGAGATC	AGCAAGCGCC	660
	TGGGCGCGGA	GTGAAACTT	TTGTGCGAGA	CGGAGAACGG	GCCGTTTCATC	GACGAGGCTA	720
	AGCGGCTGCG	AGCGCTGCAC	ATGAAGGAGC	ACCGGATTA	TAAATACCGG	CCCGGCGGGA	780
	AAACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	CGGCGGGCTG	CTGGCCCCCG	840
70	GCGGCAATAG	CATGGCGAGC	GGGGTCGGGG	TGGGCGCGGG	CCTGGGCGCG	GGCGTGAACC	900
	AGCGCATGGA	CAGTTACGCG	CACATGAACG	GCTGGAGCAA	CGGCAGCTAC	AGCATGATGC	960
	AGGACCAGCT	GGGCTACCGG	CAGCACCCGG	GCCTCAATGC	GCACGCGGCA	GCGCAGATGC	1020
	AGCCCATGCA	CCGCTACGAC	GTGAGCGCCC	TGCAGTACAA	CTCCATGACC	AGCTCGCAGA	1080
	CCTACATGAA	CGGCTCGCCC	ACCTACAGCA	TGTCTACTC	GCAGCAGGGC	ACCCCTGGCA	1140
75	TGGCTCTTGG	CTCCATGGGT	TCGGTGGTCA	AGTCCGAGGC	CAGCTCCAGC	CCCCCTGTGG	1200
	TTACCTCTTC	CTCCACTTCC	AGGGCGCCCT	GCCAGGCGGG	GGACCTCCGG	GACATGATCA	1260
	GCATGTATCT	CCCCGCGCGC	GAGGTGCCGG	AACCGCGCGC	CCCCAGCAGA	CTTCACTGT	1320
	CCCAGCACTA	CCAGAGCGGC	CCGGTGCCCG	GCACGGCCAT	TAACGGCACA	CTGCCCTCT	1380
	CACACATGTG	AGGGCCGAGC	AGCGAACTGG	AGGGGGGAGA	AATTTTCAAA	GAAAAACGAG	1440
80	GGAAATGGGA	GGGGTGCAAA	AGAGGAGAGT	AAGAAACAGC	ATGGAGAAAA	CCCGGTACGC	1500
	TCAAAAAAAA	AAAAAAATCC	CACTTCCAT	CACCCACAGC	AAATGACAGC	TGCAAAAGAG	1560
	AACACCAATC	CCATCCACAC	TCACGCAAAA	ACCGCGATGC	CGACAAGAAA	ACTTTTATGA	1620
	GAGAGATCCT	GCACTCTTT	TKGGGGACT	ATTTTGTAC	AGAGAAAAAC	TGGGAGGGT	1680
	GGGGAGGGCG	GGGGAATGGA	CCCTGTATAG	ATCTGGAGGA	AAGAAAGCTA	CGAAAACTT	1740
85	TTTAAAGATT	CTAGTGGTAC	GGTAGGAGCT	TTGCAGGAAG	TTTGCAAAAG	TCTTTACCAA	1800
	TAATATTAG	AGTATCTTC	CAACGACGA	AAAAAATGTT	TTAATTTTGG	CAAGCAACTT	1860
	TTGTACAGTA	TTTATCGAGA	TAAACATGCG	AATCAAAATG	TCCATTGTTT	ATAAGCTGAG	1920

AATTGCGCAA TATTTTCAAA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT 1980
 TTAGGACAGT TGCAAACGTG AAAAGAAGAA AATTATTCAA ATTTGGACAT TTTAATTGTT 2040
 TAAAAATTGT ACAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100
 GTTTAAAAAG GGCAAAAGTT TTAGACTGTA CTAAATTTTA TAACTTACTG TTTAAAGCAA 2160
 AAATGGCCAT GCAGGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTT GATCCCACT 2220
 TTCCATTTTG TTCAGATAAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG 2280
 GTTTGTAATA TTTCTGTAAA TTTATTGTGA TATTTTAAGG TTTTCCCCC TTTATTTTCC 2340
 GTAGTTGTAT TTTAAAAGAT TCGGCTCTGT ATTATTGAA TCAGTCTGCC GAGAATCCAT 2400
 GTATATATTT GAACTAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTCTTACT 2460
 CCATTATGCA CAGTTTGAGA TAAATAAATT TTTGAAATAT GGCACTGAA AAAAAAAAAA 2520
 AAAAAACAA AACAAAAAAA CAAAAACAA AACAAAAAAA AAAAAACAA 2580
 CACAACAA AAACAAAAA AAAAAAGA AACAAACA CAACACA CAACAAAA 2640
 CCACAACA AACACAACA CACAGAGG

Seq ID NO: 4 Protein sequence:
Protein Accession #: CAA83435.1

1 11 21 31 41 51
 MYNMMETELK PPGPQQTSGG GGNSTAAAA GGNQKNSPDR VKRPMNAFMV WSRGQRRKMA 60
 QENPKMHNSE ISKRLGAEWK LLSETEKRPF IDEAKRLRAL HMKEHPDYKY RPRRKTKTLM 120
 KDKYTLPGG LLAPGGNSMA SGVGVGAGLG AGVNQRMSY AHMNGWSNGS YSMQDQLGY 180
 PQHPGLNAG AAQMOPMHRV DVSALQYNSM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM 240
 GSVVKSEASS SPPVVTSSSH SRAPCQAGDL RDMISMYLPG AEVPEPAAPS RLHMSQHYQS 300
 GPVPGTAING TLPLSHM

Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: U91618
Coding sequence: 29-541

1 11 21 31 41 51
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGATG 60
 CATGCTACTC CTGCTTTTCA GCTCCTGGAG TCTGTGCTCA GATTGAGAAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GCCTTTAGCT TGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACCGCAA 480
 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTATTTT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTGT TGTGAAATGT TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAATAA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:
Protein Accession #: AAB50564

1 11 21 31 41 51
 MMAGMKIQLV CMLLLAFSSW SLCSDSSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNMLNS PAETGEVHE EELVARRKLP TALDGFSLTA MLTIYQLHKI CHSRAFAQHWE 120
 LIQEDILDITG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY

Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109-2940

1 11 21 31 41 51
 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTGCAG GTCCTATTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCCTA TCTCAAACAT TAAGGAAATG 300
 ATAACTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
 ATAAAGATT TAATACCTGC CACATGGAAG GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAATGT CATAGTACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCCTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAT ACATTCATTT CACACCTAAT 540
 TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGCCC ACCTCCGTTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTTCTAC 660
 ATAAATGGGC AAAATCAAA TAAAGTGACA AGGTGTTTCA CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGTCCCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGGTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
 CTACAGAACC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTACCAACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCCAC ATTCTCGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGAC TCCTTCAACT ACACAAGGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA 1140
 ATTCATACCT TCGTGGGACT TGCAGTTTC GACAGCAAG GAGAGATCAG AGCCCGCTA 1200
 CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTTGA GGTGGTTGAA 1320
 AAACGAAATG GAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCG AGATGATAAG 1380
 CTTCTTGCCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440

CTGGGTTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
 TTCCTTGTTC CAGATATATC AAATCTCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560
 TCTGGAACCTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAATAATGTC 1620
 5 AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740
 GGACGAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
 TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCTGGAACAA TACCCATCAT 1860
 TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGGCGCT CCAACTCAGC TGTGCCCCCA 1920
 10 GCCACTGTGG AAGCCTTGTG GGAAGAGAGC AGCCTCCATT TTCCTCATCC TGTGATGATT 1980
 TATGCCAATG TGAACAGGG ATTTTATCCC ATTCCTTAATG CCACTGTCAC TGCCACAGTT 2040
 GAGCCAGAGA CTGAGATGCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
 GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTCTCT CTTTGTCTGC AAATGGTAGA 2160
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAAC CCACTCTATT 2220
 CCAGGGAGTC ATGCTATGTA TGTACAGGT TACACAGCAA ACGTAATAT TCAGATGAAT 2280
 15 GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
 CCACCATGCA CCCTGAAAGT CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2460
 TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCACGGCTA CAAGCTATGA AATAAGAAATG 2520
 AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
 20 AAGCGAAATC CTGAGATGCC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC 2640
 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700
 GCAATACGAG CAATGGATAG GAACCTCCTA CAGTCTGCTG TATCTAACAT TGCCGAGGCG 2760
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 25 GGAQTTTTAA CAGCAATGGG TTTGATAGGA ATCATTGCCC TTATTATAGT TGTGACACAT 2880
 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
 ATAAATATCC AAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
 CATACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTACA 3060
 ATACAGATAA GATTTTTACA TGGTAGATCA ACAATTCCTT TTGGGGTAG ATTAGAAAAC 3120
 30 CCTTACATT TGGCTATGAA CAAATAATAA AAATTATCTT TTAAGTAAT GTCTTTAAG 3180
 GCAAAGGGAA GGTAAAGTC GGACCAAGT CAAGGAAAGT TTGTTTATT GAGGTGGAAA 3240
 AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAAGTCTG TGTAAGCAA 3300
 TCATTTAGTT ACTTTGATTA ATTTTCTT TCTCCTTATC TGTGAGTAC AGGTGCTTG 3360
 35 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT 3420
 TCTGTCTATT TGTATATAT ATTTTCAATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
 TTTCACTGTA AGAGGTAAAC TTTAACAATA TGGGTATTAC CTTGTCTCT TCATACCGGT 3540
 TTTATGACAA AGGTCTATTG AATTTATTG TNTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600
 TTTCTAAGTT TATTGCCTTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660
 TACCTAGGAA A

Seq ID NO: 8 Protein sequence:
 Protein Accession #: NP_006527.1

1 11 21 31 41 51
 45 MTQRSIAGPI CNLKFVTLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISS 60
 IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAAH 120
 GDDPYTLQVR GCGKEGKVIH FTFNPLNDN LTAGYGSRRG VFVHEWAHLR WGVFDEYNND 180
 KPFYINGQNG IKVTRCSSDI TGFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
 50 MFMSLSLVSV EFCNASTHNG EAPNLQNMOC SLRSAWDVIT DSADPHHSFP MNGTELPPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQQAEEFYLM QIVEIHTFVG IASFDSKGEI 360
 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNGKA YGSVMILVTS 420
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRIT GGLKPFVVDI SNSNSMIDAF 480
 55 SRISSTGDI FQHQIQUEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540
 FDPDGRKYIT NNFITNLTFR TASLWIPGTA KPGHWYTYTLN NTHHSLQALK VITVSRASNS 600
 AVPPATVEAF VERDSLHFPF PVMIYANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG 660
 AGADVIKNDG IYSRYFFSFA ANGRYSKLVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
 IQMNAPRKSIV GRNEEERKVG FSRVSSGGSF SVLGVPAGPH PDVFPCKII DLEAVKVEE 780
 LTLSTWAPGE DFDQQAATSY EIRMSKSLQN IQDDFNAIL VNTSKRNPPQ AGIREIFTFS 840
 60 PQISTNGPEH QPNGETHESH RIVVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
 LILKGLVTAM GLIGIICLII VVTHHTLSRK KRADKKENG T KLL

Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 336-632

1 11 21 31 41 51
 70 CTCCCTCAC CCCGCTCCAG GATGCCAGT CCCCACGACA CCTCCCACTT CCCACTGTGG 60
 CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120
 GAGCTGGCAC TCTCTGGGAG GGAGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAATAATGCC AAGTTGGGGG 240
 CCAGTGGGCG CCACATATAA ATCTCTACCC TGGGAGCCTG GCTGCCTTGC TCTCCTCTCT 300
 75 GGGTCTGTCT CTGCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
 CGCTGGCTGT GCTGGTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
 AGCTGAGTAA GGGGGAATG AAGGAACTTC TGCACAAGGA GCTGCCAGC TTTGTGGGGG 480
 AGAAGTGGA TGAGGAGGGG CTGAAGAAGC TGATGGGCAG CCTGGATGAG AACAGTGACC 540
 AGCAGGTGGA CTTCCAGGAG TATGCTGTTT TCCTGGCACT CATCACTGTC ATGTGCAATG 600
 80 ACTTCTTCCA GGGCTGCCCA GACCGACCTT GAAGCAGAAC TCTTGACTTC CTGCCATGGA 660
 TCTCTGGGC CCAGGACTGT TGATGCCCTT GAGTTTGTGA TTCAATAAAC TTTTGTGTC 720
 TGTGATAAT ATTTTAATTG CTCAGTGATG TTCCATAACC CGGCTGGCTC AGCTGGAGTG 780
 CTGGGAGATG AGGCGCTCCT GGATCCTGCT CCCTTCTGGG CTCTGACTCT CTTGGAATC 840
 TCTCAAGGC CAGGACTATG CTTTAGTCT CAATTTTGA ATTCAACA CCAGCAAAAA 900
 85 ATTGGAAATC GAGATAGGTT GCTGACTTTT ATTTTGTCAA ATAAAGATAT TAAAAAGGC 960
 AAATACCA

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

1 11 21 31 41 51
 5 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
 GSLDENSDQQ VDFQEYAVFL ALITVMCNDP FQGCPRDP

Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 336-626

1 11 21 31 41 51
 15 CTCCCTCAC CCCGTTCCAG GATGCCAGT CCCACGACA CCTCCCACTT CCCACTGTGG 60
 CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120
 GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTGGTTTCC TTAATAATGCC AAGTTGGGGG 240
 CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT 300
 20 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
 CGCTGGCTGT GCTGGTCACT ACCTTCACCA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
 AGCTGAGTAA GGGGGAATG AAGGAACCTC TGCACAAGGA GCTGCCAGC TTTGTGGGGC 480
 ATTCAGAGA ACCATGTGCT GTGAGGGCCT TCCGAGTCCA TCTGTTAAT CCTGTCAATG 540
 GAGACTTGAG AAACCAGAGC CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT 600
 25 GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660
 CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA CTCATCACTG TCATGTGCAA 720
 TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG 780
 GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTG TATTCAATAA ACTTTTTTTG 840
 30 TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCATAA CCGGCTGGC TCAGCTGGAG 900
 TGCTGGGAGA TGAGGGCTC CTGGATCCTG CTCCTTCTG GGCTCTGACT CTCCTGAAA 960
 TCTCTCCAG GCCAGAGCTA TGCTTTAGGT CTCATTTTG GAATTTCAA CACCAGCAA 1020
 AAATTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC AAATAAAGAT ATTAATAAAG 1080
 GCAATACCA

Seq ID NO: 12 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 40 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGHS REPCAVERAFR 60
 VHLFNEVIGD LRNQSPGKGS DCPKITQHRW KWMRRG

Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 58-354

1 11 21 31 41 51
 50 GTGAGTCAC CATGTGGGGG TGAGGCTGAG AGAAAACAAG TACACAGCCA CAGATCCATG 60
 ATGTGCAGTT CTCTGGAGCA GGCCTGGCT GTGCTGGTCA CTACCTTCCA CAAGTACTCC 120
 TGCCAAGAGT GCGACAAGTT CAAGCTGAGT AAGGGGGAAA TGAAGGAACT TCTGCACAAG 180
 GAGCTGCCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240
 55 AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA 300
 CTCATCACTG TCATGTGCAA TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA 360
 ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTG 420
 TATTCAATAA ACTTTTTTTG TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCATAA 480
 CCGGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCTC CTGGATCCTG CTCCTTCTG 540
 60 GGCTCTGACT TCCTGGAAA TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTG 600
 GAATTTCAA CACCAGCAA AAATTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC 660
 AAATAAAGAT ATTAATAAAG GCAATACCA

Seq ID NO: 14 Protein sequence:
 Protein Accession #: NP_005969.1

1 11 21 31 41 51
 65 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
 GSLDENSDQQ VDFQEYAVFL ALITVMCNDP FQGCPRDP

Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 62-358

1 11 21 31 41 51
 75 GGAGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGGAACTCG GCCACAGATC 60
 CATGATGTGC AGTTCTCTGG AGCAGGCGCT GGCTGTGCTG GTCCTACCT TCCACAAGTA 120
 80 CTCCTGCCAA GAGGCGGACA AGTTCAAGCT GAGTAAGGGG GAAATGAAG AACTTCTGCA 180
 CAAGGAGCTG CCCAGCTTTG TGGGGGAGAA AGTGGATGAG GAGGGCTGA AGAAGCTGAT 240
 GGGCAGCCTG GATGAGAACA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTCTCT 300
 GGCATCATC ACTGTCTATG GCAATGACTT CTTCCAGGGC TGCCAGAGC GACCTTGAAG 360
 CAGAACTCTT GACTTCTGTC CATGGATCTC TTGGGCCAG GACTGTTGAT GCCTTTGAGT 420
 85 TTTGTATTCA ATAACTTTT TTTGTCTGTT GATAATATTT TAATTGCTCA GTGATGTTCC 480
 ATAACCCGC TGGCTCAGCT GGAGTGCTGG GAGATGAGGG CCTCCTGGAT CCTGCTCCCT 540
 TCTGGGCTCT GACTCTCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 600
 TTTGGAATTT CAAACACCAG CAAAAAATG GAAATCGAGA TAGGTTGCTG ACTTTTATT 660

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

1 11 21 31 41 51
| | | | |
MMCSSLEQAL AVLVTFPHKY SCQEGDKPKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSDDQ VDFQEYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

1 11 21 31 41 51
| | | | |
AAGACGGATT CTCAGACAAG GCTTGCAAAT GCCCGCAGC CATCATTTAA CTGCACCCGC 60
AGAATAGTTA CGGTTTGTC CCCGACCTTC CCGGATCGCC TAATTTGTCC CTAGTGAGAC 120
CCCGAGGCTC TGGCCGCGCC TGGCTTCTTC GTAGCTGGAT GCATATCGTG CTCCGGGCAG 180
CGCGGGCGCA GGGCAGCGGT TCGCGCACAC CCTAGCACAC ATGAACACGC GCAAGAGCTG 240
AACCAAGCAC GGTTTCCATT TCAAAAAGGG AGACAGCCTC TACCGCGATT GTAGAAGAGA 300
CTGTGGTGTG AATTAGGAC CGGGAGGCGT CGAACCGAGG AACGGTTTCT CTTAGAGACT 360
AATTTTCTGG AGTTTCTGCC CTGCTCTGTC GTCAGCCCTC ACGTCACTTC GCCAGCAGTA 420
GCAGAGGCGG CGGCGGCGGC TCCCGGAATT GGGTTGGAGC AGGAGCCTCG CTGGCTGCTT 480
CGCTCGCGCT CTACGCGCTC AGTCCCGGCG GGTAGCAGGA GCCTGGACCC AGGCGCGGCC 540
GGCGGGCGTG AGCGCGCGGA GCCCGGCCTC GAGGTGCATA CCGGACCCCC ATTCCGATCT 600
AACAAAGGAA CTGCGCCCCA GAGAGTCCCG GGAGCGCCGC CGGTCCGTGC CCGGCGCGCC 660
GGGCCATGCA GCGACGCGCG CCGCGGAGCT CCGAGCAGCG GTAGCGCCCC CTGTAAAGC 720
GGTTCGTAT CCGGGGGTCA CTGTGAACCC TGCCGCTGTC CGGAACACTC TTCGCTCCGG 780
ACCACTCAG CCTCTGATA GCTGGACTCG GCACGCCCGC AACAAAGCAC GAGGAGTTAA 840
GAGAGCCGCA AGCGCAGGGA AGGCCTCCCC GCACGGGTGG GGGAAAGCGG CCGGTGCAGC 900
GCGGGGACAG GCACCTCGGC TGGCACTGGC TGCTAGGAT GTCGTCCTGG ATAAGSTGGC 960
ATGGACCCGC CATGGCGCGG CTCTGGGGCT TCTGCTGGCT GGTGTGGGGC TTCTGGAGGG 1020
CCGCTTTTGC CTGTCCACG TCCTGCAAAT GCAGTGCTC TCGGATCTGG TGCAGCGACC 1080
CTTCTCCTGG CATCGTGGCA TTTCCGAGAT TGGAGCCTAA CAGTGTAGAT CCTGAGAACA 1140
TCACCGAAAT TTTCATCGCA AACCAAGAAA GGTAGAAAT CATCAACGAA GATGATGTTG 1200
AAGCTTATGT GGGACTGAGA AATCTGACAA TTGTGGATTC TGGATTAAAA TTGTGGCTC 1260
ATAAAGCATT TCTGAAAAAC AGCAACCTGC AGCACATCAA TTTTACCGA AACAACTGA 1320
CGAGTTTGTG TAGGAAACAT TTCCGTCACT TTGACTTGTG TGAACGTATC CTGGTGGGCA 1380
ATCCATTATC ATGCTCCTGT GACATTATGT GGATCAAGAC TCTCCAAGAG GCTAAATCCA 1440
GTCCAGACAC TCAGGATTGT TACTGCTGTA ATGAAAGCAG CAAGAATATT CCCCTGGCAA 1500
ACCTGCAGAT ACCGAATTGT GGTTTGCCAT CTGCAATCT GGCAGCACCT AACCTCACTG 1560
TGGAGGAAGG AAGTCTATC ACATTATCCT GTAGTGTGGC AGGTGATCCG GTTCTTAATA 1620
TGTATTGGGA TGTGGTAAC CTGGTTTCCA AACATATGAA TGAACAAGC CACACACAGG 1680
GCTCCTTAAG GATAACTAAC ATTTATCCCG ATGACAGTGG GAAGCAGATC TCTGTGTGG 1740
CGGAAATCT TGTAGGAGAA GATCAAGATT CTGTCAACCT CACTGTGCAT TTGCAACCAA 1800
CTATCACAAT TCTCGAATCT CCAACCTCAG ACCACCACTG GTGCATTCCA TTCACTGTGA 1860
AAGCAACACC GAAACAGATT CTTGCTGGT TCTATAACGG GGCAATATTG AATGAGTCCA 1920
AATACATCTG TACTAAAATA CATGTTACCA ATCACACGGA GTACCACGGC TGCCCTCAGC 1980
TGGATAATCC CACTCACATG AACAAATGGG ACTACACTCT AATAGCCAAG AATGAGTATG 2040
GGAAGGATGA GAAACAGATT TCTGCTCACT TCATGGGCTG GCCTGGAATT GACGATGGTG 2100
CAAAACCAAA TTATCCTGAT GTAATTTATG AAGATTATGG AACTGCAGCG AATGACATCG 2160
GGGACACCAC GAACAGAAGT AATGAAATCC CTTCACAGA CGTCACTGAT AAAACCGGTC 2220
GGGAACATCT CTCGGTCTAT GCTGTGGTGG TGAATTGCGTC TGTGGTGGGA TTTTGCCTTT 2280
TGGTAATGCT GTTTCGTGCT AAGTTGGCAA GACACTCCAA GTTTGGCATG AAAGGTTTGT 2340
TTTTGTTTCA TAAGATCCCA CTGGATGGGT AGCTGAAATA AAGGAAAGA CAGAGAAAGG 2400
GGCTGTGGTG CTGTGTGGTT GATGCTGCCA TGTAAAGCTGG ACTCCTGGGA CTGCTGTGG 2460
CTTATCCCGG GAAGTGCTGC TTAATCTGGG TTTTCTGGTA GATGTGGGCG GTGTTTGGAG 2520
GCTGTACTAT ATGAAGCCTG CATATACTGT GAGCTGTGAT TGGGGAACAC CAATGCAGAG 2580
GTAACCTCA GCGAGCTAAG CAGCACCTCA AGAAAACATG TTAATTAAT GCTTCTCTTC 2640
TTACAGTAGT TCAATACAA AACTGAAATG AAATCCCAT TGGATTGACT TCTCTCTGA 2700
AAAGTGTGCT TTTTGACCCT ACTGGACATT TATTGACTTA ATTGCTTCTG TTTATTAATA 2760
TTGACCTGCA AAGTTAAAAA AAAATTAAAG TTGAGAACAG GTATAAGTGC AACTGAATA 2820
GTCTAATCTA CATGTAACAC ATATTTTAGT GTGATTTTCT ATACTCTAAT CAGCACTGAA 2880
TTCAGAGGGT TTGACTTTTT CATCTATAAC ACAGTGACTA AAAGAGTTAA GGGTATATAT 2940
ACCATCACTT TGGGACTTGG TAGTATTATT AAAAGGTTAT TTCTTCACT GTCAATAAAA 3000
GTCCAAATGT TTAGCTTAGG TCTGAGAGTC AAACAATGTT AAGGATTGTC TTAAGTTTCC 3060
TTAGCCAGCA AAACAAAACA AAACAAAACA AACAAATGAA AACGTTTAA AAAGAAGAAG 3120
AAGAAAAAAA ACAAGAACAA GCAGCAACAG CTGTTTGTG GGGGCTATAG ATTTAAGTTA 3180
GGCATAGTCA ATTTGAGAA TAACTAAGAGT GGAATATATG CATATGGTGA AATTATAACC 3240
TTGCCCTTTT TTATTTGCCC TCTGCGATCC ACCTGCTTTT TAGAAGTCTG CCGAGTGAGA 3300
AGGCCACAGT ATCTGCTTGG GTTTGCTATTA CAGAACTGCA GCTTTTCTAC TCTGAAAAGG 3360
CCTGGGAGCA GAATGGCTGG CCTGCTGTGA GCAGGAGAGG AGATTCTAAG AAGGATAGTC 3420
CCCCCTACAA CATACTGTCA TACTGTGGG TTTTCATGGG TAGGAAAGCT TGTCTGACC 3480
CCAGCAGCAA AGAGCTGTGA GGTGCTAAT GAATATATGC TTTATATATG CTTTCTCAT 3540
TGCTGAGAGG GCAGCCTTAG AGCTGTGGAT TTCTGCATCC CCCCTGAGTC TGACCCATGG 3600
ACACCTGTTT CATTCACTTT AGCATCACAG TGACCTTTGT ATGCTCTGTT CAGTCTGTGT 3660
CAGGCAGTAT GCTTGCTCTG AAGAGAGGTT TGGCTATCCC CACCCCAACC CACCCCAACC 3720
TGTTCCTTTT TTATCAGAG GACTTCAGAG CCAGGCCTGC AGCATTGTTG TTGAAAACAC 3780
AATCAGCTCT GACAGTTAGA CATGCACACA GACGCCATAG CTGGATTGGA AACATTGATG 3840
TTTTAAAAAT TTATTTT TGGAAATAGT TGCAAAATG CTGCAATTTA GCTTTAAGGT 3900
TCTATAGATT TTTAACTAGT CCAACACAGT CAGAAACATT GTTTTGAATC CTCTGTAAC 3960
CAAGGCATTA ATCTTAATAA ACCAGGATCC ATTTAGGTAC CACTTGATAT AAAAAGGATA 4020
TCCATAATGA ATATTTTATA CTGCATCCTT TACATTAGCC ACTAAATACG TTATTGCTTG 4080
ATGAAGACCT TTCACAGAAT CCTATGGAAT GCAGCATTTT ACTTGGCTAC TTCATACCCA 4140

TGCCTTAAAG AGGGGAGTT TCTCAAAAGC AGAAACATGC CGCCAGTTCT CAAGTTTTC 4200
 TCCTAACTCC ATTTGAATGT AAGGGCAGCT GGCCCCCAAT GTGGGGAGGT CCGAACATTT 4260
 TCTGAATTCC CATTTTCTTG TTCGCGGCTA AATGACAGTT TCTGTCTATTA CTTAGATTCC 4320
 GATCTTTCCC AAAGGTGTTG ATTTACAAAG AGGCCAGCTA ATAGCAGAAA TCATGACCCT 4380
 5 GAAAGAGAGA TGAATTTCAA GCTGTGAGCC AGGCAGGAGC TCAGTATGGC AAAGGTTCTT 4440
 GAGAATCAGC CATTTGGTAC AAAAAAGATT TTAAAGCTT TTATGTTATA CCATGGAGCC 4500
 ATAGAAAGGC TAGGATTTGT TTAAGAACTA TTTTAAAGTG TTCCAGACCC AAAAAGGAAA 4560
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Seq ID NO: 18 Protein sequence:
 Protein Accession #: CAA53571

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 20 SKNIPLANLQ IPNCGLP SAN LAAPNLVEE GKSITLSCSV AGDPVPMYMW DVGNLVSKHM 240
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Seq ID NO: 20 Protein sequence:
Protein Accession #: NP_000219

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Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: NM_003722
Coding sequence: 145-1491

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Seq ID NO: 22 Protein sequence:
 Protein Accession #: NP_003713

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Seq ID NO: 23 DNA sequence
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Seq ID NO: 24 Protein sequence:
 Protein Accession #: NP_001935.1

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10	SNVKYVMGRN	DGGYLMWDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTGKTSTGT	480
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

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	GCAAGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTCG	TAGTTTCTCC	120
	CATGTTTGAG	TCCACAGCTG	CAGATTGGGG	GTCTGTGGTA	CGCAAGAAC	TGCTATCAGA	180
	CTGCTCTGTC	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCATCTG	AGGACAGTAT	240
30	GGAGAAGGTG	AAAGTATACT	TGAGGGTTAG	GCCCTTGTTA	CCCTCAGAGT	TGGAACGACA	300
	GGAGAGATCA	GGTTGTGTCC	GTATTGAGAA	TGTGGAGACC	CTGTCTTAC	AAGCACCCAA	360
	GGAATCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGGTTTAC	420
	CTTTTCCCG	ATCTTTGGGC	CAGAAGTGGG	ACAGGCATCC	TTCTTCAACC	TAAGTGTGAA	480
	GGAGATGGTA	AAGGATGTAC	TCAAAGGGCA	GAATGCGCTC	ATCTATACAT	ATGGAGTCAC	540
35	TAACTCAGGG	AAAACCCACA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAATCT	CATCCAACAC	CTGATCTGAA	660
	GCCTTGTCTC	TCCAATGAGG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAC	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGCTAT	ATGGAGGCCT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTGAA	780
40	GAGGAGTGTC	TACATCGAAA	GTCGGATAGG	TACCAGCACC	AGCTTCGACA	GTGGCATTGC	840
	TGGGCTCTCT	TCTATCAGTG	AGTGTACCAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
	ATGGGCACAG	CCAGACATCG	CCCCACTACC	TGTCCCGGCA	AACATTGCTC	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAATC	GCTTTATGAC	CTATTAGAAC	CGCCTAGCCA	1020
	ACAGCCGCAAG	AGGCAGACTT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
	AGATCTCAAC	TGGATTCTAT	TGCAAGATGC	TGAGGAGGCG	TGGAAGCTCC	TAAAGTGGG	1140
45	TCGTAAGAAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACCAG	AACTCCAGCC	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCC	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCA	CTCTGTGATC	TGGCTGGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAACAC	CTCTCTACAC	ACCCTGGGCC	GCTGTATTGC	1380
	TGCCCTTCGT	CAAAACCCAG	AGAACCGGTC	AAAGCAGAAC	CTGGTTCCCT	TCCGTGACAG	1440
50	CAAGTTGACT	CGAGTGTTCC	AAGGTTTCTT	CACAGGCCGA	GGCCGTTCTC	GCATGATTGT	1500
	CAATGTGAAT	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGTCTAGC	CAGGTGACTT	GTGCTATGCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTCGTTTCA	CAAGGAACAT	AGTCTTCAGG	TATCCCCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
55	CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAAG	1740
	AGGAGCTCCT	ACAAGTTGTG	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GGAGATGCAT	CTCCGAGATG	AAATTGTCAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGGTGC	AGTGAACATT	TGGACACCCA	AAAGGAACAT	TTGGAGGAAA	1920
	TGTATGAAGA	AAAACATAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTGTAC	CAAGAAGAGA	1980
60	TTCAGGAGCG	GGATGAAGAG	ATTGAAGAGC	TAGAAGCTCT	CTTGACAGGA	GCCAGACAAC	2040
	AGTCAGTGGC	CCATCAGCAA	TCAGGGTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAAG	2160
	CAGAGCTAAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAATGTGTA	GAACCCACAC	2220
	CCTCAGCCAA	GCCCTTCACC	ATTGATGTGG	ACAAGAAGTT	AGAAGAGGGC	CAGAAGAATA	2280
	TAAGGCTGTT	GGCGACAGAG	CTTCAGAAAC	TTGGTGAGTC	TCTCCAATCA	GCAGAGAGAG	2340
65	CTTGTGGCCA	CAGCACTGGG	GCAGGAAAC	TTCTGCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCTTAATCAA	ACAGGACCAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAAC	2460
	TGGACCTTCG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATACTGTG	TTGAAACTCC	2520
	AAGGCCAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAAATCAG	CAACCAAACT	2580
70	AACAACCACC	AGGGAAGAAA	CCATTCTCTC	GAAATTTACT	TCCCCGAACA	CCAACCTGCC	2640
	AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCACGGCGT	TCCCTTTTAC	2700
	TCAAATCTGG	GCCTTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTCAGCT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCATA	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTTGTAT	2880
75	TATAACCACC	TATGTAATCT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTCTTAT	2940
	GCACACAAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATTG	AATTCCAAAT	3000
	GTAGCAAAAT	CATTAATAAA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
80	MSQILSPPA	GLLSDDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSTSL	EDKQVPSSE	60
	SMEKVKVYLR	VRPLLPSELE	RQEDQGCVR	ENVETLVLQA	PKDSFALKSN	ERGIGQATHR	120
85	FTFSQIFGPE	VQASPFNLT	VKEMVKDVLK	QGNWLIYTYG	VTNSGKTHTI	QGTIKDGGIL	180
	PRSLALIFNS	LQQLHPTPD	LKPLLSNEVI	WLDKQIRQE	EMKLSLNLNG	GLQEELSTS	240
	LKRSVYIESR	IGTSTSFDSG	IAGLSSISQC	TSSSQLDETS	HRWAQPDTPA	LPVPANIRFS	300

IWISFPEIYN ELLYDLLEPP SQQRKQTLR LCEQNGNPY VKDLNWIHVQ DAEAWKLLK 360
 VGRKNQSPAS THLNQNSRS HSIFSIIRLH LQEGDIVPK ISELSLCDLA GSERCKDQKS 420
 GERLKEAGNI NTSLETLGRC IAAALRQNN RSKQNLVFPF DSKLTRVFQ FPTGRGRSCM 480
 IVNVNFCAS YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 13-1424

10 1 11 21 31 41 51
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 CTTCCTCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGG TGAAGATAC 120
 15 TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCGAT 300
 GTCCATCATT TCAGGGAATG GCCAGGGGG CCCGTATGGA GGAACATTA TATCACCTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGAAAA 420
 GCTTTCCAAG TATGGAGTAA TGTACCCTCC TTGAAATTCA GCAAGATTAA CACAGGCATG 480
 20 GCTGACATTT TGGTGGTTT TGCCCGTGGG GCTCATGGAG ACTTCCATGC TTTTGATGGC 540
 AAAGTGGAA TCCTAGCCCA TGCTTTTGA CCTGGATCTG GCATTGGAGG GGATGCACAT 600
 TTGATGAGG ACGAATCTCT GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT 660
 GTTACGAGA TTGGCCATT CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG 720
 25 TTCCCCACCT ACAATATGT TGACATCAAC ACATTTCGCC TCTCTGTGA TGACATACGT 780
 GGCAATCAGT CCCTGTATGG AGACCCAAAA GAGAACCAAC GCTTGCCAAA TCCTGACAAT 840
 TCAGAACCA CTCTCTGTGA CCCCAATTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTT TCTTCAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960
 AGTGTAAAT TAAATTTCT CTTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT 1020
 30 GAAATTGAAG CAGAAATCA AGTTTCTT TTTAAAGATG ACAAATATG GTTAATTAGC 1080
 AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACTT CTTTGTGTT TCCTAACTTT 1140
 GTGAAAAAAA TTGATGCAGC TGTTTTAAAC CCACGTTTT ATAGGACCTA CTCTTTTGA 1200
 GATAACCACT ATTGAGATG TGATGAAAGG AGACAGATGA TGGACCTGG TTATCCCAA 1260
 CTGATTACCA AGAATCTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTTAAA 1320
 AACAAATACT ACTATTTCT CCAAGGATCT AACCAATTG AATATGACTT CTACTCCAA 1380
 35 CGTATACCA AACACTGAA AAGCAATAGC TGGTTTGGT GTTGAAAAAT GTGTAATTA 1440
 TGGTTTGT TAGTTCATT CAGCTTAATA AGTATTTATT GCATATTGCT TATGTCTCA 1500
 GTGTACCCT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560
 40 TTATATAAAA TACATAAAT TTTTCAATT TGAAACTCT AATTGTCTT TCTGTCTGA 1620
 CTCTACTATT AAGTTTGAAA ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 CTCTGTAAGT TGCTTCTAA CATCCTTGA CTGAGAAAT ATACTTACTT CTGGCATAAC 1740
 TAAATTAAG TATATATATT TTGGCTCAA TAAATTG

Seq ID NO: 28 Protein sequence:
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 | | | | | |
 MKFLILLILQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
 50 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFF REMPGGPVWR KHYITYRINN 120
 YTPDMNRQHV WVAIRKAFV WSNVPLKFS KINTGMADIL VVFARGAHD FHFADGKGGI 180
 LAHAFPGSG IGGDAHFDEB EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY 240
 KYVDINTFRL SADDIRIGQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300
 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
 55 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFVDNQY WRYDERRQMM DPGYPKLITK 420
 NFGGIGPKID AVFYSKNKY YFFQGSNQFE YDFLLQRIK TLKSNWFGC

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_006115.1
 Coding sequence: 236..1765

60 1 11 21 31 41 51
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 65 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGGCGT TTGTGGGGTT CCATTGAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCTGGCCAT 360
 70 TGCCGCCCTG GAGTTGCTGC CCAGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CTGCTCTCC 480
 TCTGGGAGTG CTGATGAAGG GACAACTCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
 GGAATTACCG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
 75 TCTGTACTCA TTCCAGAGC CAGAACGAGC TCAGCCCATG ACAAAGAAGC GAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
 GAAAAATGTA CTACGCTGTG GCTGTGAAGG GCTGAAGATT TTTGCAATGC CCATGCAGGA 900
 TATCAAGATG ATCCTGAAAA TGGTGCAGCT GGAATCTATT GAAGATTGG AAGTGACTTG 960
 TACCTGGAAG CTACCCACTT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
 80 GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCTTAC ATTTCCTCCG AGAAGGAAGA 1080
 GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
 TTGGGACTCT TTAATTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGTATGA 1200
 85 CCCCTTGGAA ACCCTCTCAA TAACATACTG CCGGCTTCG GAAGGGGATG TGATGCATCT 1260
 GTCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATGTAAGT CCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCTCCAGGA 1380
 CCTGGTCTTT GTGAGGTGTG GGATCACGGA TGATCAGCTC CTGCTCTTCC TGCCTTCCCT 1440
 GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC 1500

CTTGCAGAGT CTCTCGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCTC CACCTGGAGA GGCTTGCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCCGTG TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTGTAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAATGTTT AGTGTGAGTG AGGAAACAT GTTCAGTGAG GAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTTGAAAT AAGAGAGAGC AATGTGAAGC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 30 Protein sequence:
 Protein Accession #: NP_006106.1

1 11 21 31 41 51
 | | | | | |
 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCCT GCAGCGCCTC AGCACCCTC 60
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGAAT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCCGT TCAAAATGGA 240
 ACGAAGGCGT TTGTGGGGTT CCATTGAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTGTGTGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 TGCCGCCCTG GAGTTGTGTC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGACGGCC TGGCCCTTCA CCTGCCTCCC 480
 TCTGGGAGTG CTGATGAAGG GACAACTCT TCACCTGGAG ACCTTCAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
 GGAATTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
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 TATCAAGATG ATCCTGAAAA TGGTGACGCT GGAATCTATT GAAGATTTGG AAGTGACTTG 960
 TACCTGGAAG CTACCCACCT TTGGCGAAAT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
 GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCTTAC ATTTCCCGG AGAAGGAAGA 1080
 GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
 TGTGGACTCT TTATTTTTC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGATGAA 1200
 CCCCTTGAAA ACCCTCTCAA TAACCTAACTG CCGGCTTTCG GAAGGGGATG TGATGCATCT 1260
 GTCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATTAAGT CCCAGAGCCC TCCAGGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GATGAGTGTG GATCAAGGTA TGATCAGCTC CTTGCCCTCC TGCCTTCCCT 1440
 GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCATCT CCATATCTGC 1500
 CTTGCAGAGT CTCTCTCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCTC CACCTGGAGA GGCTTGCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGTG TTCTGCTCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAATGTTT AGTGTGAGTG AGGAAACAT GTTCAGTGAG GAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTTGAAAT AAGAGAGAGC AATGTGAAGC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 64-2754

1 11 21 31 41 51
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 GGCAGGTCTC GCTCTCGGCA CCTCCCGGC GCCCGCTTC TCTGGCCCT GCCCGCATC 60
 CCGATGGCCG CCGCTGGGCC CCGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCCCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
 TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCAAGT 300
 TACACAGCCA GGGCTGTGTC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCCTTGCT CATATGCAAGA GAATTCCTTG GGCCTTTTCC CATTGTTTCT TCAACAAGTT 540
 GAATCTGATG CAGCACAGAA CTATCTGTC TTCTACTCAA TAAGTGGAGC TGGAGTTGAT 600
 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 CCTGTGGATG GTGAAGAATA TGATGTTTTT GATTTGATTG CTTATGCTC AACTGCAGAT 720
 GGATATTCAG CAGATCTGCC CCTCCACTA CCTCATAGG TAGAGGATGA AAATGACAAC 780
 CACCTCTGTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC 900
 CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACTGT GGCTCTTTT TGTGCATCCC 960
 AGCACAGGCG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGTTGTT AGACAAGTAC 1020
 TCATTGATAA TGAAAGTACA AGACATGGAT GGCAGTTTTT TTGATTGAT AGGCACATCA 1080
 ACTTGATACA TAACAGTAAC AGATTCAAAT GATAATGCAC CCACTTTCAG ACAAATGCT 1140
 TATGAAGCAT TTGTAGAGGA AAATGCATTC AATGTGGAAT TCTTACGAAT ACCTATAGAA 1200
 GATAAGGATT TAATTAAACAC TGCCCAATGG AGAGTCAATT TTACCATTTT AAAGGGAAAT 1260
 GAAAAAGGAC ATTTCAAAAT CAGCACAGAC AAAGAACTA ATGAAGGTGT TCTTCTGTT 1320
 GTAAAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATTGG AGTAAACAAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTTCCAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCTT GAATGCACTC CTCAGGCCCA ATATGTGCGG 1500
 ATTAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560

	AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTGCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
	CCCCAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
5	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTGCAA	ACCAAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCACTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTTAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCTC	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
10	GCAACAAAAT	TATTTAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCTGTGG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACTTGGG	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTGTGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCTCTAAGA	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTTATGA	CCCAAACTAC	CAACAACTCT	2340
15	AGCCCAAGTT	TTTGTGGTAC	TATGGGATCA	GAATGAAAA	ATGGAGGGCA	GGAAACCATT	2400
	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGGACT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
	GAGTGGCACA	TTTGTCTCTA	ACCCGCTCTC	GGTGAAAAAT	TGCATCGATG	TAATCAGAAAT	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
	CCAGCTGGTT	CTGGGGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTTA	2700
20	AATAATTGGG	AACCCAAATG	TATTACATTA	GCAGAAGCAT	GCACAAAGAG	ATAATGTCTAC	2760
	AGTGCTACAA	TTAGGTCTTT	GTCAAGACAT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTTCA	ACATGTATGT	ATATGATGAT	TTTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCAAATTTATA	TTTTTAAAGC	CAGTTGTGTC	TTATCTTTTC	CAAAAAGTGA	AAAAATGTAA	2940
25	AACAGACAAC	TGGTAAATCT	CAAACTCCAG	CACCTGGAAT	AAGGTCTCTA	AAGCATCTGC	3000
	TCTTTTTTTT	TTTTACGGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAACA	3060
	ATAGCTAAGT	TATCTTAATA	TCCATTATT	ATGTATTTC	TTTAAGTGAT	AGTTTAAAAA	3120
	ATAAACAAGA	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGGAAAAGA	AACAATGAAG	3180
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	ATTATAACTG	AGTCTATGAG	GAATAGTTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAAAAT	3540
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35	TAGCTTTGCT	TCTCAGCTG	TTTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
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	GTCTGGGAGC	TACAAAATTT	CATTTTCTCT	CTCACTGCC	TTCTTCTGAG	TGGCAATTGGC	4020
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	ACCTCCAGCA	GAGATTCCCT	TAAGTGACTC	CAGGTTTCTC	ACCATCCTTC	AGCGTGAATT	4140
45	AATTTTAAAT	CAGTTTGTCT	TCTCCAGAGA	AATTTTAAAA	TAATAGAAGA	AATAGAAATT	4200
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	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCCTCAA	4320
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 20 KNELYNITVL AIDKDRSCT GTLAVNIEDV NDNPPPEILQE YVICKPKMG YTDILAVDPD 600
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 KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTNNSS QGFCGTMSGG MKNGGQETIE 780
 MKKGGNQMLE SCRCRGHHT LDSCRGHTE VDNCRYTSE WHSFTQPRLG EKLHRCNQNE 840
 25 DRMPQDQVYL TYNVEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 33 DNA sequence
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TGTGAACGAC	CAGACCAAAA	TCCTTGTGGT	TAATGCTGCC	TACTTTGTGG	GCAAGTGGAT	660
GAAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
CAAAACCACTG	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAAACA	TTGACAGTAT	780
CAATTGTAAAG	ATAAGTCTGA	TTCTTTTCA	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
ACCCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGGAGAAG	ATTGAAAAAC	AACTCAACTC	900
AGAGTCACTG	TCACAGTGGG	CTAATCCCAG	CACCATGGCC	AATGCCAAGG	TCAAACCTCT	960
CATTCCAAAA	TTAAGATGAT	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAACTTAGG	1020
GCTGAAACAT	ATCTTCACTG	AAGACACATC	TGATTTCTCT	GGAATGTCTG	AGACCAAGGG	1080
AGTGGCCCTA	TCAATGTGTA	TCCACAAAAG	GTGCTTAGAA	ATAACTGAAG	ATGGTGGGGA	1140
TTCCATAGAG	GTGCCAGGAG	CACGGATCCT	GCAGCACAA	GATGAATTGA	ATGCTGACCA	1200
TCCCTTTTAT	TACATCATCA	GGCACAACAA	AACTCGAAAC	ATCATTTTCT	TTGGCAAAAT	1260
CTGTTCTCCT	TAGTGGCAT	AGCCCCATGT	AAGTCTCTCC	TGACTTTTCT	GTGGATGCCG	1320
ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTTCTAGAT	ACAATAAAT	GCTAATGTTG	1380
CTGGATCAGG	AAGCCGCCAG	TACTTGTCT	ATGTAGCCTT	CACACAGATA	GACCTTTTCT	1440
TTTTTCCAAAT	TCTATCTTTT	GTTCCTTTT	TTCCCATAG	ACAATGACAT	ACGCTTTTAA	1500
TGAAAAGGAA	GTGAAAATAT	GGAAAAATAT	TTATTCATTA	TTTGTCAAAT	TGTCCGGGGT	1560
AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
TCTTCCAGC	ACTATGCTTT	CCTTCTTTGG	GATAGAGAAT	GTTCAGACA	TCTCGCTTC	1680
CCTGAAAGAC	TGAAGAAAGT	GTAGTGATG	GGACCCACGA	AACTGCCCTG	GCTCAGTGA	1740
AACTTGGGCA	CATGCTCAGG	CTACTATAGG	TCCAGAAGTC	CTTATGTTAA	GCCCTGGCAG	1800
GCAGGTGTTT	ATTAATAATC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
CTGTATGTTA	TGAACTTCTA	TGGATCAGAT	CTGGGGCAGC	AACTTATAAA	TCAACACCTT	1920
AATATGCTGC	AACAAAATGT	AGAATATTCA	GACAAAATGG	ATACATAAAG	ACTAAGTAGC	1980
CCATAAGGGG	TCAAAATTTG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	AAACACTTCG	2040
TTCCGAGAGC	TTTTTCAGATT	GTGGAATGTT	GGATAAGGAA	TTATAGACCT	CTAGTAGCTG	2100
AAATGCAAGA	CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACTTTC	ATTTTGTGATA	2160
GCTGTCCCAT	CTGTCTATGT	GGTGGGCACT	AGACTGGTGG	CAGGGGCTTC	TAGCTGACTC	2220
GCACAGGAT	TCTCACAATA	GCCGATATCA	GAATTTGTGT	TGAAGGAACT	TGTCTCTTCA	2280
TCTAATATGA	TAGCGGGAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAATA	TAAGTAAAGT	2340
GATTAAAGTG	CTACGTTTAC	CTTGACACAT	AGTTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
AGATGGCAAG	CATGTAACCT	ATATTAATAG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
CCTGTGCGG	GTTTCATGGAT	TACTTCTCTA	TAAAAAATAT	ATATTTACCA	AAAAATTTTG	2520
TGACATTCTT	TCTCCCATCT	CTTCCTTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTCTCG	2580
AGATTCAATA	TTGAATTTCT	CCTATGCTAT	TGACAATAAA	ATATTATTGA	ACTACC	

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

1	11	21	31	41	51	
MDALQLANSA	FAVDLPKQLC	EKEPLGNVLF	SPICLSTSL	LAQVGAKGDT	ANEIGQVLHF	60
ENVKDIPFGF	QTVTSVNVKL	SSPYSLKLIK	RLVYDKSLNL	STEFISSTKR	PYAKELETVD	120
FKDKLEETKG	QINNSIKDLT	DGHFENILAD	NSVNDQTKIL	VVNAAYFVKG	WMKKFPSEET	180
KECPFRINKT	DTKPVQMMNM	EATFCMGNID	SINCKIIELP	FQNKHLSMFI	LLPKDVEDES	240
TGLEKIEKQL	NSESLSQWTN	PSTMANAKVK	LSIPKFKVEK	MIDPKACLEN	LGLKHIFSED	300
TSDFSGMSET	KGVALSNIH	KVLEITEEDG	GDSIEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
NKTRNIIFPG	KFCSP					

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

1	11	21	31	41	51	
GGAGTGGGGG	AGAGAGAGGA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
TAAGAGCAAA	GATGTTTCAA	ACTGGGGGCC	TCATTGTCTT	CTACGGGCTG	TTAGCCAGGA	120
CCATGGCCCA	GTITGGAGGC	CTGCCCGTGC	CCCTGGACCA	GACCCCTGCC	TTGAATGTGA	180
ATCCAGCCCT	GCCCTTGAGT	CCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
ATGGCCTGCT	GTCTGGGGGC	CTGTGGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
TGAAGCCTGG	AGGAGGTACT	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGA	AAAGTGACGT	360
CAGTGATTCC	TGGCCTGAAC	AACATCATTG	ACATAAAGGT	CACTGACCCC	CAGCTGCTGG	420
AACTTGGCCT	TGTGCAGAGC	CCTGATGGCC	ACCGTCTCTA	TGTCAACATC	CCTCTCGGCA	480
TAAAGCTCCA	AGTGAATACG	CCCTGGTTCG	GTGCAAGTCT	GTGAGGCTG	GCTGTGAAGC	540
TGGACATCAC	TGCAGAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
TTGGTGACTG	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
CCCTCCCAT	TCAAGGTTCT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCCCTGCTG	720
AGTTGGTTCA	GGGCAACGTG	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTG	ATCAAGGTCT	840
AAGCCTTCCA	GGAAAGGGCT	GGCCTCTGCT	GAGCTGCTTC	CCAAGTCTCA	CAGATGGCTG	900
GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCTCT	960
TCCCACCAAG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAATGGGCT	CTTCTTCTGC	1020
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

5	1	11	21	31	41	51	
	MFQTGGGLIVF	YGLLAQTMQAQ	FGGLFVPLDQ	TLPLNVNPAI	PLSPTGLAGS	LTNALSNGLL	60
	SGGLLGILEN	LPLLDILKPG	GGTSGGLLGG	LLGKVTSVIP	GLNNIIDIIV	TDPQLLELGL	120
	VQSPDGHRLY	VTIPLGKLQ	VNTPLVGASL	LRLAVKLDIT	AEILAVRDKQ	ERIHVLVGLD	180
10	THSPGSLQIS	LLDGLGLPI	QGLLDSLTI	LNKVLPELVQ	GNVCPVNEV	LRGLDITLVH	240
	DIVNMLIHGL	QFVIKV					

Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115-2223

20	1	11	21	31	41	51	
	CTCAGGGCAG	AGGGAGGAAG	GACAGCAGAC	CAGACAGTCA	CAGCAGCCTT	GACAAAACGT	60
	TCCTGGAAC	CAAGCTCTTC	TCCACAGAGG	AGGACAGAGC	AGACAGCAGA	GACCATGGAG	120
	TCTCCCTGG	CCCCTCCCA	CAGATGTGTC	ATCCCCCTGG	AGAGGCTCCT	GCTCACAGCC	180
	TCACCTCTAA	CCTTCTGGAA	CCCGCCCAAC	ACTGCCAAGC	TCACCTATTGA	ATCCACGCCG	240
	TTCAATGTGC	CAGAGGGGAA	GGAGGTGCTT	CTACTTGTCC	ACAATCTGCC	CCAGCATCTT	300
25	TTTGGCTACA	GCTGGTACAA	AGGTGAAAGA	GTGGATGGCA	ACCGTCAAAT	TATAGGATAT	360
	GTAATAGGAA	CTCAACAAGC	TACCCAGGG	CCGCATACA	GTGGTCGAGA	GATAATATAC	420
	CCCAATGCAT	CCCTGCTGAT	CCAGAACATC	ATCCAGAATG	ACACAGGATT	CTACACCCAT	480
	CACGTCATAA	AGTCAGATCT	TGTGAATGAA	GAAGCAACTG	GCCAGTTCCT	GGTATACCCG	540
	GAGCTGCCCA	AGCCCTCCAT	CTCCAGCAAC	AACTCCAAAC	CCGTGGAGGA	CAAGGATGCT	600
	GTGGCCTTCA	CTGTGAACC	TGAGACTCAG	GACGCAACCT	ACCTGTGGTG	GGTAAACAAAT	660
30	CAGAGCCTCC	CGGTCACTCC	CAGGCTGCAG	CTGTCCAATG	GCAACAGGAC	CCTCACTCTA	720
	TTCAATGTCA	CAGAAATGTA	CACAGCAAGC	TACAAATGTG	AAACCCAGAA	CCCAGTGAGT	780
	GCCAGGCGCA	GTGATTCAGT	CATCCTGAAT	GTCTCTATAG	GCCCGGATGC	CCCCACCAT	840
	TCCCCTCTAA	ACACATCTTA	CAGATCAGGG	GAAATCTGA	ACCTCTCCTG	CCACGCAGCC	900
	TCTAACCCAC	CTGCACAGTA	CTCTTGGTTT	GTCAATGGGA	CTTCCAGCA	ATCCACCCAA	960
35	GAGCTCTTTA	TCCCACATCT	CACGTGAAT	AATAGTGGAT	CCTATACGTC	CCAAGCCCAT	1020
	AACTCAGACA	CTGGCCTCAA	TAGGACCACA	GTCAAGACGA	TCACAGTCTA	TGCAGAGCCA	1080
	CCCAAAACCT	TATCACCAG	CAACAACCTC	AAACCCGTGG	AGGATGAGGA	TGCTGTAGCC	1140
	TTAAACCTGT	TAACCTAGAA	TCAGAACACA	ACCTACCTGT	GGTGGGTAAA	TAATCAGAGC	1200
	CTCCCGGTCA	GTCCAGGCT	GCAGCTGTCC	AATGACAACA	GGACCCCTAC	TCTACTCAGT	1260
40	GTCAACAAGA	ATGATGTAGT	ACCCTATGAG	TGTGGAATCC	AGAACGAATT	AAGTGTGAC	1320
	CACAGCGACC	AGGTGTAGCT	GAATGCTCTC	TATGGCCGAG	ACGACCCAC	CATTTCCTCC	1380
	TCATACACCT	ATTACCGTCC	AGGGGTGAAC	CTCAGCCTCT	CCTGCCATGC	AGCCTCTAAC	1440
	CCACCTGCAC	AGTATCTTGT	GCTGATTGAT	GGGAACATCC	AGCAACACAC	ACAAGAGCTC	1500
	TTTATCTCCA	ATCATCTGTA	GAAGAACAGC	GGACTCTATA	CCTGCCAGGC	CAATAACTCA	1560
45	GCCAGTGCC	ACAGCAGGAC	TACAGTCAAG	ACAATCACAG	TCTCTGCGGA	GCTGCCCAAG	1620
	CCCTCCATCT	CCAGCAACAA	CTCCAAACCC	GTGGAGGACA	AGGATGCTGT	GGCCTTCACC	1680
	TGTGAACCTG	CCCTGAGTGT	CCTCTATGGG	CCGACACCCC	CCATCATTTT	CCCCCAGAC	1740
	GTCAGTCCCA	GGCTGCAGCT	GTCCAATGGC	AACAGGACCC	TCACCTCTAT	CAATGTCA	1800
	AGAAATGAGC	CAGAGGCTGA	TGTATGTGGA	ATCCAGAACT	CAGTGAGTGC	AAACCGCAGT	1860
50	GACCCAGTCA	CCCTGATGTT	CCTCTATGGG	CCGACACCCC	CCATCATTTT	CCCCCAGAC	1920
	TGCTCTTACC	TTTCGGGAGC	GAACCTCAAC	CTCTCTGCCC	ACTCGGCTC	TAAACCATCC	1980
	CCGAGTATT	CTTGGCGTAT	CAATGGGATA	CCGACAGCAAC	ACACACAAGT	TCTCTTTATC	2040
	GGCAAAATCA	CGCCAAATGA	TAACGGGACC	TATGCCTGTT	TTGTCTCTAA	CTTGGCTACT	2100
	GGCCGCAATA	ATTCCATAGT	CAAGAGCATC	ACAGTCTCTG	CATCTGGAAC	TTCTCTGGT	2160
55	CTCTCAGCTG	GGGCCACTGT	CGGCATCATG	ATTGGAGTGC	TGTTTGGGGT	TGCTCTGATA	2220
	TAGCAGCCCT	GGTGTAGTTT	CTTCAATTCA	GGAAGACTGA	CAGTTGTTTT	GCTTCTCTCT	2280
	TAAAGCATTT	GCAACAGCTA	CAGTCTAAAA	TTGCTTCTTT	ACCAAGGATA	TTTACAGAAA	2340
	AGACTCTGAC	CAGAGATCGA	GACCATCTTA	GCCAACTCG	TGAAACCCCA	TCTCTACTAA	2400
60	AAATACAAAA	ATGAGCTGGG	CTTGCTGGCG	CGCACTGTGA	GTCCCAGTTA	CTCGGGAGGC	2460
	TGAGGCAGGA	GAATCGCTTG	AAACCCGGAG	GTGGAGATTG	CAGTGAGCCC	AGATCGCACC	2520
	ACTGCACTCC	AGTCTGGCAA	CAGAGCAGAA	CTCCATCTCA	AAAAGAAAAG	AAAAGAAGAC	2580
	CTTGACCTGT	ACTCTTGAAT	ACAAGTTTCT	GATACCACTG	CAGTGTCTGA	GAATTTCCAA	2640
	AACTTTAATG	AACTAACTGA	CAGCTTCATG	AACTGTCCA	CCAAGATCAA	GCAGAGAAAA	2700
	TAATTAATTT	CATGGGACTA	AATGAACATA	TGAGGATTGC	TGATCTTTTA	AATGTCTTGT	2760
65	TTCCAGATT	TCAGGAAACT	TTTTTCTTT	TAAGCTATCC	ACTCTTACAG	CAATTGATA	2820
	AAATATACCT	TTGTGAACAA	AAATTGAGAC	ATTTACATTT	TCTCCCTATG	TGTCGCTCC	2880
	AGACTTGGGA	AACTATTCAT	GAATATTAT	ATTGTATGGT	AAATATAGTTA	TGTCACAAGT	2940
	TCAATAAAAA	TCTGCTCTTT	GTATAACAGA	AAAA			

Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

75	1	11	21	31	41	51	
	MESPSAPPHR	WCIPWQRLLL	TASLLTFWNP	PTTAKLTIES	TPFNVAEGKE	VLLLVHNLPO	60
	HLFGYSWYKG	ERVVDNRQII	GYVIGTQQAT	PGPAYSGREI	IYPNASLLIQ	NIQNDTGFY	120
	TLHVKISDLV	NEEATGQFRV	YPELPKPSIS	SNNKPVEDK	DAVAFTCEPE	TQDATYLWV	180
	NNQSLPVSPR	LQLSNGNRTL	TLFNVTRNDT	ASYKCETQNP	VSARRSDSVI	LVLYGPDAP	240
	TLSPNLTSYR	SGENLNLSCL	AASNPQAQYS	WFVNGTFQQS	TQELFIPNIT	VNNSGSYTCQ	300
80	AHNSDTGLNR	TVTITITVYA	EPPKPFITSN	NSNPVEDEDA	VALTCEPEIQ	NTTYLWVWNN	360
	QSLPVSPRLQ	LSNDNRTLTL	LSVTRNDVGP	YECGIQNELS	VDHSDPVILN	VLYGPDPTI	420
	SPSYTYRPG	VNLSLSCHAA	SNPPAQYSWL	IDGNIQQHTQ	ELFISNITEK	NSGLYTCQAN	480
	NSAGHSRRTT	VKITIVSAEL	PKPSISSNNS	KPVEDKDAVA	FTCEPEAQNT	TYLWVWNGQS	540
	LPVSPRLQLS	NGNRTLTLFN	VTRNDARAYV	CGIQNSVSAN	RSDPVTLDVL	YGPDTPIISP	600
85	PDSSYLSGAN	LNLSCHSASN	PSPQYSWRIN	GIPQHQTVL	FIKIPNNN	GYACFVSNL	660
	ATGRNNSIVK	SITVSASGTS	PGLSAGATVG	IMIGVLGVVA	LI		

Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

5
10
15
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1	11	21	31	41	51	
AATCCGACA	ATGGCGAAG	ACAACTCAAC	TGTTGCTTGC	TTCCAGGGCC	TGCTGATTTT	60
TGGAATGTG	ATTATTGTT	GTTCGGCAT	TGCCCTGACT	GCGAGTGCA	TCTTCTTGT	120
ATCTGACCA	CACAGCCTCT	ACCACTGCT	TGAAGCCACC	GACAACGATG	ACATCTATGG	180
GGCTGCTGG	ATCGGCATAT	TTGTGGGCAT	CTGCCTCTTC	TGCTGTCTG	TTCTAGGCAT	240
TGTAGGCATC	ATGAAGTCCA	GCAGGAAAT	TCTTCTGGCG	TATTTCAATC	TGATGTTTAT	300
AGTATATGCC	TTTGAAGTGG	CATCTGTAT	CACAGCAGCA	ACACAACGAG	ACTTTTTCAC	360
ACCCAACCTC	TTCTGAAGC	AGATGCTAGA	GAGGTACCAA	AACAACAGCC	CTCCAAACAA	420
TGATGACCAG	TGGAATAACA	ATGGAGTCAC	CAAAACCTGG	GACAGGCTCA	TGCTCCAGGA	480
CAATTGCTGT	GGCGTAAATG	GTCCATCAGA	CTGGCAAAAA	TACACATCTG	CCTTCCGGAC	540
TGGAATAAAT	GATGCTGACT	ATCCCTGGCC	TCGTCAATGC	TGTGTTATGA	ACAATCTTAA	600
AGAACCTCTC	AACCTGGAGG	CTTGTAAGT	AGGCGTGCCT	GGTTTTATC	ACAATCAGGG	660
CTGCTATGAA	CTGATCTCTG	GTCCAATGAA	CCGACAGGCC	TGGGGGGTTG	CCTGTTTGG	720
ATTTGCCATT	CTCTGTGGA	CTTTTGGGT	TCTCTGGGT	ACCATGTTCT	ACTGAGCAG	780
AATTGAATAT	TAAGAA					

Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

25
30

1	11	21	31	41	51	
MAKDNSTVRC	FQGLLIFGNV	IIGCCGIALT	AECIFFVSDQ	HSLYPLELAT	DNDIYGAAW	60
IGIFVIGICLF	CLSVLGIIVI	MKSSRKILLA	YFILMFIVYA	FEVASCITAA	TQRDFFTPNL	120
FLKQMLERYQ	NNSPPNDDQ	WKNNGVTKTW	DRLMLQDNCC	GVNGPSDWQK	YTSAPRTENN	180
DADYFPWRQC	CVMNNLKEPL	NLEACKLGVP	GFYHNQGCYE	LIISGPMNRHA	WGVANWFGPAI	240
LCWTFVWLLG	TMFYWSRIEY					

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

35
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1	11	21	31	41	51	
GCCGGACAGA	TCTGCGCGTA	TCCTGGAGCC	GGCCCAAGTTG	TGAAGTAGGA	GAGCTTTGGG	60
ACCTCTGTCC	CAAGCAAGAG	AGATGAATGG	AGAGTATAGA	GGCAGAGGAT	TTGGACGAGG	120
AAGATTTCAA	AGCTGGAAAA	GGGGAAGAGG	TGGTGGGAAC	TTCTCAGGAA	AATGGAGAGA	180
AAGAGAACAC	GACCTGATC	TGAGTAAAC	CACAGGAAAA	CGTACTTCTG	AACAACCC	240
ACAGTTTTTG	CTTCAACAA	AGACCCACA	GTCAATGCAG	TCAACATGG	ATCGATTCT	300
ACCATATAAA	GGCTGGAAGC	TTTATTTCTC	TGAAGTTTAC	AGCGATAGCT	CTCCTTTGAT	360
TGAGAAGATT	CAAGCATTTG	AAAATTTTTT	CACAAGGCAT	ATTGATTTGT	ATGACAAGGA	420
TGAAATAGAA	AGAAAGGGAA	GTATTTTGGT	AGATTTTAAA	GAAGTACAG	AAGGTGGTGA	480
AGTAACATA	TTGATACCA	ATATAGCAAC	TGAAGTAAAG	GATGCACCTG	AGAAACCTT	540
GGCTTGATG	GGTTTGGCAA	TACATCAGG	GTTAACTAAG	GACCTTGAAA	GGCATGCAGC	600
TGAGTTACAA	GCCCAGGAAG	GATTGTCTAA	TGATGGAGAA	ACAATGGTAA	ATGTGCCACA	660
TATTCATGCA	AGGGTGTACA	ACTATGAGCC	TTTGACACAG	CTCAAGAAATG	TCAGAGCAAA	720
TTACTATGGA	AAATACATG	CTCTAAGAGG	GACAGTGGTT	CGTGTCACTA	ATATAAGGCC	780
TCTTTGCACC	AAGATGGCTT	TTCTTTGTGC	TGCATGTGGA	GAAATTCAGA	GCTTTCTCT	840
TCAGATGGA	AAATACAGT	TTCCACAAA	GTGTCCGTGTG	CCTGTGTGTC	GAGGCAGGTC	900
ATTTACTGCT	CTCCGAGCT	CTCTCTCAC	AGTTACGATG	GACTGGCAGT	CAATCAAAAT	960
CCAGGAATTG	ATGCTGATG	ATCAGAGAGA	AGCAGGTCGG	ATTCCACGAA	CAATAGAAATG	1020
TGAGCTTGTT	CATGATCTTG	TGGATAGCTG	TGTCGCGGGA	GACACAGTGA	CTATTACTGG	1080
AATTGTCAAA	GTTCTCAATG	CGGAAGAAAG	TTCTCGAAAT	AAGAATGACA	AGTGATATGT	1140
CCTTTGTAT	ATTGAAGCAA	ATTCTATTAG	TAATAGCAAA	GGACAGAAAA	CAAAGAGTTC	1200
TGAGGATGGG	TGTAAGCATG	GAATGTTGAT	GGAGTTCTCA	CTTAAAGACC	TTTATGCCAT	1260
CCAAGAGATT	CAAGCTGAAG	AAAACCTGTT	TAAACTCATT	GTCAACTCGC	TTTGCCCTGT	1320
CATTTTGGT	CATGAACCTG	TAAAGCAGG	TTTGGCATT	GCACTCTTTG	GAGGAAGCCA	1380
GAAATACGCA	GATGACAAAA	ACAGAAATCC	AAATTCGGGA	GACCCACACA	TCCTTGTGT	1440
TGGAGATCCA	GGCCTAGGAA	AAAGTCAAAAT	GCTACAGGCA	GCGTGCAATG	TTGCCCCACG	1500
TGGCGTGTAT	GTTTGTGGTA	ACACCACGAC	CACCTCTGGT	CTGACGGTAA	CTCTTTCAAA	1560
AGATAGTTCC	TCTGGAGATT	TTGCTTTGGA	AGCTGGTGCC	CTGGTACTTG	GTGATCAAGG	1620
TATTTGTGGA	ATCGATGAAT	TTGATAAGAT	GGGGAATCAA	CATCAAGCCT	TGTTGGAAGC	1680
CATGGAGCAG	CAAAGTATTA	GTCTTGCTAA	GGCTGGTGTG	GTTTGTAGCC	TTCTTGCAAG	1740
AACCTTCCATT	ATTGCTGCTG	CAATCCAGT	TGGAGGACAT	TACAATAAAG	CCAAACAGT	1800
TTCTGAGAAAT	TAAAAATGG	GGAGTGCACT	ACTATCCAGA	TTTGATTGG	TCTTTATCCT	1860
GTTAGATACT	CCAAATGAGC	ATCATGATCA	CTTACTCTCT	GAACATGTGA	TTGCAATAAG	1920
AGCTGGAAAG	CAGAGAACCA	TTAGCAGTGC	CACAGTAGCT	CGTATGAATA	GTCAAGATTCT	1980
AAATACTTCC	GTACTTTGAG	TAGTTTCTGA	GAAGCCATTA	TCAGAAAGAC	TAAAGTGGT	2040
TCCTGGAGAA	ACAATAGATC	CCATTCCCA	CCAGCTATTG	AGAAAGTACA	TTGGCTATGC	2100
TGCGCAGTAT	GTGTACCCAA	GGCTATCCAC	AGAAGCTGCT	CGAGTTCTTC	AAGATTTTAA	2160
CCTTGAGCTC	CGGAACAGCA	GCCAGAGGTT	AAATAGCTCA	CCAATCACTA	CCAGGCAGCT	2220
GGAATCTTTG	ATTCGTCTGA	CAGAGGCACG	AGCAAGGTTG	GAATTGAGAG	AGGAAGCAAC	2280
CAAGAAGAGC	GCTGAGGATA	TAGTGGAAAT	TATGAAATAT	AGCATGCTAG	GAACCTACTC	2340
TGATGAATTT	GGGAACCTAG	ATTTGAGCG	ATCCAGCAT	GGTTCTGGAA	TGAGCAACAG	2400
GTCAACAGCG	AAAAGATTTA	TTTCTGCTCT	CAACAACGTT	GCTGAAAGAA	CTTATAATAA	2460
TATATTTCAA	TTTCATCAAC	TTGGCAGAT	TGCCAAAGAA	CTAAACATTC	AGGTTGCTGA	2520
TTTTGAAAT	TTTATGGAT	CACATAATGA	CCAGGGTTAC	CTCTTGAAAA	AAGGCCCAAA	2580
AGTTTACCAG	CTTCAAACTA	TGTAAAAGGA	CTTCAACCAAG	TTAGGGCTTC	CTGGGTTTAT	2640
TGCAGATTAA	AGCCATCTCA	GTGAAGATAT	GCGTGCACGC	ACAGACAGAC	AGACACACAC	2700
ACACACACAC	ACACACACAC	ACACACAGTC	AAATACTGTT	CTCTGAAAAA		2760
TGATGTCCCA	AAAGTATTAT	AATAGGAAAA	AAGCATTAAA	TATAATAAAC	TAATTTAAGA	2820

AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTATATC ACAGTGACTC AGGAGGCTGA 2880
 GGTGAGAGGA TTCCTTGAGG CCAGGGTTCG AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
 CATTCTCTAA AAAAAAAAAA AAAAAATTTA AACTTAGCTG GGTATGGTGG CACATGCTTA 3000
 TAGTCTCAGC TACTTGTGAG GCTGAGGCAG GAGGATTCTT TGAGCCCAGG AGTTTGAGGT 3060
 TACAGTGAGC CACAATCACA CCAATCCTG CACTCCAGCC TGGGCAATAA AGTAACTCTT 3120
 GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTGA AATAAATTCT 3180
 CCAAGGGGCT AAAAGTAAAT TACTTATAAA TTTTATATAG TTGTATTTT GACCTGCTTT 3240
 TTATATGTAT GAATATTTC TAAGTTTTC TAATCATATG AGGCATACAG ACAAATACAT 3300
 AAACCAATGA ATATATTACA TATTCTGTGT TCCAATAAAA CTTTATTTAT GGACACTAAA 3360
 ATTTGAATTT CATAAAATTT TCCCATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
 GCTATTTAAT AATAGGTTCT ATTTATTCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAAC 3480
 AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTGTGAAA GAATTTTGT TGGCTCACGG 3540
 AATTATTAGA AGGCAAGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATTT GTAAAAACCAT 3600
 GCCTTAGAAT TGGACTAAGG AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
 AGAAAGTGCT GCTGCCTCCC TGCCCCACCT TTGCCACTTC TGCAAGCAGA ATAGGTAGAA 3720
 GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTC TGCATGAGAT GCCTCCCTAA 3780
 ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAGACATCT GATTGAAAAA GGGTATGTTA 3840
 TATGCCCCCT TCATAGGCTG CTAGGGAGTT TTCCTGGTTC TACTTTCAGG TGGTGGGATC 3900
 AATAAGACCA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGCCAGCC 3960
 AAACATCAAA TCAATGTATA ATCCAAACAA CACTTTGTAA CATAACAAGA CTCAGGAAT 4020
 GTGAACCAT GTTGAGAAAT CTACTAAAT ACGGCTTCCC GCAACGAAG ATGAATGGAA 4080
 AATGTAAATA AAAAGAATCG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
 GATGTGGAGA CTATTGCCAT AGACCACAAT GTAAATTTT AAGTGAGGAA GGAAAAATCA 4200
 GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATA TCCAGAGCT TTGGGAGTTC 4260
 GAGGCAGGAG GATCACTTGA AGCCAGTTT GAGACCAGCC TATGCAACAC ATTGAGACCC 4320
 TATCTCTACA AAAAATGAGT TAGCTGGGCA CGGTGGTGCA TGCCTATTGT CCTACCTACT 4380
 GTGGAGGCTG AAGTAGGAAA TCACCTGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
 TTATACCACT GCATCCAGC CTGGGCAAGA GAGCAAGACC TTGTCTCTT

Seq ID NO: 44 Protein sequence:
 Protein Accession #: CAB55276.2

1 11 21 31 41 51
 MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK 60
 TPQSMQSTLD RFIPYKWKGL YFSEVYSDSS FLIEKIQAPE KPFTRHIDLY DKDEIERKGS 120
 ILVDFKELTE GGEVNLIPD IATELRDAPE KTLACMGLAI HQVLT KDOLER HAAELQAQEG 180
 LSNDGETMVN VPHIHARVYN YEPITQLKNV RANYYGKYIA LRGTVVRVSN IKPLCTKMAF 240
 LCAACGEIQS FPLPDGKYSL PTKCPVPVCR GRSFTALRSS PLTVTMDWQS IKIQELMSDD 300
 QREAGRIPRT IECBLVHDLV DSCVPDGTVT ITGIVKVSNA EEGSRNKNDK CMFLLYIEAN 360
 SISNSKGQKT KSSBDGCKHG MLMEFSLKDL YAIQEIQAEE NLFKLIIVNSL CPVIFGHELV 420
 KAGLALALFG GSKYADDKN RPIRGDPHI LVVGDPLGK SQMLQAACNV APRGVYVCGN 480
 TTTTSGLTVT LSKDSSSGDF ALEAGALVLG DQIGCGIDEF DKMGNOHQAL LEAMEQQSIS 540
 LAKAGVVCSL PARTSIIAAA NPFVGGHYNKA KTVSENLMKG SALLSRFDLV FILLDTNEH 600
 HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVVPGETIDP 660
 IPHQLLRKYI GYARQYVYPR LSTEAARVLQ DFYLELRKQS QRLNSSPITT RQLESILRLT 720
 EARARLELRE EATKEDAEDI VEIMKYSMLG TYSDEFNLD FERSQHGSGM SNRSTAKRFI 780
 SALNVAERT YNNIFQPHQL RQIAKELNIQ VADPFENFIGS LNDQGYLLKK GPKVYQLQTM

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_005416.1
 Coding sequence: 149..658

1 11 21 31 41 51
 ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG 60
 CTGAAGACCA GAAAGGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
 AAAGAGTGTG TCCAGCATCC TTTGAAGCAT GAGTTCTTAC CAGCAGAAGC AGACCTTTAC 180
 CCCACCACCT CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
 AATATTGTGT CCCACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAACAC 300
 AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA 360
 GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
 CAGGTCCCTG GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA 480
 ACCAGGCAGC ATCAAGGTCC CTGACCAAGG CTTATCAAG TTTCTGAGC CAGGTGCCAT 540
 CAAAGTCTCT GAGCAAGGAT ACACCAAGT TCCTGTGCCA GGCTACACAA AGCTACCAGA 600
 GCCATGTCTCT TCAACGGTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT 660
 TGGTGCACAG ACAAGCCCTT GAGAAGCCAA CCACCATGAT CTGGACACCC TCTTCCCATC 720
 TGTCTCTGTG TCTTAATTGT CTGTAGACCT TGTAAATCAGC ACATTGTAC CCCTAAGCCAT 780
 AGTCTCTCTC TTATTTGTAT CCTAAAATA CGTACTATAA AGCTTTTGT CACACACACT 840
 CTGAAGAATC CTGTAAGCCC CGAATTAAG CAGAAAGTCT TCATGGCTTT TCTGGTCTTC 900
 GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAAAGAAA TGCATGTTTC CTGCTCTTCC 960
 CTCATTAAAT TGCTTTTAAAT TCCA

Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_005407.1

1 11 21 31 41 51
 MSSYQQKQTF TPPPQLQQQQ VKQPSQPPPP EIFVPTTKEP CHSKVPQPGN TKIPEPGCTK 60
 VPEPGCTKVP EPGCTKVP EPGCTKVP EPGCTKVP EPGCTKVP EPGCTKVP 120
 GFIKFPEPGA IKVPEQGYTK VPVPGYTKLP EPCPSTVTPG PAQKQTKQK

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 5 GCGTCGTGTG CAGGCGTCCC CGGGCTGTGG ATAATTAGAC ACGTCTCTCC CTCATTGCC 60
 AAGGCTCGTT AGAATTCGCC CTAGAGCTGT ATCATGTATT TTCTTTCAAA TTAACCTTGC 120
 TTGCAATTAA GCTTAGGGAA CCAGCAACAA AAGCAAACCT GGGCCGAGGT CGTTCACGCG 180
 GAAAAATGGAT TAGAGAACT TCTTCCCAGA TTTAAGGGGA AAGATTCCTG CGGCCAGCGC 240
 TTTGGGGAAG GTGCCCGGAC CGCAGAGGCG ACGACAGGGG AGCAGGAAGC TGCTCACGGT 300
 AGTCGGCGTT GGGCGAGCG GTGGCCTTCC TCATCTGGGC GATGTGGGCT CCTAGAAGAG 360
 10 TAAGGATAAC ATCCTGGAAA TGACTTCTGT ACGGTTTGAG CCCAACTGCA CACTCATGAC 420
 TTGGAGCTGC CCGTGGAGT TACAGTTTAC CAAACACATT CATGAACATA ATCTCATTTA 480
 CTAAAAAATT TCTGAGAATT TTCTTTTACT AAAATTTTTT CTTATTACAA A

Seq ID NO: 48 DNA sequence:

Nucleic Acid Accession #: CAT cluster

15 1 11 21 31 41 51
 20 TTCCAAATTT TTTTCTTGT AATAAGAAAA AATTTTAGTA AAAGAAAATT CTCACAAAGT 60
 TTTTAGTAAA TGAGATTATG TTCATGAATG TGTTTGGTAA ACTGTAATC CACAGGGCAG 120
 CTCCAAGTCA TGAGTGTGCA GTTGGGCTCA AACCGTACAG AAGTCATTTC CAGGATGTTA 180
 TCCTTACTCT TCTCGAGGCC CACATCGCCC AGATGAGGAA GGCCACCGCT GCGCCCAACG 240
 CGCACTACCG TGAGCAGCTT CCGCTCCCC TGTGCTCGCC TCTGCGGTG GGGCACTTTC 300
 25 CCCAAAGCGC TGGCGCAGG AATCTTTCCC CTTAAATCGG GGAAGAAATT TCTCTAATCC 360
 ATTTTCGCGG TGAACGACCT CGGGCCAAGT TTGCTTTTGT TGCTGGTTCC CTAAGCTTAA 420
 TTGCAAGCAA AGTTAATTGT AAAGAAAATA CATGATACAG CTCTAGGGCG AATTCTAACG 480
 AGCCTTGGGC AATGAGGAA GAACGTGTCT AGTTATCCAC AGCCCCGGGA CGCCTGCACA 540
 CGACGCT

Seq ID NO: 49 DNA sequence

Nucleic Acid Accession #: CAT cluster

30 1 11 21 31 41 51
 35 TCTTCTTCT GCTGCTCGTT TGTCTCTCT GTGCTCTCT TCTTCTTTC CTGCGCGCT 60
 CCTGCGGACC TCTGTGTCT CTTCTCTGAT GGCAGGGGGC GGGAGAAGCT GACCGGTGAG 120
 ACCGTAGACC CGAAACCAT GGGGTGTACA AGCCGGTCCG CGGCTTTTTT GGGAGAAGCC 180
 GACACATGCA GACCACTTTT CCGGAACNG CATGACCATG TTATTACTAT GGGCCGCTTC 240
 40 CCCAACCAAA GTGTTTAAA CTTTTTAGGG CACCCCCAAA ATTTTTTTTT TTTTTTTTTT 300
 TTCAATTAAA AAACCTAAT ATTTATATTA AATACAAAGA TACCCAAACC CTTTATGCTT 360
 CTTTCTCTGA TCTGTCTCT TTTTCTTTGA CAGCATCTCC ATTTTTTTTT TGCTGCTTCA 420
 TCGCTGTAGC CATGGGAATC CGTTTCATTA TTATGCTAGC AATATGGAGT GCTGTATTCC 480
 TAAAGAACT GACACAGGAG AATCACTTGA ACTTGGGAGG CAGAGTTTGC AGTGAGCCGA 540
 GATTGAACCA GTGCACTCCA GCCTTGGCAG CGGAGCAAGA TTCTGTACA GTTCCTGAAG 600
 45 TGCTGGTATC GTCTGCAGC CCCATCCTCG GTTCCATTGC GCTGCCAGGC AGGGTGCTGG 660
 GACGTGGGGA GAGCTGGTCT ATATATCCCG GTGAAGCTCA GCTGTGGCAC ACCTTGGATG 720
 CCGGCTCTCT CCGGCCCCCG GGGACCTAGT ATTTTGTCCA CGAGTGTACA CCAACAAAG 780
 GAGACAGCAT CATTATGAG CCTGCAGCAT CCACCCTACT GCTGTATCCA GTTTCATTG 840
 ACTG

Seq ID NO: 50 DNA sequence

Nucleic Acid Accession #: L05187

Coding sequence: 1991..2260

55 1 11 21 31 41 51
 CTGCAGGGAG GCAGGTAGAA AAGGCTTTTG GGTTTTCAGG TGGGGGGCAG TCTAGCCTGA 60
 TCAGAAAGGA GGAAGAGGCC AGGGCAGATG TCTGGGTGGA GTGAAGGGAA AAAGTGATCC 120
 60 CAGAAGAAGG ATTAGCCCTT GAAAGTCCCT GAAAGTAGGAG AAGGGTAAAG GTGTGGTTGG 180
 TGAAGGAAAG CAGGTTTTCC CAGATTAGCA ACCAGTCAGG GGGAGGAAGG TGAGAGTGGG 240
 AGAGTCATAA GTAAATTATT CTGAATGTGT GTAGTTTAAT GGAATTGGGA AAAAGATGGG 300
 GGAATATGGAT GGAAGGTCCT GGACTCTGAG ACAAGGGGTC TATAATCAGT CCATTTCATT 360
 ATTTCTAGCT TCCACCTTCA CCAAGGCAGA CAAGGAGGGC CCACCTCAGC TCCTCTGCTC 420
 65 CCCCTCCCTT TCCCACCTAT TCATGTGTGC AAGAGTGCCC TGTCCCACAG AACACGGGGA 480
 ACAACCATCT CAATGACAAG GACAGCAGGT GGCAAGGCTC AACAGGACTC AGATGTCCTC 540
 CCAGGGTTAA CTCATGAAAC CCTCCATGAA GCCTGCTGCT CACCCCTCCC TCAAGGCAAG 600
 CCTGCACTCT GGGTCTGAGG ATGAGGGTGG CAGTGAAAT TAGGCCAGTG ACATCATTTT 660
 CAGCCAGCTA GTGCCAAAAA ATATCAGGTG GTGTTTATCA AATAAGCCGA GCCAACCGGT 720
 70 GATGAGGATG GTAGTGTGAG TCATGTGTGA CAGGTGAGGA ATGAAAACAG AGTGCCCGAG 780
 AGCTTCTATT TCCTTGAGGC AGGGCTCATT CATCTTATAA AAGCCAGCTG GCCATTGCCT 840
 TCACACCAAA CCCAAGGGAC CACACAGCCC ATTCTGCTCC GTATACCAGG TAAGTCTCTG 900
 ATTGCAACAA ACTGGCAATT CTAGTGTACT TTTTCATTAT TAGAAATTAG CTAAAGGCAA 960
 ATATGTGTAA GCAGGTAAAT CCAGGGTTTC AATGGGAGAT AGAGAATAGT GGAATATCTT 1020
 75 TATTTTAAGT TAAATTACAG TCTGGATTG AAAGGACCTT AGAGATGGTT AGGGCTCCCA 1080
 CCTCAGTAGA TAGTCATTGA ACTGGGAGTC CTGGAGAAGA TTGTTCAAAT GCCCATGGGA 1140
 AGTTCATAGC AGAATAGAAA CTCAGGCCAG AGCACTCTCA GTAACACTGC AATTTCCCCC 1200
 TGACAAGATA TTTATAGAAA TTTTAATTGA TTAGATGGAT CTCTACTGAG CATTATTATC 1260
 ATTTAAGGCA GTATGCTAGG CACTTTGGAC AAATCAATGC CCTAACGTAC TTAATTAAAC 1320
 AACATAAAAC CTAGCAGGAA GGTAAATACAT ATATATAAAT AATGAAATG CAAAGTAGAT 1380
 80 AGTAATTGGC ATGACGGAGA TGGGCGAGGA AGGGCTGTGC ACTTTTGGGA GACTTGCTCA 1440
 AGGAGACCTC TAGGGTGTCA AGTGATGTGA GCTATGATGG AGGGGTATTT GGACAAGCAG 1500
 AGATGGGAAG AAAAGCATTT GGAAGGGACT GTGTAAGCAC AGACCAGAAG CAAACCCATA 1560
 GAGGCTTAGA TGAATATAAA GCCATCCTAT AAGTCACAGG CTTTCTACAT GGTACTAGGA 1620
 85 GAGGAAAGTG GTCTGATGCC ATTTTCCAAA AGACCTAATA TGCGGACCTC ATGTCCCTCA 1680
 GAAGCCAGCT TAGTAGGGC ATTTTCCAG AACAGATATA AGGTGCCTTG GGTAGGAAGG 1740
 GAGCCAAAGAA GAGAATCCA ATAAATGGA GCAGAAGAAA TTGCTTTTA GCTCCTCCTC 1800
 TTCAAAGGCG CTGAAATTA TCCAAGCTTA TTTTATTTTT AAATGTAATG GGGGAGCTAA 1860

GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920
 TTGTATCCAT CTTTCTTTAA TTGAATCACT GTGTCAGCTT TCTGTCTCTA GAAAAAACA 1980
 CATTTGAAGC ATGAATTCCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040
 GCAGCAGCAG GTGAAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAC 2100
 CAAGGAGCCC TGCCAACCCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160
 CCAGCCCAAG ATTCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT 2220
 CACTCCAGCA CCAGCCAGC AGAAGACCAA GCAGAAGTAA TGTGGTCCAC AGCCATGCC 2280
 TTGAGGAGCT GGCCACTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATTT 2340
 GCCTATTGAC CCTGCAGTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTTGACCT 2400
 CTAAGAGAT GTCCCTTACC CTCATTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460
 GTCTCACTGA CTGAGCTAGT CTTCTGTGTG CTCGGGTGCA TTTGAGGATG GATTGCGGGA 2520
 AGGTCAAGTG ACCATCCCTA G

Seq ID NO: 51 Protein sequence:
 Protein Accession #: AAC26838

1 11 21 31 41 51
 | | | | |
 MNSQQQKQPC TPPPQPOQQQ VKQPCQPPPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
 IPEPCQPKVP EPCPSTVTPA PAQQKTKQK

Seq ID NO: 52 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120-473

1 11 21 31 41 51
 | | | | |
 CAATACAGCT AAGGAATTAT CCCTTGTAAG TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 TCAATGGACA AGATCCCCTT AAAGGACAAG TTTCAAGTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC ATGCAAGGT CCACTCTCCA CTAGCCTGG CTCTGCCCTT ATTATCTTGA 360
 TCCGGTGGCG CATGTGTAAG CCCCTAACC GCTGCTTGA AGATACTGAC TGCCCAAGAA 420
 TCAAGAAGTG CTGTGAAGGC TCTTGGCGGA TGGCCTGTTT CGTTCCCCAG TGAAGGAGC 480
 CGGTCTTGC TGCACTGTG CCGTCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCCTT CCCCTTCCA CACTGTCCAT TCTTCTCTCC ATTCAGGATG CCCACGGCTG 600
 GAGCTGCCTC TCTCATCCAC TTTCCAATAA A

Seq ID NO: 53 Protein sequence:
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 | | | | |
 MRASSFLIVV VFLIAGTLVL EAAVTGVPVK QQDITVGRVP FNGQDPVKQ VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCGSGC MACFVPQ

Seq ID NO: 54 DNA sequence
 Nucleic Acid Accession #: NM_019618
 Coding sequence: 75-584

1 11 21 31 41 51
 | | | | |
 GGCACGAGCC ACGATTCACT CCCCTGGACT GTAGATAAAG ACCCTTCTT GCCAGGTGCT 60
 GAGACAACCA CACTATGAGA GGCACTCCAG GAGACGCTGA TGGTGGAGGA AGGGCGTCT 120
 ATCAATCAAT GTGTAAACCT ATTACTGGGA CTATTAATGA TTTGAATCAG CAAGTGTGGA 180
 CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAAGTCACTG 240
 TGTCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT 300
 ATTTGGGAAT CCAGAATCCA GAAATGTGTT TGTATTGTGA GAAGGTGGA GAACAGCCCA 360
 CATTGCAGCT AAAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCCGTGAAAC 420
 CCTTCTTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC 480
 CGGACTGGTT CATTGCCTCC TCCAAGAGAG ACCAGCCCAT CATTCTGACT TCAGAACTTG 540
 GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAACCTAG CCTAGAGGTG 600
 GCAGCTTGGT CTTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTTCGTCT ACATTTTCTT 660
 AGTGTCAATT TCAGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720
 TAATGAAGAA GAAGCAATTA CTTATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA 780
 GGAGAGCTGG GTGGTATAAG GCTGTCCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT 840
 CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900
 TGAAGATGCT TCAGAGCTCA TGCGCGTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT 960
 CTCTGTTTCT TTTTGTCTT ATCCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG 1020
 CCAATATACC TCATTGTGTG TAATAGAACC TTCTTAGCAT TAAGACCTTG TAAACAAAAA 1080
 TAATTCTTGT GTTAAGTTAA ATCATTTTGT TCCTAATTGT AATGTGTAAT CTTAAAGTTA 1140
 AATAAACTTT GTGATTTTAT ATAATAAAAA AAAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:
 Protein Accession #: NP_062564

1 11 21 31 41 51
 | | | | |
 MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGG NLVAVPRSDS VTPVTVAVIT 60
 CKYPEALEQG RGDPIYLIQ NPENCLYCEK VGEQPTLQLK EQKIMDLYGQ PEPVKPFLFY 120
 RAKTGRTSTL ESVAPFDWFI ASSKRDQPII LTSELGKSYN TAFELMIND

Seq ID NO: 56 DNA sequence
 Nucleic Acid Accession #: NM_003125
 Coding sequence: 65-334

	1	11	21	31	41	51	
5	AGCAGTTCTA	AGGGACCATA	CAGAGTATTC	CTCTCTTCAC	ACCAGGACCA	GCCACTGTTG	60
	CAGCATGAGT	TCCCAGCAGC	AGAAGCAGCC	CTGCATCCCA	CCCCCTCAGC	TTCAGCAGCA	120
	GCAGGTGAAA	CAGCCTTGCC	AGCCTCCACC	TCAGGAACCA	TGCATCCCCA	AAACCAAGGA	180
	GCCCTGCCAC	CCCAAGGTGC	CTGAGCCCTG	CCACCCCAAA	GTGCCTGAGC	CCTGCCAGCC	240
	CAAGCTTCCA	GAGCCATGCC	ACCCCAAGGT	GCCTGAGCCC	TGCCCTTCAA	TAGTCACTCC	300
10	AGCACCAGCC	CAGCAGAGA	CCAAGCAGAA	GTAATGTGGT	CCACAGCCAT	GCCCTTGAGG	360
	AGCCGGCCAC	CAGATGCTGA	ATCCCCATATC	CCATTCTGTG	TATGAGTCCC	ATTTGCGTTG	420
	CAATTAGCAT	TCTGTCTCCC	CCAAAAAAGA	ATGTGCTATG	AAGCTTTCTT	TCCTACACAC	480
	TCTGAGTCTC	TGAATGAAGC	TGAAGGTCCT	AGTACCAGAG	CTAGTTTCTA	GCTGCTCAGA	540
	ATTTCATCTG	AGAGAGACTT	AAGATGAAAG	CAATGATTTC	AGCTCCCTTA	TACCCCCATT	600
15	AAATTCACCT	TCAATTCCA					

Seq ID NO: 57 Protein sequence:
Protein Accession #: NP_003116

	1	11	21	31	41	51	
20	MSSQQQKQPC	IPPPQLQQQQ	VKQPCQPPPP	EPCIPKTKEP	CHPKVPEPCH	PKVPEPCQPK	60
25	LPEPCHPKVP	EPCPSIVTPA	PAQQKTKQK				

Seq ID NO: 58 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71-2560

	1	11	21	31	41	51	
30	AAAGGGGCAA	GAGCTGAGCG	GAACACCGGC	CCGCCGTGCG	GGCAGCTGCT	TCACCCCTCT	60
	CTCTGCAGCC	ATGGGGCTCC	CTCGTGGACC	TCTCGCGTCT	CTCCTCCTTC	TCCAGGTTTG	120
	CTGGCTGCAG	TGCGCGCGCT	CCGAGCCGTG	CCGGGCGGTC	TTCAGGGAGG	CTGAAGTGAC	180
35	CTTGGAGGCG	GGAGGCGCGG	AGCAGGAGCC	CGGCCAGGCG	CTGGGGAAGG	TATTCATGGG	240
	CTGCCCTGGG	CAAGAGCCAG	CTCTGTCTAG	CACCTGATAAT	GATGACTTCA	CTGTGCGGAA	300
	TGGCGAGACA	GTCCAGGAAA	GAAGGTCACT	GAAGGAAAGG	AATCCATTGA	AGATCTTCCC	360
	ATCCAAACGT	ATCTTACGAA	GACACAAGAG	AGATTGGGTG	GTGTCTCCAA	TATCTGTCCC	420
40	TGAAAATGGC	AAGGTCCTCT	TCCCCCAGAG	ACTGAATCAG	CTCAAGTCTA	ATAAAGATAG	480
	AGACACCAAG	ATTTTCTACA	GCATCACGGG	GCCGGGGGCA	GACAGCCCCC	CTGAGGGTGT	540
	CTTCGCTGTA	GAGAGGAGGA	CAGGCTGGTT	GTTGTTGAAT	AAGCCACTGG	ACCGGGAGGA	600
	GATTGCCAAG	TATGAGCTCT	TTGGCCACGC	TGTGTCAAGG	AATGGTGCCT	CAGTGGAGGA	660
	CCCCATGAAC	ATTCTCCATCA	TCGTGACCGA	CCAGAATGAC	CACAAGCCCA	AGTTTACCCA	720
	GGACACCTTC	CGAGGGAGTG	TCTTAGAGGG	AGTCTTACCA	GGTACTTCTG	TGATGCAGGT	780
45	GACAGCCACG	GATGAGGATG	ATGCCATCTA	CACCTACAAT	GGGGTGGTTG	CTTACTCCAT	840
	CCATAGCCAA	GAACCAAGAG	ACCCACACGA	CCTCATGTTC	ACCATTCAAC	GGAGCACAGG	900
	CACCATCAGC	GTCTATCTCA	GTGGCCTGGA	CCGGGAAAAA	GTCCCTGAGT	ACACACTGAC	960
	CATCCAGGCC	ACAGACATGG	ATGGGGACGG	CTCCACCACC	ACGGCAGTGG	CAGTAGTGGA	1020
	GATCCTTGAT	GCCAAATGACA	ATGCTCCCAT	GTTTGACCCC	CAGAAGTAGC	AGGCCCATGT	1080
50	GCCTGAGAA	GAGTGGGCCC	ATGAGGTGCA	GAGGCTGACG	GTCACTGATC	TGGACGCCCC	1140
	CAACTCACCA	GCGTGGCGTG	CCACCTACCT	TATCATGGGC	GGTGACGACG	GGGACCATT	1200
	TACCATCACC	ACCCACCTCT	AGAGCAACCA	GGGCATCCTG	ACAACCAGGA	AGGGTTTGGA	1260
	TTTGTAGGCC	AAAAACCTCA	CAGCCACCAT	AGTGGTCCAC	GTGGAGGATG	TGAATGAGGC	1320
55	GCTGAAGCTC	CCAACCTCCA	CAGCCACCAT	AGTGGTCCAC	GTGGAGGATG	TGAATGAGGC	1380
	ACCTGTGTTT	GTCCACCTCT	CCAAAGTCGT	TGAGGTCCAG	GAGGGCATCC	CCACTGGGGA	1440
	GCCTGTGTGT	GTCTACACTG	CAGAAGACCC	TGACAAGGAG	AATCAAAAGA	TCAGCTACCG	1500
	CATCCTGAGA	GACCCAGCAG	GGTGGCTAGC	CATGGACCCA	GACAGTGGGC	AGGTCAACGC	1560
	TGTGGGCACC	CTGACCGGTG	AGGATGAGCA	GTTTGTGAGG	AACAACATCT	ATGAAGTCAT	1620
	GGCTTTGGCC	ATGACCAATG	GAAGCCCTCC	CACCACTGGC	ACGGGAACCC	TTCTGCTAAC	1680
60	ACTGATTGAT	GTCAATGACC	ATGGCCCATG	CCCTGAGCCC	CGTCAGATCA	CCATCTGCAA	1740
	CCAAAGCCCT	GTGCGCCAGG	TGCTGAACAT	CACGGACAAG	GACCTGTCTC	CCCACACCTC	1800
	CCCTTTCCAG	GCCCAGCTCA	CAGATGACTC	AGACATCTAC	TGGACGGCAG	AGGTCAACGA	1860
	GGAAGGTGAC	ACAGTGGTCT	TGTCCCTGAA	GAAGTTCTTG	AAGCAGGATA	CATATGACGT	1920
	GCACCTTTCT	CTGTCTGACC	ATGGCAACAA	AGAGCAGCTG	ACGGTGATCA	GGGCCACTGT	1980
65	GTGCGACTGC	CATGGCCATG	TCGAAACCTG	CCCTGGACCC	TGGAAGGGAG	GTTTCATCCT	2040
	CCCTGTGCTG	GGGGCTGTCC	TGGCTCTGCT	GTTCTCTCTG	CTGGTGTGCT	TTTGTGTTGT	2100
	GAGAAAGAAG	CGGAAGATCA	AGGAGCCCTT	CCTACTCCCA	GAAGATGACA	CCCGTGACAA	2160
	CGTCTTCTAC	TATGGCGAAG	AGGGGGGTGG	CGAAGAGGAC	CAGGACTATG	ACATCACCCA	2220
	GCTCCACCGA	GGTCTGGAGG	CCAGGCCCGA	GGTGGTCTCT	CGCAATGACG	TGGCACCAAC	2280
70	CATCATCCCG	ACACCCATGT	ACCGTCTCTG	GCCAGCCAAC	CCAGATGAAA	TCGGCAACTT	2340
	TATAATTGAG	AACCTGAAAG	CGGCTAACAC	AGACCCCAAC	GCCCCGCCCT	ACGACACCTT	2400
	CTTGGTGTTC	GACTATGAGG	GCAGCGGCTC	CGACGCCGCG	TCCCTGAGCT	CCCTCACCTC	2460
	CTCCGCCCTC	GACCAAGACC	AAGATTACGA	TTATCTGAAC	GAGTGGGGCA	GCCGCTTCAA	2520
	GAAGCTGGCA	GACTGTGACG	GTGGCGGGGA	GGACGACTAG	GCGGCTGTCC	TGCAGGGCTG	2580
75	GGGACCAAAC	GTCAGGCCAC	AGAGCATCTC	CAAGGGGTCT	CAGTTCCCCC	TTCACTGAGT	2640
	GACTTCGGAG	CTTGTTCAGG	AGTGGCCGTA	GCAACTTGGC	GGAGACAGGC	TATGAGTCTG	2700
	ACGTTAGAGT	GTTTGTCTTC	TTAGCCCTTC	AGGATGGAGG	AATGTGGGCA	GTTTGACTTC	2760
	AGCACTGAAA	ACCTCTCCAC	CTGGGCCAGG	GTTGCCTCAG	AGGCCAAGTT	TCCAGAAGCC	2820
	TCTTACCTGC	CGTAAATATG	TCAACCTCTG	GTCCTGGGCC	TGGGCTGTCT	GTGACTGACC	2880
80	TACAGTGGAC	TTTCTCTCTG	GAATGGAACC	TTCTTAGGCC	TCTGTGTGCA	ACTTAATTTT	2940
	TTTTTTTAA	GCTATCTTCA	AAACGTTAGA	GAAAGTTCTT	CAAAAGTGCA	GCCCAGAGCT	3000
	GCTGGGCCCA	CTGGCCGTCC	TGCATTTCTG	GTTTCCAGAC	CCCAATGCCT	CCCATTCCGA	3060
	TGGATCTCTG	CGTTTCTCTG	CTGAGTGTGC	CTAGGTTGCC	CCTTATTTT	TATTTTCCCT	3120
85	GTTGCGTTGC	TATAGATGAA	GGGTGAGGAC	AATCGTGTAT	ATGTACTAGA	ACTTTTTTTAT	3180
	TAAAGAAACT	TTTCCAGAAA	AAAAA				

Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

1	11	21	31	41	51	
5	MGLPRGPLAS	LLLLQVCWLQ	CAASEPCRAV	FREAETVLEA	GGAEQEPGQA	LGKVFMGCPG 60
	QEPALFSTDN	DDFTVRNGET	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG 120
	KGFFPQRLNQ	LKSNKORDTK	IFYSITGPGA	DSPPEGVFAV	EKETGWLLEN	KPLDREEIAK 180
	YELFGHAVSE	NGASVEDPMN	ISIIIVTDQND	HKPKFTQDTP	RGSVLEGVLP	GTSVMQVTAT 240
10	DEDDAIYTYN	GVVAYSIHSQ	EPKDPHDLMP	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA 300
	TDMGDGSGTT	TAVAVVEILD	ANDNAPMFDP	QKYEAHVPEN	AVGHEVQRLT	VTDLDPNSP 360
	AWRATYLMG	GDDGDHFTIT	THPESNQIL	TTRKGLDFEA	KNQHTLYVEV	TNEAPFVLKL 420
	PTSTATIVH	VEDVNEAPVF	VPPSKVVEVQ	EGIPTGEFVC	VYTAEDPDKE	NQKISYRILR 480
	DPAGWLAMP	DSGQVAVGT	LDREDEQFVR	NNIYEVMLA	MDNGSPPTTG	TGTLTLTLID 540
	VNDHGFVPEP	RQITICNQSP	VRQLNITDK	DLSPHTSPFQ	AQLTDDSDIY	WTAEVNEEGD 600
15	TVVLSLKKFL	KQDITYDVHLS	LSDHGNKEQL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL 660
	GAVLALLFLL	LVLLLLVRKK	RKIKEPLLLP	EDDTRDNVFI	YGEEGGGEED	QDYDITQLHR 720
	GLEARPEVLL	RNDVAPTIIIP	TPMYRPRPAN	PDEIGNFIIIE	NLKAANTDPT	APPYDTLLVF 780
	DYEGSGSDAA	SLSSLTSSAS	DQDQDYDILN	EWGSRFKKLA	DMYGGGEDD	

Seq ID NO: 60 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 162-428

1	11	21	31	41	51	
25	GCGTTCGGTT	GGCGGCGGAT	TCGAACGTTT	GGACTGAGGT	TTTTCTGCCT	GAAGAAGCGT 60
	CATACGGACC	GGATTGTPTT	CGCTGGCCCA	GTGTCCCGG	AGCTTGTGTG	CGATACAGAG 120
	AGCACCTCGG	AAGCTGAGGC	AGCTGGTACT	TGACAGAGAG	GATGGCGCTG	TCGACCATAG 180
	TCTCCAGAG	GAGCGGAGG	AAGCGGAAGG	CTCCCCGTGG	CTTTCTAAAG	CGAGTCTTCA 240
30	AGCGAAAGAA	GCCTCAACTT	CGTCTGGAGA	AAAGTGGTGA	CTTATTGGTC	CATCTGAACT 300
	GTTTACTGTT	TGTTTCATCGA	TTAGCAGAAG	AGTCCAGGAC	AAACGCTTGT	GCGAGTAAAT 360
	GTAGAGTCAT	TAACAAGGAG	CATGTACTGG	CCGCAGCAAA	GGTAATCTTA	AAGAAGAGCA 420
	GAGGTTAGAA	GTCAAAGAAC	ATATTCTTGA	AAGTTATGAT	GCATTCTTTT	GGGTGGTAAC 480
	AGATCATAAA	GACATTTTTT	ACACATCAGT	TAATATGGGA	TTATTAATAA	TTGG

Seq ID NO: 61 Protein sequence:
Protein Accession #: Eos sequence

1	11	21	31	41	51	
40	MALSTIVSQR	KQIKRKAPRG	FLKRVFKRKK	PQLRLEKSGD	LLVHLNCLLF	VHRLAESRST 60
	NACASKCRVI	NKEHVLAAAK	VILKRSRG			

Seq ID NO: 62 DNA sequence
Nucleic Acid Accession #: NM_000094.2
Coding sequence: 99-8933

1	11	21	31	41	51	
50	GGGCTGGAGG	GGCGCTGGGC	TCGGACCTGC	CAAGGCCACC	GCAGGGGGGA	GCAAGGGACA 60
	GAGGCGGGGG	TCCTAGCTGA	CGGCTTTTAC	TGCCTAGGAT	GACGCTGCGG	CTTCTGGTGG 120
	CCGCGCTCTG	CGCCGGGATC	CTGGCAGAGG	CGCCCCGAGT	GCGAGCCGAG	CACAGGGAGA 180
	GAGTGACCTG	CACGCGCCTT	TACGCCGCTG	ACATTGTGTT	CTTACTGGAT	GGCTCCTCAT 240
	CCATTGGCCG	CAGCAATTTC	CGCGAGGTCC	GCAGCTTTCT	CGAAGGGCTG	GTGCTGCCTT 300
55	TCTCTGGAGC	AGCCAGTGCA	CAGGGTGTGC	GCTTTGCCAC	AGTGCAGTAC	AGCGATGACC 360
	CACGGACAGA	GTTCCGCGTG	GATGCACCTG	GCTCTGGGGG	TGATGTGATC	CGCGCCATCC 420
	GTGAGCTTAG	CTACAAGGGG	GGCAACACTC	GCACAGGGGC	TGCAATTCTC	CATGTGGCTG 480
	ACCATGTCTT	CCTGCCCCAG	CTGGCCCGAC	CTGGTGTCCC	CAAGGTCTGC	ATCCTGATCA 540
	CAGACGGGAA	GTCCCGAGAC	CTGGTGGACA	CAGCTGCCCA	AAGGCTGAAG	GGCGAGGGGG 600
60	TCAAGCTATT	TGCTGTGGGG	ATCAAGAATG	CTGACCCCTG	GGAGCTGAAG	CGAGTTGCCT 660
	CACAGCCAAC	CTCCGACTTC	TTCTTCTTCG	TCAATGACTT	CAGCATCTTG	AGGACACTAC 720
	TGCCCCCTCG	TTCGCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCTGTG	ACCCGACCTC 780
	CGGATGACTC	GACCTCTGCT	CCACGAGACC	TGGTGTCTGC	TGAGCCAAGC	AGCCAATCCT 840
	TGAGAGTACA	GTGGACAGCG	GCCAGTGGCC	CTGTGACTGG	CTACAAGGTC	CAGTACACTC 900
65	CTCTGACGGG	GCTGGGACAG	CCACTGCCGA	GTGAGCGGCA	GGAGGTGAAC	GTCCGACCTG 960
	GTGAGACCAG	TGTGCGGCTG	CGGGGTCTCC	GGCCACTGAC	CGAGTACCAA	GTGACTGTGA 1020
	TTGCCCTCTA	CGCCAACAGC	ATCGGGGAGG	CTGTGAGCGG	GACAGCTCGG	ACCACTGCCC 1080
	TAGAAGGGCC	GGAACTGACC	ATCCAGAATA	CCACAGCCCA	CAGCCTCCTG	GTGGCCTGGC 1140
	GGAGTGTGCC	AGGTGCCACT	GGCTACCGTG	TGACATGGCG	GGTCTCAGT	GGTGGGCCCA 1200
70	CACAGCAGCA	GGAGCTGGGC	CCTGGGCAGG	GTTTCACTGT	GCTGCGTGAC	TTGGAGCCTG 1260
	GCACCGGACTA	TGAGGTGACC	GTGAGCACCC	TATTGGCCG	CAGTGTGGGG	CCCGCACTT 1320
	CCCTGATGGC	TCGCACTGAC	GCTTCTGTG	AGCAGACCCT	GCGCCCGGTC	ATCCTGGGCC 1380
	CCACATCCAT	CCTCTTTTTC	TGGAACCTTG	TGCCTGAGGC	CCGTGGCTAC	CGGTTGGAAT 1440
	GGCGGGGTGA	GACTGGCTTG	GAGCCACCGC	AGAAGGTGGT	ACTGCCCTCT	GATGTGACCC 1500
75	GCTACCAGTT	GGATGGGCTG	CAGCCGGGCA	CTGAGTACCG	CCTCACACTC	TACACTCTGC 1560
	TGGAGGGCCA	CGAGGTGGCC	ACCCCTGCAA	CCGTGGTTCC	CACTGGACCA	GAGCTGCCTG 1620
	TGAGCCCTGT	AACAGACCTG	CAAGCCACCG	AGCTGCCCGG	GCAGCGGGTG	CGAGTGTCTT 1680
	GGAGCCCACT	CCCTGGTGCC	ACCCAGTACC	GCATCATTTG	GCGCAGCACC	CAGGGGGTTG 1740
	AGCGGACCTT	GGTGCTTCTT	GGGAGTCAGA	CAGCATTCGA	CTTGGATGAC	GTTTCAAGCTG 1800
80	GGCTTAGCTA	CACTGTGCGG	GTGTCTGCTC	GAGTGGGTCC	CCGTGAGGGC	AGTGCCAGTG 1860
	TCCTCACTGT	CGCCGGGGAG	CCGGAAACTC	CACTTGTCTG	TCCAGGGCTG	CGGGTTGTGG 1920
	TGTTCAGATG	AACGCGAGTG	AGGGTGGCCT	GGGGACCCGT	CCCTGGAGCC	AGTGGATTTC 1980
	GGATTAGCTG	GAGCACAGGC	AGTGGTCCGG	AGTCCAGCCA	GACACTGCCC	CCAGACTCTA 2040
	CTGCCACAGA	CATCACAGGG	CTGCAGCCTG	GAACCACTA	CCAGGTGGCT	GTGTCCGTAC 2100
85	TGCGAGGCAG	AGAGGAGGGC	CCTGTCTCAG	TCATCGTGGC	TGGAACGGAG	CCACTGGGCC 2160
	CAGTGAGGAC	GGTCATGTG	ACTCAGGCCA	GCAGCTCATC	TGTACCAATT	ACCTGGACCA 2220
	GGGTTCTCTG	CGCCACAGGA	TACAGGGTTT	CCTGGCACTC	AGCCACGGC	CCAGAGAAAT 2280

	CCCAGTTGGT	TTCTGGGGAG	GCCACGGTGG	CTGAGCTGGA	TGGACTGGAG	CCAGATACTG	2340
	AGTATACGGT	GCATGTGAGG	GCCCATGTGG	CTGGCGTGGA	TGGGCCCTCT	GCCTCTGTGG	2400
	TTGTGAGGAC	TGCCCTTGAG	CCTGTGGGTC	GTGTGTGAG	GCTGCAGATC	CTCAATGCTT	2460
5	CCAGCGACGT	TCTACGGATC	ACCTGGGTAG	GGGTCACTGG	AGCCACAGCT	TACAGACTGG	2520
	CTTGGGGCCG	GAGTGAAGGC	GGCCCCATGA	GGCACCAGAT	ACTCCAGGA	AACACAGACT	2580
	CTGCAGAGAT	CCGGGGTCTC	GAAGGTGGAG	TCAGCTACTC	AGTGGAGTG	ACTGCACTTG	2640
	TCGGGGACCG	CGAGGGCACA	CCTGTCTCCA	TTGTTGTAC	TACGCCGCT	GAGGCTCCG	2700
	CAGCCCTGGG	GACGCTTAC	GTGGTGCAGC	GCGGGGAGCA	CTCGCTGAGG	CTGCGCTGGG	2760
10	AGCCCGTGCC	CAGAGCGCAG	GGCTTCCTTC	TGCACTGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
	AGTCCCGGGT	CCTGGGGCCC	GAGCTCAGCA	GCTATCACCT	GGACGGGCTG	GAGCCAGCGA	2880
	CACAGTACCG	CGTAGGGCTG	AGTGTCTTAG	GGCCGGCTGG	AGAAGGGCCC	TCTGCAGAGG	2940
	TGACTGCGCG	CACTGAGTCA	CCTCGTGTTC	CAAGCATTGA	ACTACGTGTG	GTGGACACCT	3000
	CGATCGACTC	GGTGACTTTG	GCCTGGACTC	CAGTGTCCAG	GGCATCCAGC	TACATCCTAT	3060
15	CCTGGCGGCC	ACTCAGAGG	CCTGGCCAGG	AAGTGCCTGG	GCTCCGCGAG	ACACTTCCAG	3120
	GGATCTCAAG	CTCCACAGCG	GTGACAGGGC	TAGAGCCTGG	CGTCTCTTAC	ATCTTCTCCC	3180
	TGACGCGTGT	CCTGGATGGT	GTGCGGGGTC	CTGAGGCATC	TGTACACAG	ACGCCAGTGT	3240
	GCCCGCGTGG	CTTGGCGTGG	GTGGTGTTC	TACCACATGC	CACCTAAGAG	AATGCTCACC	3300
	GTGCGGAGGC	TACGAGGAGG	GTCTGTGAGC	GTCTGGTGT	GGCACTTGGG	CCTCTTGGGC	3360
20	CACAGGCAGT	TCAGGTTGGC	CTGCTGTCTT	ACAGTCATCG	GCCCTCCCCA	CTGTTCCAC	3420
	TGAATGGCTC	CGATGAGCTT	GGCATTATCT	TGCAAGAGAT	CCGTGACATG	CCCTACATGG	3480
	ACCCAAGTGG	GAACAACCTG	GGCAGAGCGG	TGGTCACAGC	TCACAGATAC	ATGTTGGCAC	3540
	CAGATGCTCC	TGGGCGCCGC	CAGCACGTAC	CAGGGGTGAT	GGTTCGTCTA	GTGGATGAAC	3600
	CCTTGAGAGG	TGACATATT	AGCCCCATCC	GTGAGGCCCA	GGCTTCTGGG	CTTAATGTGG	3660
25	TGATGTTGGG	AATGGCTGGA	GCGGACCCAG	AGCAGCTGCG	TGCTTGGCG	CCGGTATGG	3720
	ACTCTGTCCA	GACCTTCTTC	GCCGTGGATG	ATGGGCCAAG	CCTGGACCAG	GCAGTCAGTG	3780
	GTCTGGCCAC	AGCCCTGTGT	CAGGCATCCT	TCACTACTCA	GCCCCGCCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAAGGGC	CAGAAAGGGG	AACCTGGAGA	GATGGGCTGT	AGAGGACAA	3900
	TTGGGCTCC	TGGCGACTCC	GGCCTCCCGG	GCAGGACCGG	TGCTCCCGGC	CCCCAGGGGC	3960
30	CCCTGGAAG	TGCCACTGCC	AAGGCGGAGA	GGGCTTCC	TGGAGCAGAT	GGCGCTCCAG	4020
	GCAGCCCTGG	CCGCGCCGGG	AATCCTGGGA	CCCCTGGAGC	CCCTGGCCTA	AAGGGCTCTC	4080
	CAGGGTTGCC	TGGCCCTCGT	GGGACCCCGG	GAGAGCGAGG	ACCTCGAGGG	CCAAAGGGGG	4140
	AGCCGGGGCA	TCCCGAGCAA	GTCTCGGAG	GTGAAGGACC	TGGGCTTCT	GGCGGAAAG	4200
	GGGACCCCTG	ACCATCGGGC	CCCCCTGGAC	CTCGTGGACC	ACTGGGGGAC	CCAGGACCCC	4260
	GTGGCCCCC	AGGGCTTCT	GGAACAGCCA	TGAAGGGTGA	CAAAGGCGAT	CGTGGGGAGC	4320
35	GGGGTCCCC	TGGACCTGGT	GAAGGTGGCA	TTGCTCCTGG	GGAGCCTGGG	CTGCCGGGTC	4380
	TTCCCGGAAG	CCCTGGACCC	CAAGGCCCCG	TTGGCCCCC	TGGAAGAAA	GGAGAAAAG	4440
	GTGACTCTGA	GGATGGAGCT	CCAGGCTTCC	CAGGACAACC	TGGGTCTCCG	GGTGAGCAGG	4500
	GCCACGGGG	ACCTCCTGGA	GCTATTGGCC	CCAAAGGTGA	CCGGGGCTTT	CCAGGGCCCC	4560
	TGGGTGAGGC	TGGAGAGAAG	GGCGAACGTG	GACCCCCAGG	CCCAGCGGGA	TCCCGGGGGC	4620
40	TGCCAGGGGT	TGCTGGAGCT	CCTGGAGCCA	AGGGTCTCTG	AGGGCCACCA	GGACCCACTG	4680
	GCCGCCAAGG	AGAGAAAGGG	GAGCCTGGTC	GCCCTGGGGA	CCCTGCACTG	TTGGGACCTG	4740
	CTGTTGCTGG	ACCCAAGGA	GAAAAGGGAG	ATGTGGGGCC	CGCTGGGCCC	AGAGGAGCTA	4800
	CCGGAGTCCA	AGGGGAACCG	GGCCACCCCG	GCTTGGTTCT	TCCTGGAGAC	CCTGGCCCCA	4860
45	AGGGAGACCC	TGGAGACCGG	GGTCCCATTG	GCCTTACTGG	CAGAGCAGGA	CCCCAGGTG	4920
	ACTCAGGGCC	TCCTGGAGAG	AAGGGAGACC	CTGGGCGGCC	TGGCCCCCCA	GGACCTGTTG	4980
	CGCCCCGAGG	ACGAGATGGT	GAAGTTGGAG	AGAAAGGTGA	CGAGGGTCT	CCGGGTGACC	5040
	CGGGTTTGGC	TGGAAGAGCA	GGCGAGCGTG	GCCTTCGGGG	GGCACCTGGA	GTTCGGGGGC	5100
	CTGTGGGTGA	AAAGGGAGAC	CAGGGAGATC	CTGGAGAGGA	TGGACGAAAT	GGCAGCCCTG	5160
50	GATCATCTGG	ACCCAAGGGT	GACCGTGGGG	AGCCGGGTCC	CCCAGGACCC	CCGGGACGGC	5220
	TGGTAGACAC	AGGACCTGGA	GCCAGAGAGA	AGGGAGAGCC	TGGGGACCGC	GGACAAGAGG	5280
	GTCTCTGAGG	GCCCAAGGGT	GATCCTGGCC	TCCCTGGAGC	CCCTGGGGAA	AGGGGCATTG	5340
	AAGGGTTTCG	GGGACCCCCA	GGCCACACAG	GGGACCCAGG	TGTCGAGGCG	CCAGCAGGAG	5400
	AAAAGGGTGA	CGGGGTCTCC	CCTGGGCTGG	ATGGCCGGAG	CGGACTGGAT	GGGAAACCGG	5460
55	GAGCCGCTGG	GCCCTCTGGG	CCGAATGGTG	CTGCAGGCAA	AGCTGGGGAC	CCAGGGAGAG	5520
	ACGGGCTTCC	AGGCTCTCGT	GGAGAACAAG	GCCTCCCTGG	CCCTCTGGT	CCCCCTGGAT	5580
	TACCGGGAAA	GCCAGGCGAG	CTGGGCTGAA	TGGGAAAAAC	GGAGAACCTG	GGGAAACCTG	5640
	GGGACCCCTG	AGAAGACGGG	AGGAAGGGAG	AGAAAGGAGA	TTCAGGCGCC	TCTGGGAGAG	5700
	AAGGTCTGTA	TGGCCCCAAG	GGTGAAGCTG	GAGCTCTCTG	TATCCTTGGA	CCCCAGGGGC	5760
60	CTCCAGGCTT	CGGAGGCCAG	GTGGGCCCTC	CTGGCCAGGG	TTTCTCTGGT	GTCCAGGAG	5820
	GCACGGGCCC	CAAGGGTGAC	CGTGGGGAGA	CTGGATCCAA	AGGGGAGCAG	GGCCTCCCTG	5880
	GAGAGCGTGG	CCTGCGAGGA	GAGCCTGGAA	GTGTGCCGAA	TGTGATCGG	TTGCTGGAAA	5940
	CTGCTGGCAT	CAAGGACTCT	GCCCTGCGGG	AGATCGTGGG	GACCTGGGAT	GAGAGCTCTG	6000
	GTAGCTTCTT	GCCTGTGCCC	GAACGGCGTC	GAGGCCCCAA	GGGGGACTCA	GGCGAACAGG	6060
	GCCCCCAGG	CAAGGAGGGC	CCCATCGGCT	TTCTTGGAGA	ACGCGGGCTG	AAGGGCGACC	6120
65	GTGGAGACCC	TGGCCTCAG	GGGCCACCTG	GTCTGGCCCT	TGGGGAGAGG	GGCCCCCCTG	6180
	GGCCTTCCGG	CCTTGGCCGG	GAGCCTGGAA	AGCCTGGTAT	TCCCGGGCTC	CCAGGCAGGG	6240
	CTGGGGGTGT	GGGAGAGGCA	GGAAAGGCCAG	GAGAGAGGGG	AGAACGGGGA	GAGAAAGGAG	6300
	AACGTGGAGA	ACAGGCGAGA	GATGGCCCTC	CTGGACTCCC	TGGAACCCCT	GGGCCCCCTG	6360
	GACCCCTCTG	CCCCAAGGTG	TCTGTGGATG	AGCCAGGTCC	TGGACTCTCT	GGAGAACAGG	6420
70	GACCCCTCTG	ACTCAAGGGT	GCTAAGGGGG	AGCCGGGCGAG	CAATGGTGAC	CAAGGTCCCA	6480
	AAGGAGACAG	GGGTGTGCCA	GGCATCAAAG	GAGACCGGGG	AGAGCCTGGA	CCGAGGGGTC	6540
	AGGACGGCAA	CCCGGGTCTA	CCAGGAGAGC	GTGGTATGGC	TGGGCTGAA	GGGAAGCCGG	6600
	GTCTGCGAGG	TCCAAAGAGG	CCCCCTGGCC	CAGTGGGTGG	TCTGGAGAC	CCTGGACCAC	6660
75	CTGGTGGCCC	GGGTCTTGGT	GGCCTTGCA	GACCCCAAGG	ACCTTCTGGC	CTGAAGGGGG	6720
	AGCCTGGAGA	GACAGGACCT	CCAGGACGGG	GCCTGACTGG	ACCTACTGGA	GCTGTGGGAC	6780
	TTCTTGGACC	CCCCGGCCTT	TCAGGCTTGG	TGGGTCCACA	GGGGTCTCCA	GGTTTGGCTG	6840
	GACAGTGGG	GAGAGCAGGG	AAGCCGGGAG	CCCAGGTCG	AGATGGTGCC	AGTGAAGGAG	6900
	ATGGAGACAG	AGGGAGCCCT	GGTGTGCCAG	GGTCACCAGG	TCTGCCTGGC	CCTGTGCGAC	6960
80	CTAAAGGAGA	ACCTGGCCCC	ACGGGGGGCC	CTGGACAGGC	TGTGGTGGG	CTCCCTGGAG	7020
	CAAAGGGAGA	GAGAGGAGCC	CCTGGAGGCC	TTGCTGGAGA	CCTGGTGGGT	GAGCCGGGAG	7080
	CCAAAGGTGA	CCGAGGACTG	CCAGGGCCGC	GAGGCGAGAA	GGGTGAAGCT	GGCCGTGCAG	7140
	GGGAGCCCGG	AGACCTTGGG	GAAGATGGTC	AGAAAGGGGC	TCCAGGACCC	AAAGGTTTCA	7200
	AGGGTGACCC	AGGATCTGGG	GTCCCGGGCT	CCCCTGGGCC	TCCTGGCCCT	CCAGGTGTGA	7260
85	AGGGAGATCT	GGGCTTCCCT	GGCCTGCCCC	GTGCTCTGGG	TGTGTGTTGG	TTCCCGGGTC	7320
	AGACAGGCCC	TGAGGAGAGG	ATGGGTGAGC	CAGGCCCTAG	TGGAGAGCGG	GGTCTGGCAG	7380
	GCCCCCAGG	GAGAGAAGGA	ATCCAGGAC	CCCTGGGGCC	ACCTGGACCA	CCGGGGTCAG	7440
	TGGGACCACC	TGGGCGCTCT	GGACTCAAAG	GAGACAAGGG	AGACCCTGGA	GTAGGGCTGC	7500

5 CTGGGCCCCC AGGCGAGCGT GGGGAGCCAG GCATCCGGGG TGAAGATGGC CGCCCCGGCC 7560
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 GTGATGTTGG GAGTGCAGGA CTAAGGGGTG ACAAGGGAGA CTCAGCTGTG ATCCTGGGGC 7680
 10 CTCCAGGCCC ACGGGGTGCC AAGGGGGACA TGGGTGAACG AGGGCCTCGG GGCTTGGATG 7740
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 15 CCCCAGGCCG CCCCGGGCTG GCAGGACACA AAGGAGAGAT GGGGGAGCCT GGTGTGCCCG 8100
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 20 CCGGAGAGAG AGTGGTGGG GCTCCTGGGG TCCCTGGAGC TCCTGGCGAG AGAGGGGAGC 8400
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 25 TCCATGCTGT GCCTGTGCTC CGCGTCTCTC ATGCAGAGGA GGAAGAGCGG GTACCCCTCTG 8640
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 ACACCTTGGC CTGGTACCAT CGGGCTGTGA CAGGCAGCAC AGAGGCCTGT CACCTTTTGT 8820
 30 TCATGCTGTG GGTGTGGAGG AATGCCAACC GTTTTGGGAC CCGTGAGGCC TCGAGCGGCC 8880
 GCTGCCACCC CCGGTGTGTC CAGAGCCAGG GGACAGGTAC TGCCACAGGAC TGAGGCCAG 8940
 ATAATGAGCT GAGATTGAGC ATCCCTGGA GAGTCCGGG TCTCAGCAGA ACCCCACTGT 9000
 CCCTCCCTCT GGTGCTTGGT GCTTGTGTGC ACGTGAGCGT GCGAGTGCAC GTCCGTTATT 9060
 TCAGTGACTT GGTCCCGTGG GTCTAGCCTT CCCCCCTGTG GACAAACCCC CATTGTGGCT 9120
 CCTGCCACCC TGGCAGATGA CTCACTGTGG GGGGGTGGCT GTGGGCAGTG AGCGGATGTG 9180
 35 ACTGGCGTCT GACCCGCCCT TTGACCAAG CCTGTGATGA CATGGTGGCT ATTCGGGGG 9240
 GCATTAAAGC TGCTGTTTAA AAAGGCAAAA AA

Seq ID NO: 63 Protein sequence:
 Protein Accession #: NP_000085.1

35 1 11 21 31 41 51
 | | | | | |
 MTLRLVLAAL CAGILAEAPR VRAQHRERV CTRLYAADIV FLIDGSSSIG RSNFREVRSP 60
 LEGLVLFPFG AASAGQVRFA TVQYSDPRT EFGLDALGSG GDVIRAIREL SYKGNNTRTG 120
 40 AAILHVADHV FLPLQARPGV PKVCILITDG KSQDLVDTAA QRLKGQVKL FAVGIKNADP 180
 EELKRVASQP TSDFFFFVND FSIILRLTLLPL VSRRVCTTAG GVPVTRPPDD STSAPRDLVL 240
 SEPSSQSLRV QWTAASGVPY GYKQVYPLT GLGQPLPSER QEVNVPAGET SVRLRGLRPL 300
 TEYQVTIVIAL YANSIGEAVS GTARTTALEG PELTIQNTTA HSLLVAVRSV PGATGYRVTW 360
 RVLSGGPTTQ QELGPGQGSV LLRLDLEPGTD YEVTVSTLFG RSVGPATSLM ARTDASVEQT 420
 45 LRPVILGPTS ILLSNLTVPE ARGVLEWRR ETGLEPPQKV VLPSTDVTRYQ LDGLQPGTEY 480
 RLTLTYLLEG HEVATPATVV PTGPELPVSP VTDLQATELP GQVRVWSWSP VPGATQYRII 540
 VRSTQGVERT LVLPGSQFAT DLDVQAGLS YTVRVSVARVG PREGSASVLT VRREPETPLA 600
 VPGLRVVVDG ATRVAVWGP VPGASGFRIS WSTGSGPESS QTLPPDSTAT DITGLQPGTT 660
 YQVAVSVLRG REEGPAIVIV ARTDPLGPVR TVHVTVQASS SVTITWTRVP GATGYRVSWH 720
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 SVRVLTALVD REGTPVSIIV TTPPEAPPAL GTLHVVRQGE HSLRLRWEVP PRAQGFLHWH 900
 QPEGQEQSR VLGPELSSYH LDGLEPATQY RVRLSVLPGA GEGPSAEVTA RTESPRVPSI 960
 55 ELRVVDTSID VTLTWTVPVS RPSPLFPLNG SHDLGILQR IRDMPYMDPS GNNLGTAVVT 1020
 GVSYIFSLTP VLDGVRGPEA SVTQTPVCPR GLADVVLPH ATQDNAHRAE ATRRVLERLV 1080
 LALGPLGPA QVGLLSYSH RPSPLFPLNG SHDLGILQR IRDMPYMDPS GNNLGTAVVT 1140
 AHRYMLAPDA PQRRGHVGP MVLLVDEPLR GDIFSPIREA QASGLNVVML GMAGADPEQL 1200
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 60 APGLKSGPL PGPRGDPGER GPRGPKGEPG APQGVIGGEG PGLPGRKGDPE GSPGPPGPRG 1380
 PLGDPGPRGP PGLPGTAMKG DKGDRGERGP PGPGEIGIAP GEPGLPGLPG SPGPQGPVGP 1440
 PGKKGKGGDS EDGAPGLPGQ PGSPGEQGPR GPPGAIGPKG DRGFPGLPGE AGEKGERGPP 1500
 GPAGSRGLPG VAGRPGAKGP EGPPGPTGRQ GEKGEPRGP DPAAVVGPAVA GPKGEKGDVG 1560
 PAGPRGATGV QGERGPPGLV LPGDGPKGD PGDRGPIGLT GRAGPPGDSG PPGEKCDPGR 1620
 65 PGPPGPVGP GRDGEVGEKG DEGPDPGDL PGKAGERGLR GAPGVRGVPG EKGDDQDPGE 1680
 DGRNGSPGSS GPKGDRGEPG PPGPPGRLVD TGPAGREKGE PGDRGQEGPR GPKGDPGLPG 1740
 APGERGIEGF RGPFGQGDG CVRGPAGEKG DRGPPGLDGR SGLDGKPGAA GPSGPNAGAG 1800
 KAGDPGRDGL PGLRGEQGLP GPSPPGLPG KPGEDGKPLG NGKNGEPGDP GEDGRKGEKG 1860
 DSGASGREGR DGPKGERGAP GILGPQPPG LPGPVGPFGG GPPGVPGGTG PKGDRGETGS 1920
 70 KGEQGLPGER GLRGEFGSV NVDRLLTAG IKASALREIV ETWDESSGSF LPVPERRRGP 1980
 KGDSEQGGP GKGPPIGPPG ERGLKGRDGD PGPPGPPGLA LGERGPPGPS GLAGEPGKPG 2040
 IPLPFRAGG VGEAGRPGER GERGEKGERG EQGRDGPPLG PGTGPPGPPG GPKVSVDEPG 2100
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 75 GPTGAVGLPG PPGPSGLVPG QGSPGLPGQV GETGKPGAPG RDGASGKGDG RGSFVPGSP 2280
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 80 DSAVILGPPG PRGAKGDMGE RGRPLDGDG GPRGNDGDP DKSGKEGPD KGSAGLPLGR 2580
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 85 APERGEQQR FPGAPGRGEK GEALTEDDI RGVFRQEMSQ HCACQGFQIA SGSRLPLSYA 2820
 ADTAGSQLHA VVPLRVSHAE EZERVPEDD EYSEYSEYSV EYQDPEAPW DSDDPCLPL 2880
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 TAQD

Seq ID NO: 64 DNA sequence
Nucleic Acid Accession #: NM_006945,
Coding sequence: 1-219

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10	TGTCCACAGC	CTCGCCCAAC	TCCAGAGTGC	CAGCAGAAAT	ATCCTCTCTGT	GACACCTTCC	180
	CCACCCCTGCC	AGCCAAGATC	ATCAGCAGAG	AGCAAGTAA			

Seq ID NO: 65 Protein sequence:
Protein Accession #: NP_008876

15 1 11 21 31 41 51 60

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MSYQQQQCKQ PCQPPPVVCPT PKCPEPCPPP KCPEPCPPPK CPQPCPPQOC QQKYFPVTPS 60

PPCQPKYPPK SK

Seq ID NO: 66 DNA sequence
Nucleic Acid Accession #: NM_005629.1
Coding sequence: 639-2546

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	CCGCCGCCAC	CACCGCCACC	GGAGTCCGGG	GCCAGCCCGG	CAGCCTCCGC	GGGCCCGCGG	180
30	CGGGCGGGCG	GGCGCGGGCG	ACAGGCCCTC	GCTCCGCGCG	TGCTTTGACG	ACCGCGGGCG	240
	CCGATGTGCG	CCGCCGCCCG	TTAGGATGAG	TCTCGGGTCG	GGCGAGGAGC	CGCCGCAGCC	300
	GCGCGCGGCC	GAGCGCGGGG	CAGGAGCCCT	GGGAGCCGCC	CGCCGCCCGC	CCGCCGCCCG	360
	GCCCGGGCCG	GAGCGCGCCC	GCGCGCCCCC	GGGCCCCCGA	CACACATGAG	ATTTCTCAGG	420
	CTCACTTTCA	AGTGTTCGT	GGACTGCTTC	TGACTGCGCC	GCCCCGCGCC	CGCACCCCGC	480
35	CGTCCGCGCG	CGGCCCCGTC	CCCCGCGCCG	CGCCGCCCCC	GGCCCCCGCC	CGCCGCCCGC	540
	CCTCGGGGCC	CTCCCCGGTG	CCGCGGGTGC	CCCCGCCCTC	ACCGCGCGCC	CCGCTGAGGC	600
	GCCCGCAGCC	CGGCCCGGCC	GTGCGGCGCG	CGGGGGCCAT	GGCGAAGAAG	AGCGCCGAGA	660
	ACGGCATCTA	TAGCGTGTCC	GGCGACGAGA	AGAAGGGCCG	CTCATCGCG	CCCGGGCCCG	720
	ACGGGGCCCC	GGCCAAGGGC	GACGGCCCCG	TGGGCTGGG	GACACCCGCG	GGCGCGCTGG	780
40	CCGTGGGCCG	GCGCGAGACC	TGAGACGCGC	AGATGGACTT	CATCATGTGC	TGCGTGGGCT	840
	TCGCCGTGGG	CTTGGGCAAC	GTGTGCGCGT	TCCCTTACCT	GTGCTACAA	AACGGCCGAG	900
	TGTGTGTCTT	TATTCCTCAT	GCTCTGATCG	CCCTGGTTGG	AGGAATCCCC	ATTTTCTTCT	960
	TAGAGATCTC	GCTGGGCCAG	TTTCAAGAAG	CCGGACGCA	CAATGTCTGG	AACATCTGTC	1020
	CCCTGTTC	AGGCCTGGG	TAGCCTTCCA	TGTTGATCGT	CTTCTACTGC	AACACCTACT	1080
45	ACATCATGGT	GCTGGCGCTG	GGCTTCTATT	ACCTGGTCAA	GTCTTCTTAC	ACCACGCTGC	1140
	CTTGGGCGAC	ATGTGGCCAC	ACCTGGAACA	CTCCGAGCT	CGTGAGATC	TTCGCCCATG	1200
	AAGACTGTGC	CAATGCCAGC	CTGGCCAAAC	TCACCTGTGA	CCAGCTTGCT	GACCGCGGCT	1260
	CCCCCTGCTT	CGAGTTCTGG	GAGAACAATT	CTTTGAGGCT	GTCTGGGGGA	CTGAGAGGTG	1320
	CAGGGGCGAC	CAACTGGGAG	GTAGCCCTTG	GTCTGTGGCG	CTGTGTGGTG	CTGTGCTTACT	1380
50	TCTGTGTCTG	GAAGGGGGTG	AAATCCACGG	GAAAGATCGT	GTACTTCTGC	GCTACATCTC	1440
	CCTACGTTGG	CTGGTCTGAG	CTGCTGGTGC	GTGGAGTGCT	GCTGCTTGGC	GCCCTGGATG	1500
	GCATCACTTA	CTATCTCAAG	CTGACTGGT	CRAAGCTGGG	GTCCCTCAG	GTGTGGATAG	1560
	ATGGCGGGAC	CCAGATTTTC	TTTTCTTACG	CCATTGGCCT	GGGGGCCCTC	ACAGCCCTGG	1620
	GCAGTACAA	CCGCTTCAAC	AACAACCTTG	ACAAGGCTCT	CATCATCTGC	GCTCATGCTA	1680
	ACAGTGGGAC	CAGCTTCTTT	GCTAGCTTGC	TGGTGTATCC	CTCTCTGGGC	TTCTATGGCT	1740
55	CAGAGCAGGG	CGTGACATCA	TCCAAGGTGG	CAGAGTCAGG	GCCGGGCGTC	GCCTTCATCG	1800
	CCTACCCGCG	GGCTGTACAG	CTGATGCCAG	TGGCCCACTC	CTGGGCTGCC	CTGTTCTTCT	1860
	TCATGCTGTT	GCTGCTTGGT	CTCGACAGCC	AGTTTGTAGG	TTGGGAGGCG	TTTATCAGCC	1920
	GCTTCTCTGA	CTTCTCTCCG	GGCTCTTACT	ACTTCCGTTT	CCAAAGGGAG	ATCTCTGTGG	1980
60	CCCTCTGTGT	TGCCCCCTGC	TTTGTCTATC	ATCTCTCCAT	GGTGACTGAT	GGCGGGATGT	2040
	ACGTGTTTCCA	GCTGTTTTCAG	TACTACTCGG	CCAGCGGCAC	ACCCCTGTCT	TGGCAGGCCT	2100
	TTTGGGAGTG	CGTGGTGGTG	GCTTGGGTGT	ACGGAGCTGA	CCGTTTCTG	GACGACATCT	2160
	CCTGTATGAT	CGGGTACCGA	TTTCTGCCCT	GGATGAATGT	GTGCTGGTCC	TTCTTACACC	2220
	CGCTGTGCTG	CATGGGCATC	CTTATCTTCA	ACGTTGTGTA	TACAGAGCGG	CTGTGCTTAC	2280
65	ACAACACCTA	CGTGTACCGG	TGTTGGGGTG	AGGCCATGGG	CTGGGCCTTC	GCCTGTCTCT	2340
	CCATGCTGTG	CGTGCCTGTC	CACCTCTCTG	GCTGCCTCCT	CAGGGCCAA	GGCACCATCG	2400
	CTGAGCGCGT	CGACGACCTG	ACCCAGCCCA	TCTGGGCGCT	CACACCATTG	GAGTACCGAG	2460
	CTCAGGACGC	AGATGTGAGG	GGCTTGACCA	CCCTGACCCC	AGTGTCCGAG	AGCAGCAAGT	2520
	TCGTCGTGGT	GGAGAGGTGC	ATGTGACAAC	TCAGCTTACA	TCACGAGCTC	ACCTCTGGTA	2580
70	GCCATGTGAG	CCCGCTGCTC	AGCCCAACCG	CACCCCTCCA	GGGGCGCTGC	CTTTCCCTGA	2640
	CACTTTTTGG	GCTCTGCTCG	GGGAGGAGGG	GAGAAAGCAC	CATGAGTGGT	CACATAAACA	2700
	ACTTTTTTCA	TTTTTAATAA	AACGCCAAAA	ATATCACAA	CCACCAAAAT	TAGATGCCTC	2760
	TCCCCCTCCA	GCCCTTACCG	AGCTGTGCTT	AGGGCCCGCC	TAGTGCCCCA	CCCCCAACCA	2820
	CAGTGTCTGA	CTCCTCTCTC	CCCTGCCACG	CCCAACCCCT	GCCCACTCTT	CCAGGCTCTG	2880
75	CTCTGCGACA	CACCCGTGGG	TGACCCCTCA	CCCCAGAAG	AGCATGTGCA	GCTTGGGAAA	2940
	TGTGAGGAG	GGAAGGAGAG	AGAGACGGGA	GGGAGGAGAG	AGAGAGAGAG	GAGGCGAGGG	3000
	GAGGGGCGAG	AGAACCAAGG	CRAATATTTT	AGCTGGGGTA	TACCCCTCTC		

CTTCTGTGTA GCAGCTTTAA CCCAGGTTTG TCTGTACGT CCAGTCCCGA GACGGCTGAG 3780
 TGACCCCAAG AAAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGCTGGGTGA 3840
 GGGTGGCGGG CCTGCGGGGA CATTCTACTG TGCTAAAAAG CCACTGCAGA CATAGCAATA 3900
 AAAACATGTC ATTTTCC

Seq ID NO: 67 Protein sequence:
 Protein Accession #: NP_005620.1

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 INVWNICPLF KGLGYASPMI VFYCNYYIM VLANGFYLV KSFTTTLFWA TCGHTWNTPD 180
 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVL RSGGLEVPGA LNWEVTLCLL 240
 ACWVLVYFCV WGVKSTGKI VYFTATFPYV VLVVLLVRGV LLPGALDGI YLKPDSWKL 300
 GSPQVWIDAG TQIFPSYAI LGALTALGSY NFFNNNCYKD AIIILALINS TSFFAGFVVF 360
 SILGFMAAEQ GVHISKVAES GPGLAFIAYP RAVTLMVPAP LWAALPFMML LLLGLDSQFV 420
 GVEGFITGLL DLLPASVYFR PQREISVALC CALCFVIDLS MVTGGMVYV QLFDYYSASG 480
 TTLWQAFWE CVVVAWVYGA DRFMDDIACM IGYRPCPMWK WCVSFTPLV CMGIFIFNVV 540
 YVEPLVYNN YVYPWNGEAM GWAFALSSML CVPLHLLGCL LRAKGTMAER WQHLTQPIWG 600
 LHHLEYRAQD ADVRLTLTLT PVSESSKVVV VESVM

Seq ID NO: 68 DNA sequence
 Nucleic Acid Accession #: NM_021953.1
 Coding sequence: 178-2469

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 AATGCCCAA GTGAACATC AGAGGAGGAA CCTAAGAGAT CCCTGCCCCA ACAGGAGTCT 300
 AATCAAGCAG AGGCCTCAA GGAAGTGGCG GAGTCCAACT CTTGCAAGTT TCCAGCTGGG 360
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 GGGCCCAACA AATTATCTCT CATCAGCTGT GGGGGAGGCC CAACTCAGCC TCCAGGACTC 540
 CGGCCTCAA CCCAACCCAG CTATGATGCC AAAAGGACAG AAGTGACCCT GGAGACCTTG 600
 GGACCAAAAC CTGCACTAGG GGATGTGAAT CTTCCTAGAC CACTGAGAGC CCTTTGCGAG 660
 CAGAAACGGG AGACTGTGAG AGATCGGTGAG GCAGCAGGCT GCATATCAA CAATAGCCTA 720
 TCCAACATCC AGTGGCTTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG 780
 CAAGAGATGG AGGAAAAGGA GAATGTGAC CTGGAGCAGC GACAGGTAA GGTGAGGAG 840
 CCTTCGAGAC CATCAGCTGC CTGGCAGAAC TCTGTGCTG AGCGCCACC CTACTCTTAC 900
 ATGGCCATGA TACAATTGCG CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAC 960
 ATCTATACGT GGATTGAGGA CCATCTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG 1020
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 AATGGCAAGG TCTCCTCTG GACCATTAC CCCAGTGCCA ACCGCTACTT GACATTGGAC 1140
 CAGGTGTTA AGCCACTGGA CCCAGGCTCT CCACAATTGC CCGAGCACTT GGAATCACAG 1200
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 AAGGTGCTGC TAGCTGAGGA GGGGATAGCT CCTCTTTCT CTGCAAGACC AGGGAAGAG 1500
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Seq ID NO: 69 Protein sequence:
Protein Accession #: NP_068772.1

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LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
10     LSNIQWLRLM SSDGLGSRSI QEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS 240
YMAIIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNL S LHD MFVRETS 300
ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QQRPNPELR RNMTIKTELP 360
LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSEL ARHSKRVRIA 420
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15     SPPLLEWSP APSFKESSH SWEDSSQSPT PRPKKSYSL RSPTRCVSEM LVIQHRERRE 540
RSRSRRKQHL LPPCVDEPEL LFSSEGPSTR WAAELPFPAD SSDPASQLSY SQEVGGPFKT 600
PIKETLPIHS TPSKSVLERT PESWRLTPPA KVGGLDFSPV QTSQASDPL PDPLGLMDLS 660
TTPLQSAPPL ESPQRLSSE PLDLISVFPF NSSPSDIDVP KGPSPEPQVS GLAANRSLTE 720
20     GLVLDTMNDS LSKILLDISF PGLDEDPLGP DNINWSQFIP ELQ

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Seq ID NO: 70 DNA sequence
Nucleic Acid Accession #: BC006529.1
Coding sequence: 178-2424

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AATGCCCAA GTGAAACATC AGAGGAGGAA CCTAAGAGAT CCCTGCCCCA ACAGGAGTCT 300
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35     GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAAGAGAG TGGCAGTAGT 480
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40     CAGAAACGGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA 720
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45     ATCTATACGT GAGATTGAGG TCCCTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG 1020
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CAGGTGTTTA AGCAGCAAGG ACGACCGAAT CCAGAGCTCC GCGGGAACAT GACCATCAAA 1200
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60     TTCCAGCAG ACTCCTCTGA CCCTGCCTCC CAGCTCAGCT ACTCCAGGA AGTGGGAGGA 1920
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CTCCCCAGAA CCCCTGAATC CTGGAGGCTC ACGCCCCAG CCAAGTAGG GGGACTGGAT 2040
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65     ATAGACGTCC CCAAGCCAGT CTCCCGGAG CCACAGGTTT CTGGCCTTGC AGCCAATCGT 2280
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70     ATCCCGGGCA CTCCAAGGCT CAGTGCACCC CAAGCCTCTG AGTGAGGACA GCAGGCAGGG 2520
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75     AAATAGTATA AATTCTCCAA ATTATCCTCT AATATATAAT GTAAGCTTAT TTCTTAGAT 2820
CATTATCCAG AGACTGCCAG AAGGTGGGTA GGATGACCTG GGGTTTCAAT TGACTTCTGT 2880
TCCTTGCTTT TAGTTTGTAT AGAAGGGAAG ACCTGCAGTG CACGGTTTCT TCAGGCTGA 2940
GGTACCTGGA CTTGGGTTC TTCACTGCAG GGACCCAGAC AAGTGATCT GCTTGCCAGA 3000
GTCCTTTTTC CCCCTCCCTG CCACCTCCCC GTGTTTCCAA GTCAGCTTTC CTGCAAGAAG 3060
80     AAATCCTGGT TAAAAAGTC TTTTGTATTG GGTGAGGAGT TGAATTGGG GTGGGAGGAT 3120
GGATGCAACT GAAGCAGAT GTGGGTGCCC AGATGTGCGC TATTAGATGT TTCTCTGATA 3180
ATGTCCCCAA TCATACCAGG GAGACTGGCA TTGACGAGAA CTCAGGTGGA GGCTTGAGAA 3240
GGCCGAAAGG GCCCTGACC TGCCTGGCTT CCTTAGCTTG CCCCTCAGCT TTGCAAGAG 3300
CCACCCTAGG CCCAGCTGA CCGCATGGGT GTGAGCCAGC TTGAGAACAC TAACTACTCA 3360
85     ATAAAGCGA AGGTGAAAAA AAAAAAATA AAAAAA

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Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

	1	11	21	31	41	51	
	MKTSRRPLI	LKRRRLPLPV	QNAPSETSEE	EPKRSPAQQE	SNQAEASKEV	ABSNSCKPFA	60
5	GIKIINHPTM	PNTQVVAIPN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
	LRPQQTSTYD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
	LSNIQWLRRM	SSDGLGSRSI	KQEMEEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSRPPYS	240
	YMAMIQFAIN	STERKRMTLK	DIYTWIEDHF	PYFKHIAPKG	WKNISIRHNS	LHDMFVRETS	300
10	ANGKVSFWTI	HPSANRYLTL	DQVFKQKRP	NPELRRNMTI	KTELPLGARR	KMKPLLPVRS	360
	SYLVPIQFPV	NQSLVLQPSV	KVPLPLAASL	MSELARHSK	RVRIAPKVL	AEEGIAPLSS	420
	AGPGKEEKL	FGEGFSPLLP	VQTIKEBEIQ	PGEEMPHLAR	PIKVESPPLE	EWSPSPSPFK	480
	ESSHSHWEDS	SQSPTPRPKK	SYSGLRSPTR	CVSEMLVIQH	RERRERSR	RKQHLLPPCV	540
	DEPELLFSEG	PSTSRWAAEL	FFPADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISSTPSKS	600
15	VLPRTFESWR	LTPPAKVGG	DFSPVQTPQG	ASDPLPDPLG	LMDLSTTPLQ	SAPPLESQOR	660
	LLSSEPLDLI	SVPPGNSPFS	DIDVFKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSLSKIL	720
	LDISFPGLDE	DPLGPDNINW	SQFIPELQ				

Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

	1	11	21	31	41	51	
25	GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCC	60
	CCAGGTGGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAACGCGAG	ATTCTAATG	180
	AAAATAGCC	CCGTCGGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCC	TCCTGTTCAA	240
30	AATGCCCAAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTGCCCCA	ACAGGAGTCT	300
	AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAA	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
35	CGGCCTCAAA	CCCAAAACAG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600
	GGACCAAAAC	CTCAGCTAG	GGATGTGAAT	CTTCCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGAAACAGGA	GAATTTGTAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
40	CCTTCGAGAC	CATCAGCTGC	CTGGCAGAAC	TCTGTGCTG	AGCGGCCACC	CTACTCTTAC	900
	ATGGCCATGA	TACAATTCGC	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAAGAC	960
	ATCTATACGT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCCGCCACAA	CCTTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGCTGCTC	1080
	AATGGCAAGG	TCTCCTTCTG	GACCATTAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
45	CAGGTGTTTA	GCTCACTGGA	CCCAAGGCTC	CCCAAAATGC	CCGAGCACTT	GGAATCACAG	1200
	CAGAAACGAC	CGAATCCAGA	GCTCCGCCGG	AACATGACCA	TCAAAACCGA	ACTCCCCCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCCCGG	TGAACCACTC	ACTGGTGTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCTGG	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCCC	1440
50	AAGGTTTTTG	GGGAACAGGT	GGTGTGTTGT	TACATGAGTA	AGTTCTTTAG	TGGCGATCTG	1500
	CGAGATTTTG	GTACACCCAT	CACAGCTTGT	TTTAAATTTA	TCTTCTTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCAG	GACCAGGGAA	AGAGGAGAAA	1620
	CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
55	TGGAAGAGT	GGCCCTCCCC	GGCCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
	GATTCGTCCC	AATCTCCAC	CCCAGAGCCC	AAGAAGTCCT	ACAGTGGGCT	TAGGTCCCCA	1860
	ACCCGGTGTG	TCTCGGAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
	TCTCGGAGGA	AACAGCATCT	ACTGCCTCCC	TGTGTGGATG	AGCCGGAGCT	GCTCTTCTCA	1980
	GAGGGGCCCA	GTACTTCCCG	CTGGGCCGCA	GAGCTCCCGT	TCCCAGCAGA	CTCCTCTGAC	2040
60	CCTGCCTCCC	AGCTCAGCTA	CTCCCAGGAA	GTGGGAGGAC	CTTTAAGAC	ACCCATTAAG	2100
	GAAACGCTGC	CCATCTCCTC	CACCCGAGC	AAATCTGTCC	TCCCCAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CGCCCCAGC	CAAAGTAGGG	GGACTGGATT	TCAGCCAGT	ACAAACCTCC	2220
	CAGGGTGCTC	CTGACCTCC	GCCTGACCCC	CTGGGGCTGA	TGGATCTCAG	CACCACTCCC	2280
	TTGCAAAATG	CTCCCCCCTC	TGAATCACCG	CAAAGGTCC	TCAGTTCAGA	ACCCTTAGAC	2340
65	CTCATCTCCG	TCCCTTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
	TCCCGGAGC	CACAGGTTTC	TGGCCTTGCA	GCCAATCGTT	CTCTGACAGA	AGGCCTGGTG	2460
	CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGTCTG	ACATCAGCTT	TCCTGGCCTG	2520
	GACGAGGACC	CAGTGGGCCC	TGACAAATC	AACTGGTCCC	AGTTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
70	AGTGACCCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTTCTGCT	CCTCATAGCT	2700
	CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCTTA	GCCACTGTCT	GGACCTTTGT	2760
	TTCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
	AAAGGCAATG	GTGAAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGCA	2880
	GTCTCTTACC	TTCCCTGATC	TTTGACGGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
75	TTATCCTCTA	ATTATAAATG	TAAAGCTTAT	TCCTTAGATC	ATTATCCAGA	GACTCCAGGA	3000
	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCTTGCTTTT	AGTTTGTATA	3060
	GAAGGGAAGA	CCTGCAGTGC	ACGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
	TCACCTCAGG	GACCCAGACA	AGTGATCTG	CTTGCCAGAG	TCCTTTTTCG	CCCTCCCTGC	3180
	CACCTCCCCG	TGTTTCCAAG	TCAGCTTTCC	TGCAAGAAGA	AATCCTGGTT	AAAAAGTCT	3240
80	TTTGATTGG	GTCAGGAGTT	GAATTTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
	TGGGTGCCCA	GATGTGCCT	ATTAGATGTT	TCTCTGATAA	TGTCCTCAAT	CATACCAGGG	3360
	AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCCTGACCT	3420
	GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAGAGGC	CACCTTAGGC	CCCAGCTGAC	3480
	CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACTACTCAA	TAAAGCGGAA	GGTGACAA	3540
85	AAAAAAAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1

1 11 21 31 41 51
 5 MKTSPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AESNSCKPFA 60
 GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPNNKFILIS CGGAPTQPPG 120
 LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
 LSNIQWLKRM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSRPPYS 240
 YMAMIQFAIN STERKMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNLS LHMFPVRETS 300
 10 ANGKVSFWTI HPSANRYLTL DOVFKPLDPG SPQLPEHLES QQKRPNPPELR RNMTIKTELP 360
 LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSEL ARHSKRVRIA 420
 PKVFGQVVF GYMSKFFSGD LRDFGTPITS LFNFIPLCLS VLLAEEGIAP LSSAGPGKEE 480
 KLLFGEFGFP LLFVGTIKEE EIQGEEMPH LARPIKVESP PLEEWPSAP SFKEESSHSW 540
 EDSSQSPTPR PKKSYSLGRS PTRCVSEMLV IQHRERRERS RSRKQHLPL PCVDEPELLF 600
 15 SEGPSTSRWA AELPPADSS DPASQLSYSQ EVGGPFKTP I KETLPISSTP SKSVLPRTPE 660
 SWRLTPPARV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAPPLES PQRLLSSEPL 720
 DLISVFFGNS SPSDIDVPKP GSPEPQVSGL AANRSLTEGL VLDTMNDSLS KILLDISPFG 780
 LDEPLGPDN INWSQFIPEL Q

20 Seq ID NO: 74 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 111-416

1 11 21 31 41 51
 25 GGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
 TCATCCTTCT ACTCGTGACG CTTCCCAGCT CTGGCTTTT GAAAGCAAAG ATGAGCAAACA 120
 CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
 ATGACAAGAT TGAGAAGCCA AGCCTGTGTA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
 30 TTAGTGCCTG TGACAAAAG GGCACAAATT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
 AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCA 360
 CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCTGTTC CGGGGCGAGC CAGTGACCCA 420
 GCCCCACCAA TGGGCTCCA GAGACCCAG GAACAATAA ATGTCTTCTC CCACCAGA

35 Seq ID NO: 75 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 40 MSNTQAERSI IGMIDMFHYK TRDDKIEKP SLLTMMKENF PNFLSACDKK GTNYLADVFE 60
 KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

45 Seq ID NO: 76 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 111-416

1 11 21 31 41 51
 50 GGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
 TCATCCTTCT ACTCGTGACG CTTCCCAGTT CTGGCTTTT GAAAGCAAAG ATGAGCAAACA 120
 CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
 ATGGCAAGAT TGAGAAGCCA AGCCTGTGTA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
 55 TCAGTGCCTG TGACAAAAG GGCATACATT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
 AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCG 360
 CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCTGTTC TGGGGGAAGC CAGTGATCCA 420
 GCCCCACCAA GGGGCTCCA GAGACCCAG GAACAATAA TGTCTCTCTC CACCAGA

60 Seq ID NO: 77 Protein sequence:
 Protein Accession #: XP_048124.1

1 11 21 31 41 51
 65 MSNTQAERSI IGMIDMFHYK TGRDGKIEKP SLLTMMKENF PNFLSACDKK GIHYLATVFE 60
 KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

70 Seq ID NO: 78 DNA sequence
 Nucleic Acid Accession #: Z73678.1
 Coding sequence: 253-2433

1 11 21 31 41 51
 75 GGGGTGGTGC AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TCGCCAGTGC 60
 CAGAGAGGGA CGAACCAGGG TGGAGCGGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
 CCTCGCACTC TATGGCCGTA GGGAGCCGCT GAGAGCGAGA AGAGCACGCT CCTGCCCGCC 180
 CGCTGCACCG CACCTCGCCT CGCCTCTCTG CTCTCCTAGG CCCCAGCCGC GCGCCACCCG 240
 80 CCTCCCGCCA CATGAACCA CTCGCCGCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG 300
 GACCAGGACA ACTCCACGTT GGCTTTGCCG TCGGACCAAA AGATGAAAAC AGGCACGTCT 360
 GGCAGGCAGC GCGTGACGAG GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAGTCT 420
 85 TCCAGTCTGT ACAGCCAGG CCACTCCAAT CGAGGTCCA TGTATGATGG CTTGGCTGAC 480
 AATTACAAC ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCA GGCAGGGAAT 540
 GGCTCATGGG GATATCCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
 TTCAGCTCTT ACAGCACTGG AGCGGCTGG AGCCCGGGG ACCCCGGGG CAGCTGTAAC 660
 ACCACCGGCG CAGGCAGCGA CATCTGCTTC ATGCAGAAAA TCAAGGCGAG CCGCAGTGAG 720
 CCGCACTCT ACTGTGACCC ACGGGGCACC CTGCGCAAGG GCACGCTGGG CAGCAAGGGC 780
 CAGAAGACCA CCCAGAACCG CTACAGCTTT TACAGCACCT GCAGTGGTCA GAAGGCCATA 840
 AAGAAGTGCC CTGTGCGCCC GCCCTCTTGT GCCTCCAAGC AGGACCCTGT GTATATCCCG 900

	CCCATCTCCT	GCAACAAGGA	CCTGTCCTTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
	AGTGAGGACA	TCGAGTGCAG	TGGGCTGACC	ATCCCCAAGG	CTGTGACGTA	CCTGAGCTCC	1020
	CAGGATGAGA	AGTACCAGGC	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACGAGAACGT	CCAGCAGGCC	GCGGCAGGGG	CCCTGCGCAA	CCTGGTGTTC	1200
	AGGAGCACC	CCAACAAGCT	GGAGACCCGG	AGGCAGAAATG	GGATCCGCGA	GGCAGTCAGC	1260
	CTCCTGAGGA	GAACCGGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTGTCTTCCA	ATGACGAGCT	GAAGGAGGAA	CTCATTGCGG	ACGCCCTGCG	TGTTCTGGCC	1380
10	GACCGGCTCA	TCATTCCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
	GTGGTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGCAGGCC	GCCAGACGAT	GCGTAACTAC	TCAGGGCTCA	TTGATTCCCT	CATGGCCTAT	1560
	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GACGACAAGT	CTGTGGAAAA	CTGCATGTGT	1620
	GTTCTGCACA	ACCTCTCCTA	CCGCCTGGAC	GCCGAGGTGC	CCACCCGCTA	CCGCCAGCTG	1680
15	GAGTATAACG	CCCGCAACGC	CTACACCGAG	AAGTCCTCCA	CTGGCTGCTT	CAGCAACAAG	1740
	AGCGACAAGA	TGATGAACAA	CAACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
	AAGGGCAGCG	GCTGGTTGTA	CCATTTCAGAT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	AAGAGCAAGA	AAGATGCTAC	CCTGGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGACAGCC	1920
	AGCAAGGGGC	TGATGTCCAG	TGGCATGAGC	CAGTTGATTG	GGCTGAAGGA	AAAGGGCCTG	1980
20	CCACAAATTG	CCCGCTCCTT	GCAATCTGGC	AACTCTGATG	TGGTGGGCTC	CGGAGCCTCC	2040
	CTCCTGAGCA	CCAGTCCCGC	CCACCCTCTG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCAGCCAC	ACTGGCAATA	CCAGCAACTC	CGAAGACATC	2160
	TTGTCTCTCG	CCTGCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAAG	2220
	CAGTACTTCT	CAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAAG	CAGTGCCTCA	2280
25	CCCAAGGCCG	CAGAAGCTGC	CCGGCTTCTC	CTGTCTGACA	TGTGGTCCAG	CAAGGAACTG	2340
	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACTTCAC	CTCCGATTTC	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCAG	CTGAGAAGCC	CTCAGGCCCTC	GCTGGATGGG	GTTTTCTGTC	2520
	CATCTGTGTC	AGTATTTGGG	AAAGTTTACA	AGAAACTGAG	AAGAAACCTA	AAAACCTGTG	2580
30	ATAGTGGAAA	CTTTTTTAGA	TTTTTTTTTT	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
	AGGGAGGTTG	GGGCGGGGGG	GGCTTTCTTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
	TTTCTTCCTC	TGAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
	GCGTGCATGT	TGTGTGTGT	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TAAGCTATTT	TGTTGCAGCT	CATAAGGTGG	TGAAAAGGAC	TCTCTGTGT	TTCTTACTCA	2880
35	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCTGCTCATA	ATTCTGAAA	TGTGTGGTGC	2940
	CAGGCAAGG	GGCCCTACAC	TGCAGTCAGG	CCCTCAGAGG	AGTCTGACAG	GCTTCTTACC	3000
	AGTGGTCTCC	AAGGGTGCAG	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	GCTTTCCACG	AAGGGAGGTC	TGGTGTATCT	CATGGGAGAA	TCTGGGGTGT	CTGTAGTGTG	3120
	ACCCCTCCAG	CAGCCGCCAC	AGGACTGAGG	TGGGTAGGT	GTGAGGTTCC	AGAGGACAGC	3180
40	AGGACACTCT	CGCATACTTT	GCCAAATGAG	GCCTGCTCAG	AGGAGTAGGA	GCTGAAAGAT	3240
	GGTGCCTTCC	ACCCCTCTGG	GCTGTGTGCC	CATCAGAGCA	GGCTCAGCCT	GCAAGGGCCC	3300
	TGCAITCAGA	GGTCTTGTAA	TCTACTTGT	GCAGGAGAAA	GAAGGTAAAA	AATGATTTTT	3360
	TTAAGAAAAG	CTATTTTATT	GCAGCTCTTT	CCCAAGAGCT	GTCTGGGAA	TGGCTGGTCT	3420
	TCATATTTCC	AGTGAGAGG	GGAAACAATG	GGGCTGGGCA	TATACCTATT	CCGGCTTCTA	3480
45	GTGGATGGA	TGTGGGCTAT	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGCTGTG	3540
	AGTCAATTGA	GGGAGTGT	GGGTCCCAGG	AGACTTGGAC	GGGGGGAGTT	TGGGTAGACT	3600
	AGGAAAGGAA	AGTGGCATAT	CAGGGTACCG	GTACCGGCAA	GCTCACATCT	CAGCCAGGGG	3660
	CCATGCCCCA	CTTCCCTGA	CCCCAGCTGT	CTTGTCTCCA	CTCTGTGAAA	CCCAAGGGG	3720
	ATGTGATAAA	CAGGGCTATT	AGGGGTATCA	GCCACGTCGA	GCCCCCAGAC	TCGTGTCACT	3780
50	CTAGACCAGC	AGCAGCAGGA	GGGCTCCCGA	GGGCTTATG	AGAAAACTG	TGTGGACATC	3840
	CCTTGGTGA	CACCTAAGCA	GAGCAGAGCC	CAGCGCTCCC	AAGCCTTCTC	CCTTCCAGCT	3900
	TCTACCTCCA	TGCTAGCATT	GCTGGTGTTA	GAGAGGAATT	AACCTCTCTG	TCTGTGCCCT	3960
	TCCTTAGAAG	AATATAAGAT	GCTCTCTCTC	CTCACCCTTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCCTCTTCTG	CACCACCCCC	GAGTCCAAAC	CCACCTCTTG	CCCCAGCATT	CAGGCTGGAA	4080
55	AACTACTGAT	TGGACTCAGT	ATGACAACCTG	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCTCCGGA	GAGGTGTCCC	CGGCTGTAG	CCAGCTGTGC	TGTGGTGTG	TGGGTCTGTC	4200
	ATACCTCTCC	TGCTTCTGCT	TCACACTGGG	AGGCCCACTC	CTGGCTCACC	TCTCCCTCTC	4260
	AGGGACCCAC	GTGGGAGCCT	GGATCCCTGG	ACTGTCTCTG	GCATAGGTTT	CAGGGGCCCTC	4320
	CTTGTGTGTC	ATCAGAACCC	AGAGGAATTC	TTCTCCTAAA	AAATACGTAT	GGCATACCAA	4380
60	CTGTGCGGG	GCAGTGTCTC	AAGCACTTAG	ACTACATCAG	GGAAGAACAC	AGACCACATC	4440
	CCCGTCTCA	TGCGGCTTAT	GTTTTCTGGA	GGAAAGTGG	GACACAAGTC	CTTGGCTTTA	4500
	GGGCTCCCC	GGCTGGGGG	TGTGCAGTCC	GGTCAGGGCG	GGAGGGGAAA	TGCACCGCTG	4560
	CATGTGAACC	CTAGTGCCTC	AGCCGAGTGC	CCCTTCCCCT	TAGCACTACC	CTGGCTCTCT	4620
	GCATCCCCCT	GCCTCATGTT	CCTCCACCTT	TCAAAGAATG	AAGAGCCCCA	TGGGCCAGC	4680
65	CCCTGCCCTG	GGAAACAGGC	AGCCTTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
	AGGGCTGACT	TTGGTGACAC	TGCCAATGCC	CTCTCAGGCC	AGCTCAGGTC	ACCCGGGCCCT	4800
	CTGACCAGG	CCTGTCACTT	TGAGAGGGGC	AAAACCTGAGA	GGGGCTTTTC	CTAGAGAAAG	4860
	AGAACCAAGGA	GCTTGCCAGG	CTTCATGTAG	CCGACACACG	TCTCAGGATT	TTAAGTCCAC	4920
	ATTGGCCTCA	CACCTAGCCTA	GGCCAATGCC	CAAAATAAGG	AGTTCCAATT	TGGGGCCAAA	4980
70	TGAGGAAGGA	CACAGACTCT	GCCCTGGGAT	CTCCTGTGCT	AGCGGCCAAT	GACAAATCCA	5040
	GTCATTGGCC	ACCAGCCACC	TCTGCAGTGG	GGACCACACT	AGCAGCCCTG	ACTCCACACT	5100
	CCTCCTGGGG	ACCCAAGAGG	CAGTGTGTCT	GTCTGCGTGT	CCACCTTGG	ATCTGGCTGA	5160
	ACTGGCTGGG	AGGACCAAGA	CTGCGGCTGG	GGTGGGCAGG	GAAGGGAAGC	CGGGGGCTGC	5220
	TGTGAGGGAT	CTTGGAGCTT	CCCTGTAGCC	CACCTTCCCC	TTGCTTCATG	TTTGTAGAGG	5280
75	AACTTGTGTC	CGGCCAGGCC	CAGTTTCTTT	GTGTGATACA	CTAATGTATT	TGCTTTTTTT	5340
	GGAAATAGAG	AAAATCAATA	AATTGCTAGT	GTTTCTTTGA	AAAAA		

Seq ID NO: 79 Protein sequence:
Protein Accession #: CAA98022.1

80	1	11	21	31	41	51	
	MNHSPLKTL	AYECFQDQDN	STLALPSDQK	MKTGTSGRQR	VQEQVMVTVK	RQKSKSSQSS	60
	TLSHSNRGS	YDGLADNYNY	GTTSRSSYS	KFQAGNGSWG	YPIYNGTLKR	EPDNRFRSSY	120
	SQMENWSRHY	PRGSCNTTGA	GSDICFMQKI	KASRSEPDLY	CDPRGTLRKG	TLGSKGQKTT	180
85	QKRYSPYSTC	SQQAIAIKCP	VRPPSCASKQ	DPVYIPPIPC	NKDLSPFGHSR	ASSKICSEDI	240
	ECSGLTIPKA	YQALIGAYYIQ	HTCFQDESAK	QQVQLGGIC	KLVDLLRSPN		300
	QNVQAAAGA	LRNLVFRSTT	NKLETRRQNG	IREAVSLRR	TGNAEIQKQL	TGLLWNLST	360

DELKEELIAD ALPVLADRV IIPFSGWCDGN SNMSREVVDP EVFFNATGCL RNLSADAGR 420
 QTMNRNYSGLI DSLMAYVQNC VAASRCDDKS VENCMCVLHN LSYRLDAEVP TRYRQLEYNA 480
 RNAYTEKSST GCFPSNKSDBM MNMNYDCPLP EBETNPKGSG WLYHSDAIR YLNLGMSKSK 540
 5 DATLEACAGA LQNLTASKGL MSSGMSQLIG LKEKGLPQIA RLLQSGNSDV VRSGASLLSN 600
 MSRHPLLRHV MGNQVFEVPT RLLTSHTGNT SNSEDILSSA CYTVRNLMAS QPQLAKQYFS 660
 SSMNLNINI NL CRSSASPKAA EAARLLLSDM WSSKELQGV L RQQGFDRNML GTLAGANSLR 720
 NFTSRP

Seq ID NO: 80 DNA sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180-1658

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 20 TGGAGCCCGA CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC 240
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 TCTCTGTGGG CCTTTTGGTT AACCGCTTTG GCCGGCGGAA TTCAATGCTG ATGATGAACC 480
 25 TGCTGGCCTT CGTGTCCGCC GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA 540
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 30 AGAACCGGGC CAAGAGTGTG CTAAGAAGC TGGCGGGGAC AGCTGACGTG ACCCATGACC 900
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 35 CTGTGCTGTC GCTGTTTGTG GTGGAGCGAG CAGGCCGGCG GACCCTGCAC CTCATAGGCC 1200
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 40 CAGCTGCCAT TGGCGTTGCA GGCTTCTCCA ACTGGACCTC AAATTTCAAT GTGGGCATGT 1440
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 55 GCCGGGTCT AGTCTCCTTT GCACTGAGGG CCACACTATT ACCATGAGAA GAGGGCCTGT 2340
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Seq ID NO: 81 Protein sequence:
 Protein Accession #: NP_006507.1

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 GNKDLWPLLL SIIFIPALLQ CIVLPFCPE PRPLLINRNE ENRAKSVLKK LRGTADVTHD 240
 75 LQEMKEESRQ MMREKKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSIPEK 300
 AGVQPPVYAT IGSIVNTAP TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 LPWMSYLSIV AIFGFVAFPE VGPPIPWFI VAELEFSQGR PAIAVAFGS NWTNPFIVGM 420
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Seq ID NO: 82 DNA sequence
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 ACATTACAGAG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTTG 780
 AAATCAAACC TTGTAACTCA TTTATTGCTG ATGGCCACTC TTTTCTCTGA CTCCCTCTG 840
 CCTCTGAGGG CTTCAGTATT GATGGGGAGG GAGGCCTAAG TACCACTCAT GGAGAGTATG 900
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 AGGGCTGCCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC 1080
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 ACCAGCTGGC ACAGGTGCAC AGATTCAATA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200
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Seq ID NO: 83 Protein sequence:
 Protein Accession #: AAH01291

1 11 21 31 41 51
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 MALLALLLVV ALPRVWTDAN LTARQRPED SQRTDEGDNR VVCHVCEREN TFECQNPERRC 60
 KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEPMPF FYLKCKKIRY 120
 CNLEGPPIINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLSL

Seq ID NO: 84 DNA sequence
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 Coding sequence: 229-2726

1 11 21 31 41 51
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 CGCCGCGCGC CGCGCGCGCC GCGCGCGCGC AGCCCAACCAT GTCTCGCGCG 240
 AAGCAAGGCA AACCCAGCA CTTAAGCAAA CGGGAATTCT CGCCGAGGCC TCTTGAAGCC 300
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	TATTTTAAAT	TGTCCTTAAT	TCGTTGCTGA	GCAAACATGT	TGCTGTTTCC	AGTTCGGTTC	3180
5	TGAGAGAAAA	AGAGAGAGAG	AGAGAAAAAG	ACCATGCTGC	ATACATTCTG	TAATACATAT	3240
	CATGTACAGT	TTTATTTTAT	AACGTGAGGA	GGAAAAACAG	TCTTTGGATT	AACCCCTTAT	3300
	AGACAGAATA	GATAGCACTG	AAAAAAATATC	TCTATGAGCT	AAATGTCTGT	CTCTAAAGGG	3360
	TTAAATGTAT	CAATTGGAAA	GGAAGAAAAA	AGGCCTTGAA	TTGACAAAT	AACAGAAAAA	3420
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10	CACATCGATG	GTTCTTCTA	CTTGTTATAA	ACTTGTAGCT	TAATTGAGCA	TGCGGTGAGG	3540
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15	TGCTTTAATA	ATGTCCTTTT	AAAAATACTG	GCACCAAAAG	AAATAGATCC	AGATCTACTT	3900
	GGTTGTCAAG	TGGACAATCA	AATGATAAAC	TTTAAGACCT	TGTATACCAT	ATTGAAAGGA	3960
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25	GAGTATAAAA	TAAACCTGCT	CAGATAGGAC	AATTAAGTGC	ACTGTACAAT	TTTCCAGTT	4440
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	CATTGAGGAG	CTGCTTTTAA	AAACTAAAAA	AAAAAAACT	TTGCCAGCCA	TTTACTTGAC	4560
	TATTGAGCTT	ACTTACTTGG	ACGCAACATT	GCAAGCGCTG	TGAATGGAAA	CAGAATACAC	4620
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30	CTTTTTTAAA	TATAAATGTT	AAGAAAAATT	TTTTTTAAAA	AACACTTCAT	TATGTTTAGG	4740
	GGGGAAGTGC	ATTTTAGGGT	TCCATTGTCT	TGGTGGTGT	ACAAGACTTG	TTATCCATT	4800
	AAAAATGGTA	GTGGAAATTC	TATGCCTTGG	ATACACACCG	CTCTTCAGGT	TGTAAAAAAA	4860
	AAAAACATAC	ATTGGGGGAA	GGTTAAGAT	TATATAGTAC	TTAAATATAG	GAAAAATGCAC	4920
	ACTCATGTTG	ATTCCTATGC	TAAAATACAT	TTATGGTCTT	TTTTCTGTAT	TTCTAGAATG	4980
35	GTATTTGAAT	TAAATGTTCA	TCTAGTGTTA	GGCACTATAG	TATTTATAT	GAAGCTTGTA	5040
	TTTTTAACTG	TGCTTTGTTT	TCTTAAAGG	TATCAATGTA	CCTTTTTTGG	TAGTGGAAAA	5100
	AAAAAAGACA	GGCTGCCACA	GTATATTTTT	TTAATTGGC	AGGATAATAT	AGTGCAAAAT	5160
	ATTGTATGTC	TTCAAAAAAA	AAAAAAGAG	AGAAACAAAA	AAGTGTGACA	TTACAGATGA	5220
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40	GGGGTTGTAC	ATATCCTTTT	TTGTTCCCTT	TTCTGCTGTC	CATAGTGTAT	GCAGTACTGC	5340
	AAAGTAATAA	CCTTGGTTTG	TTATGTAGTG	TGCTTTTGT	CCCTTTCCCT	CTATCACCCCT	5400
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	AAAAAAAAC	CAATGTTTTG	CAGTTTTTTT	CATTGCCAAA	AACTAAATGG	TGCTTTATAT	5520
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50	CTGCATTAA	CTGTTCATAC	ACCCATTTTG	TCCCTTTATT	GAAAAAATAA	AAAAAATTAA	5940

Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

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60	CPKQEHIAK	LLHWRLSSP	RSAHALIPT	PGMSAEYAPQ	GICKDEPSSY	TCTTCKQPFT	180
	SAWFLQHAQ	NTHGLRIYLE	SEHGSPITPR	VGIPSGLGAE	CPSQPPLHGI	HIADNNPFNL	240
	LRIPGVSRE	PASMLAEGFRP	PTPLPFSPPP	RHLDLPHRIE	RLGAEEMALA	THHPSAFDRV	300
	LRINPMAMEP	PMDFSRRLR	ELAGNTSSPP	LSPGRPSPMQ	RLLQPFQPGS	KPPFLATPPL	360
	PPLQSAPPPS	QPPVKSKECE	FCGKTFKQFS	NLVVHRRSHT	GEKPYKCNLC	DHACTQASKL	420
65	KRHMKTHMK	SSPMVTKSD	GLSTASSPEP	GTSDLVGSAS	SALKSVVAKF	KSENDPNLIP	480
	ENGDEEEED	DEEEEEEED	EEBELTESER	VDYGFGLSLE	AARHHENSSR	GAVVGVGDES	540
	RALPDVMQGM	VLSSMQHFSE	AFHQVLGEKH	KRGHLAEAE	HRDTCDEDSV	AGESDRIDDG	600
	TVNNGRCSPG	ESASGGLSKK	LLLGSPPSL	PFSKRIKLEK	EFDLPPATMF	NTENVYSQWL	660
	AGYAASRLQK	DPFLSFGDSR	QSPFASSEH	SENGSLRFS	TPPGELDGGI	SGRSGTSGGG	720
70	STPHISGPGT	GRPSSKEGRR	SDTCEYCGKV	FKNCSNLTVH	RRSHTGERPY	KCELCNYACA	780
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Seq ID NO: 86 DNA sequence
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Coding sequence: 53-1576

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	CGTGACCTCT	CAGCGGAACA	TCACGCTGCT	CAACGGCGTG	GCCATCATCG	TGGGGACCAT	240
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85	GCTGGCGCTG	GTGGTGTGGG	CCGCGTGGG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
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	CTACGGCTCG	CTGCGCGCT	TCCTCAAGCT	CTGGATCGAG	CTGCTCATCA	TCCGGCTTC	480
	ATCGCAGTAC	ATCGTGGCCC	TGGTCTTCGC	CACCTACCTG	CTCAAGCCGC	TCTTCCCCAC	540

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 GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCGC 660
 CAAGCTCCTG GCCTCGGCCG TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAATCGGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAAATTACT TGAATTTCTG 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
 CATCGTGACG CTGGGTGACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCCTGGATC ATCCCGTCT TCGTGGGCCT GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
 GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCCTGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCA CGTGTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTCTCCGTG ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTG TCGGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATCGCGTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCA 1440
 CATCATCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAA ACAAGCCCAA 1500
 GTGGCTCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
 CCCCAGGAG ACATAGCCAG GAGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 87 Protein sequence:
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 | | | | |
 MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLNGVAIIV 60
 GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYAEGLTTI SKSGGDYAYM 120
 LEVYGSPLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL PFTCPVPEEA AKLVACLCLV 180
 LLTAVNCYSV KAAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
 GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNPLAIIII SLPIVTLVYV LTNLAYFTTL 300
 STEQMLSSEA VAVDFGNHYL GVMSWIIPVF VGLSCPGSVN GSLFTSSRLF FVGSREGHLP 360
 SILSMIHQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCLVAL AIIIGMIWLRH 420
 RKPELERIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GPTIILSLGP VYFVGWVWKN 480
 KPKWLLQGIF STTVLCQKLM QVVPQET

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 168-989

1 11 21 31 41 51
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 TAAAAAGCAA AAGAATTGCG GGCCGCGTGC ACACGGGCTT CCCCAGAAAC CTTCCCCGCT 60
 TCTGGATATG AAATTCAGAG TGCTTGCTGA GTCCATATGC CGGCTGCTGG GAGCCAGGAG 120
 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
 TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
 TGTCTCTGGT CTTTCATCTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
 GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGTCC AACGTCTGCT 360
 TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
 CATGCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
 ACCGAGAAGC CCAATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
 GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCAGCGTG GACATCGCCT 600
 TTCTCATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAGTGCC 660
 ACGCAGATCC ATATCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
 TTTTCAACCT CTTTCATGGT GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC 780
 TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA 840
 TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCTG CAAACAAGAC GACCTCCTTT 900
 CGGGTGACCT CATCTTCTG GGTCTCAGCA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
 GAGACCATGT GAAGAAAAC ATCTTGTGAG GGGCTGCGCT GACTGGTCTG GCAGGTTGGG 1020
 CCTGGATGGG GAGGCTCTAG ACTCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
 CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
 TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200
 GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

Seq ID NO: 89 Protein sequence:
 Protein Accession #: NP_005259.1

1 11 21 31 41 51
 | | | | |
 MNWSIFEGLL SGVKNYSTAF GRINLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
 SNVCFDEFPF VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
 GKRRGGLNWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
 SEKNIFTLFM VATAAICILL NLVELIYLV S KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
 DDLLSGDLIF LGSDSHPLL PDRPRDHVKK TIL

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002391.1
 Coding sequence: 26-457

1 11 21 31 41 51
 | | | | |
 CGGGCGAAGC AGCGCGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCTCCT 60
 CGCCCTGCTG GCGCTCACT CCGCGTCCG CAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
 CCGGGGAGC GAGTGCCTG AGTGGGCTG GGGGCCCTG ACCCCAGCA GCAAGGATTG 180
 CGGCGTGGT TTCCGCGAG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCAAGGT 240
 GCCCTGCAAC TGGAGAGAG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAAGTGGG 300
 TCGTGTGAT GGGGCGACAG GCACCAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360

CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCA AGACCAAAGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAG GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCCCTGGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
 CACCAAGTGC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
 ACTCCCAAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAGGAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAAGC TCTTCTTTT 780
 TAATAT

Seq ID NO: 91 Protein sequence:
 Protein Accession #: NP_002382.1

1 11 21 31 41 51
 | | | | |
 MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DOGVGFREGT 60
 CGAQTRIRRC RVPNCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGLTKKA RYNAQCQSTI 120
 RVTKPCTPKT KAKAKAKKKG GKD

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_005130.1
 Coding sequence: 98-802

1 11 21 31 41 51
 | | | | |
 CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCACTGGATC 60
 CGTGTGCTCA GAACAAGGTG AACGCCACGC TGCAGCCATG AAGATCTGTA GCCTCACCTC 120
 GCTCTCCTTC CTCTACTTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAAGTGAA 180
 GAATGACTTC CACAGCAAAAG TGGTCTCAGA ACAAAGGAC ACTCTGGCCA ACACCCAGAT 240
 TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAAGACC AAGCCAACCTG 300
 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360
 GGACCATGAA TTTTCCCTGTG TCCTTGTGTC CAATCCAACC TCATGCCTAA AGCTCAAGGA 420
 TGAGAGAGTC TATTGGAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
 ATATTCCAAG ACAGCTGTGA AAACCCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540
 TAAGCTAGTC AGCTCCATC TATTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600
 GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCTC TCTAGCCTAG CAGTGACCCA 660
 GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
 GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT 780
 AGTGCAGGAC ACGTCATGCT AATGAGGTCA AAAGAGAAGC GGTTCCTTTA AGAGATGTCA 840
 TGTGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACCTT 900
 TGTGCTTAGT GAGTGCACAG AAATATTAA ACAAGTTTG TATTTTGTG TTTTGTGTTT 960
 TGGAAATTTG CTTATTTTTC TTGGATGCGA TGTTTCAGAG CTGTTTCTCT CAGCATGTAT 1020
 TTCCATGGCC CACACAGCTA TGTGTTTGTG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
 GAGTGATAAT TTCAGTGCAA CGAACTTTCT GCTGAATTAA TGTAATAAA ACTCTGGGTG 1140
 TTTTCAAAA AAAAAAAA AAA

Seq ID NO: 93 Protein sequence:
 Protein Accession #: NP_005121.1

1 11 21 31 41 51
 | | | | |
 MKICSLTLLS FLLAAQVLL VEGKKVKVNG LHSKVVSEKQ DTLGNTQIKQ KSRPGNKGKP 60
 VTKDQANCRW AATQEEGIS LKVBCTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 RSQKDICRYS KTAVKTRVCR KDFPESLKL VSSTLFGNTK PRKEKTEMSP REHIKGETT 180
 PSSLAVTQTM ATKAPCEVED PDMANQRKTA LEPCGETWSS LCTFFLSIVQ DTSC

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: NM_012101
 Coding sequence: 125-1891

1 11 21 31 41 51
 | | | | |
 CTCCTCACAG GTGTGTCTCT AGTCCTCGTG GTTGCCCTGCC CCACTCCCTG CCGAGACGCC 60
 TGCCAGAAAG GTACCTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120
 TGCATGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTGG AGCCAGAAAG CCAGGGATGC 180
 CCGGAGCCCG TCGGGCCCCA GTGGCAGCCT GGAGAATGGC ACCAAGGCTG ACGGCAAGGA 240
 TGCCAAGACC ACCAACGGGC ACGGCGGGGA GGCAGCTGAG GGCAAGAGCC TGGGCGAGCG 300
 CCTGAAGCCA GGGGAAGSTA GGAGCGCCCT GTTGGCGGGC AATGAGTGGC GGCAGCCCAT 360
 CATCCAGTTT GTCGAGTCCG GGGACGACAA GAACTCCAAC TACTTCAGCA TGGACTCTAT 420
 GGAAGGCAAG AGGTGCGCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCCT 480
 TACCTTTGCC GAAAAGGGCG ACGTGCACAA GTCCATTTC TCGGAGTCCC GGAAGCCAC 540
 GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCGGG CCGACACGGG 600
 CCTTTTTC CAAGTCCAAGT CCGGCTCCGA GGAGGTGCTG TGCGACTCCT GCATCGGCAA 660
 CAAGCAGAAG CGGTCAAGT CCTGCCTGGT GTGCCAGGCC TCCTTCTGCG AGCTGCATCT 720
 CAAGCCCCAC CTGGAGGGCG CCGCCTTCCG AGACCACAG CTGCTCGAGC CCATCCGGGA 780
 CTTTGAGGCC CGCAAGTGT CCGTGCATGG CAAGACGATG GAGCTCTTCT GCCAGACCGA 840
 CCAGACCTGC ATCTGCTACC TTTGCATGTT CCAGGAGCAC AAGAATCATA GCACCGTGAC 900
 AGTGGAGGAG CCAAGGCCG AGAAGGAGAC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA 960
 GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT 1020
 CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGCG 1080
 GGACCTGGAG AAGCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC 1140
 TGTGAGCAAA GTGAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGCTGCATGA 1200
 GGACAAGCAG ACCCGGAGC AGCTGCATAG CATCAGGAC TCTGTGTTGT TTCTGCAGGA 1260
 ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCCACCT ATCATGTCTT 1320
 GCTGGAGGGG GAGGCGCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380
 ATGCATGCGC CACGTTGAGA AGATGTGCAA GCGGACCTG AGCCGTAAC TCAATTGAGAG 1440
 GAACACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG 1500

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GGGTGAGTGG AGTGACCCGG ACACCATGAA GAGATACTCC ATGTACCTGA CACCCAAAGG 1560
TGGGGTCCGG ACATCATACC AGCCCTCGTC TCCTGGCCGC TTCACCAAGG AGACCACCCA 1620
GAAGAATTTC AACATCTCT ATGGCACCAG AGGTAACCTAC ACCTCCCGGG TCTGGGAGTA 1680
CTCCTCCAGC ATTCAGAACT CTGACAATGA CCTGCCCGTC GTCCAAGGCA GCTCCTCCTT 1740
CTCCCTGAAA GGCTATCCCT CCCTCATGCG GAGCCAAAGC CCCAAGGCC AGCCCCAGAC 1800
TTGGAATCT GGCAAGCAGA CTATGCTGTC TCACTACCGG CCATTCTACG TCAACAAAGG 1860
CAACGGGATT GGGTCCAACG AAGCCCCATG AGCTCCTGGC GGAAGGAACG AGGCGCCACA 1920
CCCTGCTCT CTCTCTGAC CTGCTGCTCT TGCTCTCTA AGCTACTGTG CTTGTCTGGG 1980
TGGGAGGGAG CCTGGTCTG CACCTGCCCT CTGCAGCCCT CTGCCAGCCT CTTGGGGGCA 2040
GTTCCGGCCT CTCGGACTTC CCCACTGGCC ACACCTCCATT CAGACTCCTT TCCTGCCCTG 2100
TGACCTCAGA TGGTCACCAT CATTCCTGTG CTCAGAGGCC AACCCATCAC AGGGGTGAGA 2160
TAGGTTGGGG CTGCCCCATA CCCGCCAGCC TCCTCCTCTC GGGCTGGATC TGGGGGCTAG 2220
CAGTGAGTAG CCGCATGGTA TCAGCCTGCC TCTCCCGCCC ACGCCCTGCT GTCTCCAGGC 2280
CTATAGACGT TTCTCTCCAA GGCCCTATCC CCCAATGTTG TCAGCAGATG CCTGGACAGC 2340
ACAGCCACCC ATCTCCCAAT CACATGGCCC ACCTCCTGCT TCCCAGAGGA CTGGCCCTAC 2400
GTGCTCTCTC TCGTCTTACC TATCAATGCC CAGCATGGCA GAACCTGCAG TGGCCAAGGG 2460
CTGCAGATGG AAACCTCTCA GTGTCTTGAC ATCACCCTAC CCAGGCGGTG GGTCTCCACC 2520
ACAGCCACTT TGAGTCTGTG GTCCCTGGAG GGTGGCTTCT CTGACTGGC AGGATGACCT 2580
TAGCCAAGAT ATTCTCTGT TCCTCTGCT GAGATAAAGA ATTCCTCTAA CATGATATAA 2640
TCCACCCATG CAAATAGTA CTGCCCCAGC TACCATTAC CATTTGCCA CAGAATTCA 2700
TTCAGTCTAC ACTTTGGCAT TCTCTCTGGC GATGGAGTGT GGCTGGGCTG ACCGCAAAAG 2760
GTGCTTACA CACTGCCCCC ACCTCAGCC GTTCCCCAT CAGAGGCTGC CTCTCCTTC 2820
TGATTACCCC CCATGTTGCA TATCAGGGT CTCAAGGATT GGAGAGGAGA CAAAACCAAG 2880
AGCAGCACAG TGGGGACATC TCCCGTCTCA ACAGCCCCAG GCCTATGGGG GCTCTGGAAG 2940
GATGGGCCAG CTGACAGGGG TTGGGGAGGG AGACATCCAG CTTGGGCTTT CCCCTTGGGA 3000
ATAAACCAAT GGTCTGTC

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Seq ID NO: 95 Protein sequence:
Protein Accession #: NP_036233.1

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1 11 21 31 41 51
MEAADASRSN GSSPEARDAR SPSPGPSGSLE NGTKADGKDA KTTNGHGGEA AEGKSLGSAL 60
KPEGGRSALF AGNEWRRPII QFVESGDDKN SNYFSMDSME GKRSPYAGLQ LGAAKKPPVT 120
FAEKGDVRKS IPSESRRPTV SIMEPGETRR NSYPRADTGL FSRSKSGSEE VLCDSCIGNK 180
QKAVKSCILVC QASFCEHLHK PHLEGAAFRD HQLLEPIRDF EARKCPVHGK TMEFLFCQTDQ 240
TCICYLQMFQ EHKNHSTVTV EEAKAEKETE LSLQKEQLQL KIIIEIDEAE KWQKEKDRIK 300
SFTTNEKAIL EQNFRDLVRD LEKQKEEVRA ALBQREQDAV DQVKVIMDAL DERAKVLHED 360
KQTRQLHSI SDSVLFQEF GALMSNYSLP PPLPTYHVLL EGEGLQSLG NFKDDLNVLC 420
MRHVEKMCKA DLSRNFIERN HMENGSDHRY VNNTYNSFGG EWSAPDTMKR YSMYLTTPKGG 480
VRTSYQSSSP GRFTKETTKQ NFNPLYGTGK NYTSRVWEYS SSIQNSDNDL PVVQSSSSFS 540
LKGYPPLMRS QSPKAQPQTW KSGQKTMLSH YRPFYVKNKN GIGSNEAP

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Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: NM_080668.1
Coding sequence: 83-841

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75
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1 11 21 31 41 51
GGCACGAGGG CAGCGAGTGG CCTTCCCGGT TGGCGCGCGC CCGGGGCGGC GGCCTGAGAG 60
GAGCTCGAGA CGGAGCCTAG TTATGCTCTG GAGGCGAAGC CGGTCCGAG GAGCCGCTCA 120
GCGCTCCGGG CCAAGGGCCC CATCTCCTAC TAAGCCTCTG CGGAGGTCCC AGCGGAAATC 180
AGGCTCTGAA CTCCCGAGCA TCCTCCCTGA AATCTGGCCG AAGACACCCA GTGCGGCTGC 240
AGTCAGAAAG CCCATCGTCT TAAAGAGGAT CGTGGCCCAT GCTGTAGAGG TCCAGCTGT 300
CCAATCACCT CGCAGGAGCC CTAGGATTTT CTTTCTCTTG GAGAAAGAAA ACGAGCCCCC 360
TGGCAGGGAG CTTACTAAGG AGGACCTTTT CAAGACACAC AGCGTCCCTG CCACCCCCAC 420
CAGCACTCCT GTGCCGAACC CTGAGGCCGA GTCCAGTCCC AAGGAAGGAG AGCTGGACGC 480
CAGAGACTTG GAAATGTCTA AGAAAGTCAG GCGTCTCTAC AGCCGCTGG AGACCTGGG 540
CTCTGCTCT ACCTCCACCC CAGGCCGCGC GTCTGCTTT GGCTTCGAGG GGCTGCTGGG 600
GGCAGAGAC TTGTCCGGAG TCTGCCAGT GGTGTGCTCC AAACCTCACG AGGTCCCCAG 660
GGTTTGTGCA AAGCCCTGGG CCCCAGACAT GACTCTCCCT GGAATCTCCC CACCACCCGA 720
GAAACAGAAA CGTAAGAAGA AGAAAATGCC AGAGATCTTG AAAACGGAGC TGGATGAGTG 780
GGCTGCGGCC ATGAATGCCG AGTTTGAAGC TGCTGAGCAG TTTGATCTCC TGGTTGAATG 840
AGATGCACTG GGGGGTGCAC CTGGCCAGAC TCTCCCTCCT GTCCTGTACA TAGCCACCTC 900
CCTGTGGAGA GGACACTTAG GGTCCCCTCC CTTGGTCTTG TTACTGTGT GTGTGCTGGT 960
GCTGCGCATG AGGACTGTCT GCCTTTGAGG GCTTGGGCAG CAGCGGCAGC CATCTTGGTT 1020
TTAGGAAATG GGGCCGCTG GCCCAGCCAC TCACTGGTGT CTTGTCTCT GTGCTCCTGT 1080
CCTTCTATC TCCCAAAGT ACCATAGCCA GTTTCAGAT GGGCCACAGA CTGGGGAGGA 1140
GAATCAGTGG CCCAGCCAGA AGTTAAAGGG CTGAGGGTTG AGGTGAGAGG CACCTCTGCT 1200
CTTGTGGGA GGGGTGGCTG CTTGGAATA GGCCAGGGG CTCTGCCAGC CTCGGCCTCT 1260
CCCTCCTGAG TTGCTTCTG TTGGTGGCTT TCTTCTTGAA CCCACCTGTG TAAAGAGGTT 1320
TTCAGTTCGG TGGTTTCCC CTTTGATTCT GTAAATAGTC CCAGAGAGAA TTCGTGGGCT 1380
GAGGGCAATT CTGCTTGGA GGAAGAAGCT GGACATTCAG CTTGTGGAGT CTGAGTTTGT 1440
AAGGATGTAG GGAGCCTTAG TTGGGTCTCA GACCATAAGT GTGTACTACA CAGAAGCTGT 1500
GTTTTCTAGT TCTGGTCTGC TGTGAGATG TTGTGTAAT GCCAGGTGTA TAGGGCGCTG 1560
GCTGCTTGGG GCAAAGGGTG CATTTCAGGG TGTGGCCACC AGGTGCTGTG AGTTTCTGTG 1620
GCTCATGGCC TCTGGGCTGG TCCCTTGCAC AGGGGCCACG CTGGAGTCTT ACCACTCTGC 1680
TGCAAGGGTG GAAGGTGGCC CTTCTTGTA CCCATACCCA TTTCTTACAA AATAAGTTAC 1740
ACCGAGTCTA CTTGGCCCTA GAAGAGAAAG TTGAAGAGTC CCAGACCTAC TAGCATTTTG 1800
CAACTATGCT TGTAAAGTTC TCGGAAAGTT TCCTCGCGTA CCAGACAGCG GCGGGGGCTG 1860
ATAGCAATTT TAGTTTTTGG CCTCCCTATC CTCTCACATG AGAACACTGC CTGGATGCAT 1920
CTCATGATCT CTGGAGAATT TCCCCATCT TCTCTTCTT CCATCGTGTG GATTCAATAG 1980
TTTGGATTG AAGGCTGCCC TGCCCCGAC TCTCTGCGG CACCCCTGGC CATTGTACCT 2040
TTTGTATGTT AGAAGTTCGT GGAAGTAGAC GCTGAGGTGT GCAGAGGAGC TGGTGGATAA 2100
CAGAGAATGC CAGGGAAGAT GAGTGTCTGG TCAGGGTACT TGGATGAAAC GGTGCAGGCC 2160
AGGCGGGCCC TAATAAAACC CTCTGCCAGG TCTGGGAGTC CCAGGCCATC TGCTCAACGC 2220

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TCTGTGGTTT GTACAGACCTG CAAGCAAGCC CCCTGCTGGG GAAGCCTAGG TGTCTCTGAG 2280
 CTGAACCGCA CTGAAGAAGT CTTGTCTCTA CTGGCTGATG CAGCAGAAGT CTTGGGAAAT 2340
 GTCTTAGTCC TGCAGAAATCA GGAGTCACCA GATGATGCAG AGTTGAGATC ATCATTGCAA 2400
 AGTTCTCTGT TCCTGAGGAA CTAAATTTAA GGAAAAATG GGATTTTGT TTAGAGTTGG 2460
 AAAAAAAGCC TGATTAAAGA GTTTCTGCCT GTTAAAAAAA AAAAAAATA AAAAAA

Seq ID NO: 97 Protein sequence:
 Protein Accession #: NP_542399.1

1 11 21 31 41 51
 MSGRRTRSGG AAQRSGPRAP SPTKPLRRSQ RKSSELSPSI LPEIWPKTPS AAIVRKPVL 60
 KRIVAHAVEV PAVQSPRRSP RISFFLEKEN EPPGRELTKE DLFKTHSVPA TPTSTPVPNP 120
 EAESSSKEGE LDARDLEMSK KVRYSYRLE TLGSASTSTP GRRSCFGFGE LLGAEDLSGV 180
 SPVVCCKLTE VPRVCAKPWA PDMTLPGISP PPEKQKRKKK KMPEILKTEL DEWAAAMNAE 240
 FEAAEQFDLL VE

Seq ID NO: 98 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 58-12444

1 11 21 31 41 51
 GGGGCATTTC CGGGTCCGGG CCGAGCGGGC GCACGCGCGG GAGCGGGACT CGGCGGCATG 60
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 GCGGACCGCT GCGGTGCTGC CCTGGCGGT CATCAACTGA TCCGCGGCT GGGCAGGAA 180
 TCGTCTCTGA GCAGCAGCCC CGCGGTGCTG GCATTACAGA CATCTTAGT TTTTCCAGA 240
 GATTTCCGGT TGCTTGTATT TGTCCGGAAG TCACTCAACA GTATTGAAT TCGTGAATGT 300
 AGAGAAGAAA TCCTAAAGTT TTTATGTATT TTCTTAGAAA AAATGGGCCA GAAGATCGCA 360
 CCTTACTCTG TTGAATTTAA GAACACTTGT ACCAGTGT TT ATACAAAAGA TAGAGCTGCT 420
 AAATGTAAAA TTCCAGCCCT GGACCTTCTT ATTAAGTTAC TTCAGACTTT TAGAAGTTCT 480
 AGACTCATGG ATGAATTTAA AATTGGAGAA TTATTTAGTA AATTCTATGG AGAACTTGCA 540
 TTGAAAAAAA AAATACCAGA TACAGTTTAA GAAAAAGTAT ATGAGCTCCT AGGATTATTG 600
 GGTGAAGTTT ATCCTAGTGA GATGATAAAT AATGCAGAAA ACCTGTTCG CGCTTTCTG 660
 GGTGAACCTT AGACCCAGAT GACATCAGCA GTAAGAGAGC CCAAACTACC TGTTCGGCA 720
 GGATGTCTGA AGGGGTGTG CTCACCTCTG TGCAACTTCA CTAAGTCCAT GGAAGAAGAT 780
 CCCCAGACTT CAAGGGAGAT TTTTAATTTT GTACTAAAGG CAATTCGTCC TCAGATTGAT 840
 CTGAAGAGAT ATGCTGTGCC CTCAGCTGGC TTGCGCCTAT TTGCCCTGCA TGCATCTCAG 900
 TTTAGCACCT GCCTTCTGGA CAACTACGTG TCTCTATTG AAGTCTTGT AAAGTGGTGT 960
 GCCCACACAA ATGTAGAATT GAAAAAGCT GCACCTTCAG CCTTGGATC CTTTCTGAAA 1020
 CAGGTTTCTA ATGATGGTGG GAAAAATGCA GAAATGCATA AAAATAAACT GCAGTACTTT 1080
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 GACTTCATGT ACGTTGAGCT CATTACGCGC TGCAAGCAGA TGTTCCTCAC CCAGACAGAC 1260
 ACTGGTGACG ACCGTGTTTA TCAGATGCCA AGCTTCTCTC AGTCTGTTGC AAGCGTCTTG 1320
 CTGTACCTTG ACACAGTTCC TGAGGTGTAT ACTCCAGTTC TGGAGCACCT CGTGGTGATG 1380
 CAGATAGACA GTTCCCAACA TCAGCTCCA AAAATGCAGC TGGTGTGTTG CAGAGCCATA 1440
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 GTGGTGATC AGGGTTAAT CAGAAATATG TCTAAACCAG TGGTCTCTCC AAAGGGCCCT 1560
 GAGTCTGAAT CTGAAGATCA CCGTGTCTCA GGGGAAGTCA GAACTGGCAA ATGGAAGGTG 1620
 CCCACATACA AAGACTACGT GGATCTCTTC AGACATCTCC TGAGCTCTGA CCAGATGATG 1680
 GATTCTATT TAGCAGATGA AGCATTCTTC TCTGTGAATT CCTCCAGTGA AAGTCTGAAT 1740
 CATTACTTTT ATGATGAATT TGTAAATCC GTTTGAAGA TTGTTGAGAA ATTGGATCTT 1800
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	SIGFNTIGDVQ	VMAHLPDVCV	NLMKALKMSP	YKDILETHLR	EKITAQSIEE	LCAVNLYGPD	1440
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	PSLDLSCQKL	QAVTLLPFFT	SLTGGSELEL	RRVLEQLIVA	HFPMQSREFF	PGTFRFNYYV	1560
	SLFSETINTE	LLKNLDLAVL	ELMQSSVDNT	KMVSAILNGM	LDQSFREERAN	QKHQGLKLAT	1620
	TILQHWKCCD	SWWAKDSPL	TKMAVLALLA	KILQIDSSVS	FNTSHGSPFE	VFTTYISLLA	1680
	KTDLDLHLKG	QAVTLLPFFT	SLTGGSELEL	RRVLEQLIVA	HFPMQSREFF	PGTFRFNYYV	1740
25	DCMKKFLDAL	ELSQSPMLLE	LMTEVLCREQ	QHVMEELFQS	SFRRIARRGS	CVTQVGLLES	1800
	VYEMFRKDDP	RLSFTFRQSV	DRSLTLTLWH	CSLDALREFF	STIVVDAIDV	LKSRTFKLNE	1860
	STFDTQITKK	MGYYKILDMV	YSRLPKDDVH	AKESKINQVF	HGSCITEGNE	LTKTILKLCY	1920
	DAFTENMAGE	NQLLERRRLY	HCAAYNCAIS	VICCVFNLK	FYQGFLESEK	PEKNLLIFEN	1980
	LIDLKRRYNF	PVEVEVPMER	KKKYIEIRKE	AREAANGSDS	GPSYMSLSLY	LADSTLSEEM	2040
30	SQDFSTGQV	SYSYSSQDPR	PATGRFRRRR	QRDPTVHDDV	LELEMDLNR	HECMAPLTAL	2100
	VKMHRSLSGP	PQGEEDSVPR	DLPSWMKPLH	GKLGNPVPL	NIRLFLAKLV	INTEEVFRPY	2160
	AKHWLSPLQL	LAASENNGGE	GIHYMVVEIV	ATILSWTGLA	TPTGVPKDEV	LANRLNLFML	2220
	KHVFHFKRAV	FRHNLEIKT	LVECWKCLDS	IPYRLIFKEF	SGKDPNSKDN	SVGIQLLGIV	2280
	MANDLPPYDP	QCGIQSSEYF	QALVNMMSFV	RYKEVYAAAA	EVGLGILRYV	MERKNILEES	2340
35	LCELVAQKQL	QHNTMEDFK	IVCLNKVTKS	FPPLADRFMN	AVFLLPKFH	GVLTLCLEV	2400
	VLCRVEGME	LYFQKSKDF	VQVMRHRDDE	RQKVCLEIY	KMPKPKFVE	LRLELNPVVE	2460
	FVSHPTTCCR	EQMYNLMWI	HDNYRDPSE	TDNDSQEIFK	LAKDVLQGL	IDENPGLQLI	2520
	IRNFWSHETR	LPSNTLDRL	ALNSLYSPKI	EVHFLSLATN	FLEEMTSMSP	DYPNPMFEHP	2580
	LGSECFQEYT	IDSDFRFRST	VLTMPFVETQ	ASQGTLOTRT	QEGSLSARWP	VAGQITLCEY	2640
40	QHDFTLTQTA	DGRSSFDWLT	GSSTDPLVDH	TSPSSDSLFF	AHKRSERLQR	APLKSVCQDF	2700
	GKRLGLPGED	EVDNKVKGAA	GRDOLLRLRR	RFMRDQEKLS	LMYARKGVAE	QKREKEIKSE	2760
	LKMKQDAQV	LYRSYRHKDI	PDIIKHSSSL	ITPLQAVAR	DPPIAKQLFS	SLFSGILKEM	2820
	DKFKTLSEKN	NITQKLLQDF	NRFLNTPFSF	FPFVSCIQD	ISQHAALLS	LDPAAVSAGC	2880
	LASLQQPVG	RLLEALRL	LPAELPAKRV	RGKARLPD	LRWVELAKLY	RSIGEDVLR	2940
45	GIFTSEIGTK	QITQSALLAE	ARSDYSEAAK	QYDEALNKQD	WVDGEPTAE	KDFWELASLD	3000
	CYNHLAEWKS	LEYCSTASID	SENPPDLNKI	WSEPFYQETY	LPYMIRSKLK	LLLQGEADQS	3060
	LLTFIDKAMH	GELQKAILLE	HYSQELSLLY	LLQDDVDRAK	YYIQNGIQSF	MQNYSSIDVL	3120
	LHQSLTLKQL	QITQSALLAE	FISFISKQGN	LSSQVPLKRL	LNTWTNRYPD	AKMDPMNIWD	3180
	DIITNRCFFL	SKIEEKLTP	PEDNSMNVQ	DGDPSDRMEV	QEEDIEDISS	IRSCKFSMKM	3240
50	KMIDSARKQN	NFSLAMKLLK	ELHKESKTRD	DWLVSQVQSY	CRLSHCRSRS	QCCSEQVLT	3300
	LKTVSLLDEN	NFSSYLSKNI	LAFRDQNIL	GTTYRIIANA	LSSEPACLAE	IIEEDKARRIL	3360
	ELSGSSSEDS	EKVIAGLYQR	AFQHLSEAVQ	AAEBEAQPPS	WSCGPAAGVI	DAYMTLADFC	3420
	DQDLRKEEEN	ASVIDSABLQ	AYPALVVEKM	LKALKLNSNE	ARLKFPRLQ	IIERYPEETL	3480
	SLMTKEISSV	PCWQCTISW	HMVALLDKDQ	AVAVQHSVEE	ITDNYQQAIV	YPFIISSSEY	3540
55	SFKDTSTGHK	NKEFVARIKS	KLDQGGVIQD	FINALDQLSN	PELLFKDWSN	DVRAELAKTP	3600
	VNKNIEKMY	ERMYAALGDP	KAPGLGAPRR	KFIQTFGKEF	DKHFGKGGSK	LLRMKLSDFN	3660
	DTNMLLLK	NKDSKPPGNL	KECSWMSDF	KVEFLRNELE	IPGQYDGRGK	PLPEYHVRIA	3720
	GFDERVTVMA	SLRRPKRIII	RGHDEREHPF	LVKGGEDLRQ	DQVEQLFQV	MNGILAQDSA	3780
	CSQRALQLRT	YSVVPMTSRL	GLIEWLENTV	TLKDLLNTM	SQEEKAAYLS	DPRAPPCEYK	3840
60	DWLTMSGKH	DYVAGTMYK	GANRTETVTS	FRKRRESKVA	DLKRAFVRM	STSPAEFLAL	3900
	RSHFASSHAL	ICISHWILGI	GDRHLNFMV	AMETGGVIGI	DFGHAFGSAT	QFLFVPELMP	3960
	FRLTRQFINL	MLPMKETGLM	YSIMVHALRA	FRSDPGLLTN	TMDVVFKEPS	FDWKNFEQKM	4020
	LKKGGSWQIE	INVAEKWYYP	RQKICYAKRK	LAGANPAVIT	CEDELLGHEK	APAFRDYVAV	4080
	ARGSKDHNIR	AQEPESGLSE	ETQVKCLMDQ	ATDPNILGRT	WEGWEPWM		

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_000673
Coding sequence: 101-1225

70	1	11	21	31	41	51	
	ATGTGAAGGC	ACAAGCTGCT	GTTATATACA	ACAGAGTGAA	CTGAGCATCA	GTCAGAAAAA	60
	GTCTATGTTT	GCAGAAATAC	AGATCCAAGA	CAAAGACAGG	ATGGGCACTG	CTGGAAAAAGT	120
	TATTAAATGC	AAAGCAGCTG	TGCTTTGGGA	GCAGAAAGCA	CCCTTCTCCA	TTGAGGAAAT	180
75	AGAAGTTGCC	CACCAAGAG	CTAAGAAAGT	TCGCATTAAAG	ATTTTGGCCA	CAGGAATCTG	240
	TCGCACAGAT	GACCATGTGA	TAAAAGGAAC	AATGGTGTCC	AAGTTTCCAG	TGATTGTGGG	300
	ACATAGAGCA	ACTGGGATCT	TAGAGAGCAT	TGGAGAAGGA	GTGACTACAG	TGAAACCAGG	360
	TGACAAAGTC	ATCCCTCTCT	TTCTGCCACA	ATGTAGAGAA	TGCAATGCTT	GTGCAACCC	420
	AGATGGCAAC	CTTTGCATTA	GGAGCGATAT	TACTGGTCTG	GGAGTACTGG	CTGATGGCAC	480
	CACCAAGATT	ACATGCAAGG	GCAACACAGT	ACACCACTTC	ATGAACACCA	GTACATTTC	540
80	CGAGTACACA	GTGGTGGATG	AATCTTCTGT	TGCTAAGATT	GATGATGCAG	CTCCTCTTGA	600
	GAAAGTCTGT	TTAATTGGCT	GTGGGTTTTT	CACTGGATAT	GGCGCTGCTG	TTAAACTTGG	660
	CAAGGTCAAA	CTGCTTCCA	CTTGCGTCTG	CTTTGGCCTG	GGAGGAGTTG	GCCTGTCTAG	720
	CATCATGGGC	TGTAAGTCAG	CTGGTGTCAT	TAGGATCATT	GGGATTGACC	TCAACAAAGA	780
	CAAAATTGAG	AAGGCCATGG	CTGTAGGTGC	CACTGAGTGT	ATCAGTCCCA	AGGACTCTAC	840
85	CAAAACCATC	AGTGAAGTGC	TGTCAGAAAT	GACAGGCAAC	AACGTGGGAT	ACACCTTTGA	900
	AGTTATTGGG	CATCTTGAAA	CCATGATTGA	TGCCCTGGCA	TCTGTCCACA	TGAACCTATG	960
	GACCAAGCTG	GTTGTAGGAG	TTCCTCCATC	AGCCAAGATG	CTCACCTATG	ACCCGATGTT	1020

GCTCTTCACT GGACGCACAT GGAAGGGATG TGTCTTTGGA GGTTTGAAAA GCAGAGATGA 1080
 TGTCCCAAAA CTAGTGACTG AGTTCTCTGGC AAAGAAAATTT GACCTGGACC AGTTGATAAC 1140
 TCATGTTTFA CCATTTAAAA AAATCAGTGA AGGATTTGAG CTGCTCAATT CAGGACAAAG 1200
 5 CATTGGAACG GTCCTGACGT TTTGAGATCC AAAGTGGCAG GAGGTCTGTG TTGTCATGGT 1260
 GAACCTGGAGT TTCTCTTGTG AGAGTTCCCT CATCTGAAAT CATGTATCTG TCTCACAAT 1320
 ACAGCATAA GTAGAAGATT TGTGAAGAC ATAGAACCCT TATAAGAAT TATTAACCTT 1380
 TATAACATT TAAAGTCTTG TGAGCACCTG GGAATTAGTA TAATAACAAT GTTAATATTT 1440
 10 TTGATTTACA TTTTGTAAAG CTATAATTGT ATCTTTTAAG AAAACATACA CTGGGATTTT 1500
 TATGTTGAAA TGGAGATTTT TAAGAGTTT AACCAGCTGC TGCAGATATA TAACTCAAAA 1560
 CAGATATAGC GTATAAAGAT ATAGTAAATG CATCTCCAG AGTAATATTC ACTTAACACA 1620
 TTGAACTAT TATTTTATAG ATTTGAATAT AAATGTATTT TTTAAACACT TGTATGAGT 1680
 TAACTTGGAT TACATTTTGA AATCAGTTCA TTCCATGATG CATATTACTG GATTAGATTA 1740
 AGAAAGACAG AAAAGATTAA GGGACGGGCA CATTTTTCAA CGATTAAGAA TCATCATTAC 1800
 15 ATAACCTGGT GAAACTGAAA AAGTATATCA TATGGGTACA CAAGGCTATT TGCCAGCATA 1860
 TATTAATATT TTAGAAAATA TTCCTTTTGT AATACTGAAT ATAAACATAG AGCTAGAGTC 1920
 ATATTATCAT ACTTATCATA ATGTTCAATT TGATACAGTA GAATTGCAAG TCCTTAAGTC 1980
 CCTATTCACT GTGCTTAGTA GTGACTCCAT TTAATAAAAA GTGTTTTTAG TTTTAAACAA 2040
 CTAACCG

Seq ID NO: 101 Protein sequence:
 Protein Accession #: NP_000664

1 11 21 31 41 51
 25 | | | | |
 MGTAGKVIK KAALVWEQKQ PFSIEIEVA PPKTEKVRK ILATGICRTD DHVIKGTMSV 60
 KFPVIVGHEA TGIVESIGEG VTTVKPGDKV IPLFLPQCRE CNACRNPDPN LCIRSDITGR 120
 GVLADGTTTF TCKGKPVHVF MNTSTFTTEYT VUDESSVAKI DDAAPPEKVC LIGCGFSTGY 180
 GAAVKTGKVK PGSTCVVFLG GGVGLSVIMG CKSAGASRII GIDLNKDKFE KAMAVGATEC 240
 30 ISPKDSTKPI SEVLSEMTGN NVGYTFEVIH HLETMIDALA SCHMNYGTSV VVGVPSSAKM 300
 LTYDPMLEPT GRTWKGCVEF GLKSRDDVPK LVTEFLAKKF DLDQLITHVL PFKKISEGFE 360
 LLNSGQSIRT VLTF

Seq ID NO: 102 DNA sequence
 Nucleic Acid Accession #: NM_006783.1
 Coding sequence: 1..786

1 11 21 31 41 51
 40 | | | | |
 ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60
 GGGAAAGTGT GGATCACAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120
 CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
 AAAAAATGTT GCTATGACCA CTTTTTCCCG GTGTCCCA CA TCCGGCTGTG GGCCTCCAG 240
 CTGATCTTCG TCTCACCCCG AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
 45 GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
 ATTAAAAAGC ACAAGGTTCC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
 TTTTCCGAA TCATCTTTGA AGCAGCCCTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
 TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGC 540
 TTTATTTCTA GGCCAAACAGA GAAGACCGTG TTTACCATT TTAGATTTC TGCGTCTGTG 600
 50 ATTTGATGTC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTATAG 660
 AGATCAAGAA GAGCAGACAG GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
 CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
 AGCTAA

Seq ID NO: 103 Protein sequence:
 Protein Accession #: NP_006774.1

1 11 21 31 41 51
 60 | | | | |
 MDWGLHTFI GGVNKHSTSI GKVVITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
 KNVCYDHFFP VSHIRLWALQ LIPVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDPKDIED 120
 IKKKVRIEG SLWWTYTSII PFRIIFEAAF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
 FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLKVCFR RSKRAQTQKN HPNHALKESK 240
 QNEMNELISD SQNNAITGFP S

Seq ID NO: 104 DNA sequence
 Nucleic Acid Accession #: NM_020411
 Coding sequence: 86-526

1 11 21 31 41 51
 70 | | | | |
 GGACCTGGGA AGGAGCATAG GACAGGGCAA GCGGGGATAA GGAGGGGCAC CACAGCCCTT 60
 AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTT 120
 ACTGGGCGTC TTCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC 180
 75 GCGGACTCGG GTCCCTGAGG TCTGGATTCT TTCTCGCTA CTGAGACACG GCGGACACAC 240
 ACAAACACAG AACCACACAG CAGTCCCGAG GAGCCAGTA ATGGAGAGCC CAAAAAGAA 300
 GAACACGACG CTGAAAGTCG GGATCTTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
 ACAGCTGAGA TCCCACTGCG CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
 ACCGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAGAGGGA 480
 80 AACTGTAAAT ATGCCAGAAG CAGGTGAAGA GCAACACAA GTTTAAATGA AGACAAGCTG 540
 AAACAACGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG 600
 CAGCTTTCAC CAAAAA AAAA

Seq ID NO: 105 Protein sequence:
 Protein Accession #: NP_065144.1

1 11 21 31 41 51

MLLWCPQCA CSLGVFPSP SPVWGTRRSC EPATRVPEVW ILSPLLRHGG HTQTQNHAS 60
PRSPVMESPK KKNQQLKVG LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG 120
SGVKVKIIPK EEHCKMPEAG EEQPPQV

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: J04129
Coding sequence: 99-587

1 11 21 31 41 51
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCTGGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAGG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCC CTCTGAGGGT CCACATCACC TCACTGTGTG 240
CCACCCCCGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTG 300
AGAAAGAAGT CCTTTGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAAGCA GGCCACGCTG CTGATACTG ACTACGACAA TTCTCTGTTT CTCTGCCTAC 420
AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCCTGCCC AGGCACCTAT 540
GGTACTTGCT GGAATTGAAA CAGATGGAAG AGCGTGCCG TTTCTAGCTC ACCTCGCCT 600
CCAGGAAGAC CAGACTCCCA CCCTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC 660
TTTCAAAGAA TAACCAACAG TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCT 720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGITA TTAATAAACC CTTGAGCAT G

Seq ID NO: 107 Protein sequence:
Protein Accession #: AAA60147

1 11 21 31 41 51
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLP T EDNLEIVLHR 60
WENNSCVEKK VLGEKTNPK KFKINYTVAN EATLLD TDYD NFLFLCLQDT TPIQSMCCQ 120
YLARVLVEDD EIMQGFIRAF RPLRHLWYL LDLKQMEEP RF

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 48-794

1 11 21 31 41 51
TCCAGGCAG CAGTTAGCCC GCCGCCGCC TGTGTGTCCC CAGAGCCATG GAGAGAGCCA 60
GTCTGATCCA GAAGGCCAAG CTGGCAGAGC AGGCCGAACG CTATGAGGAC ATGGCAGCCT 120
TCATGAAAGG CGCCGTGGAG AAGGGCGAGG AGCTCTCCTG CGAAGAGCGA AACCTGCTCT 180
CAGTAGCCTA TAAGAACGTG GTGGCGGCC AGAGGGCTGC CTGGAGGGTG CTGTCCAGTA 240
TTGAGCAGAA AAGCAACGAG GAGGGCTCGG AGGAGAAGGG GCCCGAGGTG CGTGAGTACC 300
GGGAGAAGGT GGAGACTGAG CTCCAGGGCG TGTGCGACAC CGTGCTGGGC CTGCTGGACA 360
GCCACCTCAT CAAGGAGGCC GGGGACGCC AGAGCCGGT CTCTACCTG AAGATGAAGG 420
GTGACTACTA CCGTACCTG GCCGAGGTG CCACCGGTGA CGACAAGAAG CGCATCATG 480
ACTCAGCCCG GTCAGCCTAC CAGGAGGCCA TGGACATCAG CAAGAAGGAG ATGCCGCCA 540
CAAACCCCAT CCGCCTGGG CTGGCCCTGA ACTTTCCGT CTTCACCTAC GAGATCGCCA 600
ACAGCCCGCA GGAGGCCATC TCTCTGGCCA AGACCACTTT CGACGAGGCC ATGGCTGATC 660
TGCACACCCT CAGCGAGGAC TCCTACAAAG ACAGCACCCT CATCATGCAG CTGCTGCGAG 720
ACAACCTGAC ACTGTGAGC GCCGCAACG CCGGGGAAGA GGGGGCGAG GCTCCCCAGG 780
AGCCCCAGAG CTGAGTGTG CCGGCCACG CCGCGCCTG CCCCCTCCAG TCCCCACCC 840
TGCCGAGAGG ACTAGTATGG GGTGGGAGGC CCCACCCTTC TCCCTAGGC GCTGTTCTTG 900
CTCCAAAGGG CTCCTGTGG AGGACTGGC AGAGCTGAGG CCACCTGGGG CTGGGGATCC 960
CACTCTCTT GCAGCTGTG ACCGACCTA ACCACTGGT ATGCCCCAC CCCTGCTCTC 1020
CGCACCCGCT TCCTCCGAC CCCAGGACCA GGCTACTTCT CCCCTCCTCT TGCCTCCCTC 1080
CTGCCCCGTC TGCTCTGAT CGTAGGAATT GAGGAGTGTG CCGCCTGTG GCTGAGAACT 1140
GGACAGTGGC AGGGCTGGG GATGGGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 1200
CGCGCGCGCC AGTGCAAGAC CGAGATTGAG GGAAAGCATG TCTGCTGGGT GTGACCATGT 1260
TTCCTCTCAA TAAAGTTCCT CTGTGACACT C

Seq ID NO: 109 Protein sequence:
Protein Accession #: NP_006133.1

1 11 21 31 41 51
MERASLIQKA KLAEQAEYE DMAAFMKGAV EKGEELSCEE RNLLSVAYKN VVGQRAAWR 60
VLSSIEQKSN EEGSEEGPE VREYREKVT ELQGVCDTVL GLLDHSLIKE AGDAESRVFY 120
LKMKGDIYRY LAEVATGDDK KRIIDSARSA YQEAMDISK EMPPTNPRL GLALNFSVFH 180
YEIANSPEEA ISLAKTTFDE AMADLHTLSE DSYKDSTLIM QLLRDNLTW TADNAGEEGG 240
EAPQEPQS

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: NM_000695
Coding sequence: 407-1564

1 11 21 31 41 51
CACGAGTTGG TTTGGGAGCT GCCAGTCTCC TGGGAGGATC GCAGTCAGCA GAGCAGGGCT 60
GAGGCCTGGG GGTAGGAGCA GAGCCTGCGC ATCTGGAGGC AGCATGTCCA AGAAAGGGAG 120
TGGAGGTGCA GCGAAGGACC CAGGGGCGA GCCACGCTG GGGATGGACC CCTTCGAGGA 180
CACACTGGG CGGCTGGTG AGGCCTTCAA CTGAGGGCGC ACGCGGCGG CCGAGTTCCG 240
GGCTGCGCAG CTCCAGGGCC TGGGCCACTT CCTTCAAGAA AACAAGCAGC TTCTGCGCGA 300

	CGTGCTGGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTGTGACT	ACGCTCTCAA	GAACCTTTCG	GCGTGGATGA	AGGATGAACC	420
	ACCGTCCACG	AACCTGTTCA	TGAAGAGCTA	CTCGGTCTAG	ATCTCGAAGG	AACCTTTTGG	480
5	CCTGGTCTCT	ATCATCGCAC	CCTGGGAAGTA	CCCATTTGAAC	CTGACCCCTGG	TGCTCTCTGGT	540
	GGGCAACCTC	CCCGCAGGGA	ATTGCGTGTG	GCTGAAGCCG	TCAGAAATCA	GCCAGGGCAC	600
	AGAGAAGGTC	TGCTGCTGAG	TGCTGCCCCA	GTACCTGAGC	CAGAGCTGCT	TTCGCGTGGT	660
	GCTGGGCGGA	CCCCAGGAGA	CAGGGGACGT	GCTAGAGCAC	AAGTTGGACT	ATCTTCTTCT	720
	CACAGGGAGC	CCTCGTGTGT	GCAAGATTGT	CATGACTGCT	GCCACCAAGC	ACGTGACGCC	780
10	TGTCACCTCT	GAGCTGTGGG	GCAAGAACCCT	TGCTACGCTG	GACGACAACT	GCGACCCCCA	840
	GACCGTGGCC	AACCGCGTGG	CCTGGTTCCT	CTACTTCAAT	GCCGGCCAGA	CCTGCGTGGC	900
	CCCTGTACTAC	GTCTCTGTGCA	GCCCCAGATG	CAGGAGGAGG	CTGCTGCCCC	CCCTGACAGG	960
	CACCATCACC	CGTTTCTATG	GCGACGACCC	CCAGAGCTCC	CCAAACCTTG	GCGCATCAT	1020
	CAACCGAGAA	CAGTTCACAG	GGCTGCGGGC	ATTGCTGGGC	TGCGGCCCGG	TGGCCATTGG	1080
	GGGCGCAGAG	AACGAGAGCG	ATCGCTACAT	CGCCCCACAG	GTGTCGTGGG	ACGTGACAGA	1140
15	GAGCGTGGAC	GTGATGACGG	AGGAGATCTT	CGGGCCCCAT	TGCCCCATG	TGAACGTGCA	1200
	CTTCTCCAAC	AGGACAGCAG	TTGTGAACCA	GATGCTGGAG	CGGACCCAGA	CGGCGAGCTT	1320
	TGGAGCGAAT	GAGGGCTTCA	CTCATACATC	TTCTGCTGCC	TGTGCATTCT	GGGGAAGTCG	1380
	CCACAGTGGT	ATGGGCCGGT	ACCACGGCAA	GTTACCTTTC	GACACCTTCT	CCCACCACCG	1440
20	CACCTGCGCT	CTCGGCCCTT	CGGGCTGGGA	GAATTTAAAG	GAGATTCGCT	ACCCACCTTA	1500
	TACCGCATGT	AACCAGCAGT	TGTTACGCTG	GGGCATGGGC	TCCGAGAGCT	GCACCTCCTT	1560
	GTGAGCGTCC	CACCCGCCCT	CAACGGGTCA	CACAGAGAAA	CCTGAGTCTA	GCCATGAGGG	1620
	GCTTATGCTC	CCAACTCACA	TTGTTCTCTC	AGAGCCGACG	CTCCCCACAG	CTCAGGTTTC	1680
25	TGGAGCTGTC	ACATGACTGC	ATCTGCTGCT	CAGGGCTGCG	AAAGCAAGGT	CTTGCTTCTA	1740
	TCTGGGGGAC	GCTGCTCGAG	AGAGGCCGAG	AGGCCGAGA	ACATGCCAGG	TGTCCTCACT	1800
	CACCCCCAC	TCCCCAAATT	GACGCCTTTG	CCCTCTCGGT	CAGGGTGGC	CAGGCCCACT	1860
	CACAGGGGCA	GTGTCACTCT	GGAATAATCA	TGTCCTGGCT	TCTTTAGGGG	CATCAGCCCT	1920
	GAACGGTTGA	GAGCGTGGAG	CCCTCCAGGC	CTTGTCTCTC	CCCTCTAGGC	ACACGCGCAC	1980
30	TTCCACCTCT	CGCCCAATCC	AACGTGACCA	GCACTGCCTC	CCCCAGGAT	CCTCTCACAT	2040
	CCCCACATGG	TCTCTGCACC	ACCCCTCTGG	TCACACCCG	ACCCCTGACT	CACCCACAGC	2100
	AGCTCCATCC	ACTGGGAAAA	CTGGGGTTTG	CATCACTCCA	CTGCACAGTG	TTAGTGGGAC	2160
	CTGGGGGCAA	GTCCCTTTGAC	TTCTCTGAGC	CTCAGTTTCC	TTATGTGAAA	GTTGCTGGAA	2220
	CCAAATATGA	TGCACCTTAT	CCAAACTCTA	ATAAAAATGA	FTCGGGGGAG	CACATAGGAA	2280
	CCCTCACACA	CACATGCCCG	TAACAGGATT	TATCACCAAG	ACAAGCCTGC	ATGTAAGACC	2340
	AGACACAGGG	CTCATGTGAAA	AGGACGCTCT	CAAAAGACTG	AGTATTTCCAG	ATGAGCTGCA	2400
35	GATGCTTATC	TACCACGGCC	GTCTCCACCA	GA AAAACCAT	GCCAACTCCT	GCGATCAGCT	2460
	TGTGACTTAC	AAACCTTGTG	TAAAGAGCTG	TTACATCATG	TTCTGTCTCT	TAAACAGTTC	2520
	CCCTTGGCTG	TGTCCTCTGT	TGTATGCTCT	GGATCCTTCC	AAGCACTCAT	AGCCCCAGTA	2580
	GGAACTCCTCT	GCTCCTCCCA	AATAAAATCA	TCGTGTC			

Seq ID NO: 111 Protein sequence:
Protein Accession #: NP_000686

45	1	11	21	31	41	51	
	MKDEPRSTNL	FMKLDSVFIW	KEPFGVLVII	APWNYPLNLT	LVLLVGLTLP	GNCVVLPKPE	60
	ISQGTGKVL	EVLPQYLDQS	CFAVVLGGPQ	ETGQLLEHLK	DYIFTGSPR	VGKIVMTAAT	120
50	KHLPTVLTLE	GKNKPCYVDD	NCDPQTVANR	VAWFCYFNAG	QTCVAPDYVL	CSPEMQERLL	180
	PALQSTITFR	YGGDPQSSPN	LGRIINQKFP	QLRLALLGCC	RVAIGGQSNR	SDRYIAPTVL	240
	VDVQTEPEFM	QEEIFGPIPL	IVNVQSVDEA	IKFINRQKEP	LALYAFSNSR	QVVNQMLERT	300
	SSGSFGNGNE	FTYISLLSPG	FVGCVHSGMG	RYHGKFTFDT	FSHHRTCLLA	PSGLEKLKEI	360
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Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58-2298

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	GGCCAGACTG	GGAGAAATC	TGAGAAGGGA	CCAGTTTGT	GGCGGAAGCG	TGTAAAATCA	120
	GAGTACATG	GCTGAGACGA	GCTCAAGGAG	TTCAGACGAG	CTGATGAAGT	AAAGAGTATG	180
	TTTAGTTCCA	ATGCTCAGAA	AAATTTGGAA	AGAACGGAAA	TTCTAAACCA	AGAAATGGAAA	240
65	CAGCGAAGGA	TACAGCCTGT	GCACATCCTG	ACTTCTGTGA	GCTCATTGCG	CGGGACTAGG	300
	GAGTGTTCGG	TACCCAGTGA	CTTGGATTTT	CCAACACAAG	TCATCCCCAT	AAAGACTCTG	360
	AATGCAGTTG	GTTCAAGTCA	CATAATGTAT	TCTTGGTCTC	CCCTACAGCA	GAAATTTATG	420
	GTGGAAGATG	AAACTGTTTT	ACATAACATT	CCTTATATGG	GAGATGAAGT	TTTAGATCAG	480
	GATGGTATCT	TCATTGAAGA	ACTTAATAAA	AATTAATGAT	GGAAAGTACA	CGGGGATAGA	540
70	GAATGTGGGT	TTATAAATGA	TGAAATTTTT	GTGGAGTTGG	TGAATGCCCT	TGGTCAATAT	600
	AATGATGATG	ACGATGATGA	TGATGGAGAC	GATCCTGAAG	AAAGAGAAGA	AAAGCAGAAA	660
	GATCTGGAGG	ATCACCAGGA	TCATAAAGAA	AGCCGCCAC	CTCCGAAATT	TCCTTCTGAT	720
	AAAATTTTGG	ATGCCCATTC	CGAATGTTT	CCAGATAAAG	GCACAGCAGA	AGAACTAAAG	780
	GAAAAATATA	AAGAACTCAC	CGAACGACG	CTCCCAGCG	CACCTCTCC	TGAATGCTCC	840
75	CCCAACATAG	ATGGACCAA	TGCTAAATCT	GTTCAGAGAG	AGCAAAGCTT	ACACTGTATT	900
	CATACGCTTT	TCTGTAGCGG	ATGTTTTAAA	TATGACTGCT	TCTACATCTT	TTTTCATGCA	960
	ACACCCAACA	CTTTAAGCG	GAAAGAACCA	GAAACAGCTC	TAGACAACA	ACCTTTGTGA	1020
	CCACAGTGTT	ACCAGCATTT	GGAGGAGGCA	AAGGAGTTTG	CTGTGCTCT	CCACGCTGAG	1080
80	CGGATAAAGA	CCCCACCAA	ACGTCACGGA	GGCCGCAGAA	GAGGACGGCT	TCCCAATAAC	1140
	AGTAGCAGCG	CCGACACCCC	CACCAATTAAT	GTGCTGGAAT	CAAGAGGATC	AGACAGTGAAT	1200
	AGGGAAGACG	GAGCTGAAC	GGGGGAGAG	AACAAATGATA	AAGAAGAAGA	AGAGAAGAAA	1260
	GATGAAACTT	CGAGCTCCTC	TGAAGCAAAT	TCTCGGTGTC	AAACACCAAT	AAAGATGAAG	1320
	CCAAATTTATG	GAACCTCTGA	GAAATGTGGG	TGGAGTGGTG	CTGAAGCCCTC	AATGTTTAAA	1380
	GTCCTCATTT	GCCTTTACTA	TGACAAATTC	TGTGCCATT	CTAGGTTAAT	TGGGACCAA	1440
85	ACATGTAGAC	AGGTGTATGA	GTTTAGAGTC	AAAGAATCTA	GCATCATAGC	TCCAGCTCCC	1500
	CTCGGAGGAT	TGGATATCTC	TCCAAGGAAA	AAGAAGAGGA	AACACCGGTT	TGGGCTGCA	1560
	GACTGCAGAA	AGATACAGCT	GAAAAGGAC	GGCTCCTCTA	ACCATGTTTA	CAACTCATCA	1620

5
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15

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CCCTGTGATC ATCCACGGCA GCCTGTGTAC AGTTCGTGCC CTTGTGTGAT AGCACAAAAT 1680
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GAAATGGAAG TCCCTTGACA TCTGCTACCT CCTCCCCTC CTCTGAAACA GCTGCCTTAG 2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAAATTCGT 2400
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GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
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20 Seq ID NO: 113 Protein sequence:
Protein Accession #: NP_004447

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KORRIQPVHI LTSVSSLRGT RECSVTSDDL FPTQVIPLKT LNAVASVPIM YSWSPLOQNF 120
MVEDETVLHN IPYMGDEVLD QDGFPIELI KNYDGKVHGD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DPEEREKEQ KDLBDHRDDK ESRPPRKFPD DKILEAISM FPDKGTAEBL 240
KEKYKELTEQ QLPGLPPEC TPNIDGPNK SVQREQSLHS FHTLPCRRCP KYDCFHHPFH 300
ATPNTYKRNK TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GRRRRRLPN 360
NSSRPSPTPI NVLESKDIDS DREAGTETGG ENNDKEEEK KDRTSSSSEA NSRCQPIKM 420
KPNIEPPENV EWSGAESMF RVLIGTYIDN FCAIARLIGT KTCRQVYEF VKESSIIAPA 480
PAEDVDTPPR KKKRKRHLWA AHCRKIQLKK DGSSNHVINY QPCDHPRPQPC DSSCPCVIAQ 540
NFCEKFCQCS SECQNRFPGC RCKAQCNKQ CPCYLAVREC DPDLCLTCGA ADHWDSKNVS 600
CKNCISQRGS KKHLLAPSD VAGWGFIDK PVQKNEFISE YCGEIIISQDE ADRRGKVYDK 660
YMCSEFLNINL NDFVVDATRK GNKRIRFANH VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
ELFVDYRYSQ ADALKYVGIE REMEIP

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40 Seq ID NO: 114 DNA sequence
Nucleic Acid Accession #: NM_001827
Coding sequence: 96-335

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CGGCAAGATA CTTGACGAAA CACTACGAGT ACCGGCATGT TATGTTACCC AGAGAACTTT 180
CCAAACAAGT ACCTAAACT CATCTGATGT CTGAAGAGGA GTGGAGGAGA CTGGGTGCC 240
AACAGAGTCT AGGCTGGGTT CATPACATGA TTCATGAGCC AGAACCACAT ATTCTTCTCT 300
TTAGACGACC TCTTCCAAAA GATCAACAAA AATGAAGTTT ATCTGGGGAT CGTCAAATCT 360
TTTTCAAAAT TAATGTATAT GTGTATATAA GGTAGTATTC AGTGAATACT TGAGAAATGT 420
ACAAATCTTT CATCCATACC TGTGCATGAG CTGTATTCTT CACAGCAACA GAGCTCAGTT 480
AAATGCAACT GCAAGTAGGT TACTGTAAAG TGTTTAAGAT AAAAGTTCTT CCAGTCAGTT 540
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60 Seq ID NO: 115 Protein sequence:
Protein Accession #: NP_001818

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Seq ID NO: 116 DNA sequence
Nucleic Acid Accession #: CAT cluster

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AGAGGTGTGT TCCAGGAAA GCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC 180
GCAGCCAACA GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGCTCTGT GGAGGATGGG 240
AAGGACTGAT CCACATTCCT ACCAGGAAGT TTAGCAGAAC CCCCCTGCTG CAATGGACC 300
CCTTGAAGG ACCTGGCTCA GGCTGGACCA CCTCTTGAGA GGGAGGAGCT CTGGATTGTA 360
TCAAGAAATC TTGCTGAGC ATGCTGCCTC ATGCTATATA TACCAACACT TTGGGAGGCC 420
AGTGTGGGAG GATCTCTTGA GCCCAGGAGT TCAAGACTAG CCTGGGCAAC ACAGAGAGAA 480
CCCATCTCTA AATAATAAAT AATAATAAAA TAAAAAATTA GCAGGGCATG GTGGCATGTG 540
CCTGTAGTTC CAGCTACCCA GGAGGCTGAG GCAAGAGGAT GGCTGGAGCC TGGGATGTTG 600
AGGCTGCAAT GAACTGTGAT TACCCACTG CACTCCAGCC TGGGCAAAAG AGCGAGAGAA 660
CTGTCTCTAA ATAATAATTA TAATAATAAT CTTATTTTGG AGAATAAAGA GACCTCTGGA 720
TTTGAGGTGC CATTTGGGTA GAAAGAAAAG ACGTTTACAC CGAGAAATAG TCTGTGTTGC 780
CCTGAAGGAG CAGAGGGATG CATCGCTGGA GGTGACCTAC AGTTGAAGAA GACTCATTAT 840
GACAGACCTT GTCCTTCTTC CTTGTGGAAA GTGTTTCCTC TGCTGCTACT GCTCATGAGA 900
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CCGCCTCCCA TGTCTGCTGT GCCTTTGTAC TCAGCAATTC TTGTTTGTCT CATTATCTTC 1020
CAGCCGGATA CAGAGTGAAT AGTTAACAC ACTTAGGTCA AATAGGATCT AATTTTGTG 1080
TCCTGCTCCG TGTAAAGAGG CCAGTGTTTG TGTGTTGCAA GCAGCCTTGG AATAGTAATC 1140

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 GTGAAGGCTC GTGTTCTCCA TCCTCAACTT TCTTTGCTTC GATCATACAC AAGAATACAT 1320
 TTGGAAGGGC AAAAATGAA CACTGTGCTT CATTGCAGCC GTGTTTTGTG ACACAGATGC 1380
 ACAGTCTGCT GTGAAGACCT TCTCTCAAGT GGCATTTGGG AGTCCATGCC AGATCATGGT 1440
 GCTTCATGAG AGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCTCCCCC 1500
 CAGTGTGTGC TGATGACACA TACACACCTG ACAATAGCTT GAGTCTTCTC TGTTCCTTTT 1560
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 Nucleic Acid Accession #: BC012178.1
 Coding sequence: 204-2285

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 TTGGCCTTAC AGAAAATGGA AAAGTAATAC TGAAGAATTT CCTTTATGAT ATAGCTGGAT 840
 GCAGTGGAAC CTTACCGGTG CAGAACAGAG AACTTGAGTG TATTCGAGAG ATCAAAGAGA 900
 GAGTAGGCAC GTCAAAGATT TTGTTTTTAC TCAGTGGTGG AGTAGACTCA ACAGTTTGTA 960
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 ATTTTCATAA AGATGAAGTG AGAATTTTGG GCAGAGAACT TGGACTTCCA GAAGAGTTAG 1500
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 CTTATATTGG TAAGGACTTT CCTGAAACCA ACAATATTTT GAAAATAGTA GCTGATTTT 1620
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 AGGATCAGGA GAAGCTGATG CAAATTACCA GTCTGCATTC ACTGAATGCC TTCTTGCTGC 1740
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Seq ID NO: 118 Protein sequence:
 Protein Accession #: AAH12178.1

1 11 21 31 41 51
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 SKKLYGAQPH PEVGLTENSF VILKNFLYDI AGCSGTFVQ NRELECIREI KERVGTSKVL 240
 VLLSGGVDSST VCTALLNRLAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
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Seq ID NO: 119 DNA sequence
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 Coding sequence: 27..1967

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30	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
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	CCTCCAAAGG	GACTAGAGTT	AAGCCTCCTG	CTCCCTTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
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	TCCCGTGT	CAGTGTCTCC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
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Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

65	1	11	21	31	41	51	
	MGLPRLVCAF	LLAACCCCPR	VAGVPGEAEQ	PAPELVEVEV	GSTALLKCGL	SQSQGNLSHV	60
	DWFSVHKR	TLIFVRVQSQ	GQSEPEGEYQ	RLSLQDRGAT	LALTQVTPQD	ERIFLCQGR	120
	PRSQEYRIQL	RUYKAPPEFN	IQVNPGLIPV	NSKEPEEVAT	CVGRNGYPIPI	QVIWYKNGRP	180
	LKEEKNRVHI	QSSQTVESSG	LYTLQSLKA	QLVKEDKDAQ	FYCELNRYLP	SGNHMKESRE	240
70	VTVPVPYPT	KVWLEVEPVG	MLKEGDRVEI	RCLADGNPPP	HFSISKQNP	TREAEETTN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPEQLLV	NYVSDVRVSP	AAAPERQEGSS	360
	LTLTCEAESS	QDLEFQWLRE	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
	QLVKLAIFGP	PWMAFKERKV	WVKENMVLNL	SCREASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
	LSTLNLVLT	ELLETVGECT	ASNDLGKNTS	ILFLELVNLT	TLTPDSNTTT	GLSTSTASPH	540
75	TRANSTSTER	KLPEPESRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLP	RRSGKQEIIL	600
	PPSRKTELTV	EVKSKDLPEE	MGLLQSSGD	KRAPGDQGEK	YIDLRLH		

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

80	1	11	21	31	41	51	
	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAAGCCA	60
	TGGAGACTTC	AGCATCTCTC	TCCCAGCCTC	AGGACAAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTTC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAACA	ATATGAGAGA	AACAAGTCTT	CTTCTCTCTC	CTTCTCTTCC	TCCTCATCCT	240
	CCTCATCTTC	TTCATCTCTC	TCCTCTCTCAG	GTCCTGGGCA	TGGGGAGCCT	GACGTTTTGA	300

5
10
15
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AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCTCT GGGGAATCAG 360
GACTCCGAAG GAGAGGCTCT GACCCAGCAA GTGGAGAAAGT GGAGGCCTCT CAGTTAAGAA 420
GACTGAATAT AAAGAAAGAT GATGAGTTTTC TCATTTCGT CCTCCTGTGC TTTGCCATCG 480
GGGCCTTGCT GGTGTGTTAT CACTATTACG CAGACTGGTT CATGTCTCTT GGGGTGCGCC 540
TGCTCACCTT CGCCTCCCTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
ACAGCGTCTT CCAAGGCTTC ATCCCCCTCT TCCAGAAGTT TAGGCTGACA GGGTTCAGGA 660
AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCAGTGT GACCACCACT 720
GCGACCCCTG AGCCCAACAG GGCAGAGCAG CATTCTGAGA GACGCACAGG AGACCAAGCC 780
AGACCAATAA ACAGAAACACT TTTCTTCCA TGTGTTCTGA ATGTTGGCAC CAGCCCGGGC 840
AGGGGCATCT CATTGTTGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
GGTGGGTGTG GGGCCTGAGG CTTACAGTA CCTGGACCAG CAGGAAGATT CTGGGAGGTC 960
ACTGCTCTCA GAGGACAGCA AGGGACCTCT AGCTCTGCAA GCTGTGATCT GTCTGGGTTT 1020
ATGGTTTTTC TCAATCCCA GGCATCTGCT ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
GGGAGAGATG GATGGTCCAC TGCTTTGAGG CAGGGAGCCA TCGGCTGGG GCCCTTGCT 1140
GAACCTGATG CAGTAAGATG GCTGAGGACT AAAACCATTT TTTTTCAGCC CAAAAAATAA 1200
GGCAGGAAAA TGATCATCAG AAATAAATG GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
TCCTGCACTT TTGGGAGGCT CAGGCTAAGG GTCGCTTGAA GCTGAGAGTT CAAGACCAAC 1320
CTGGGCAACA TAGTGAGACC CCCATCTCTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
TACATACCTG TACATACCTG CGGTTCCAGC TACTCAAGAG GCTGAGGCAG GAGGACTGCT 1440
TGAGCCACAG AGTTTCAGGC TGCACTGAGG TACGATCAAG CCACCTGCACT CCAGCCTGGG 1500
CGACAGAGCA AGATCGTTTC TCTAAAATT

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25 Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_060776

30

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1 11 21 31 41 51
METSASSSQP QDNSQVHRET EDVDYGETDF HKQDGKAGLF SQEQYERNKS SSSSFSSSSS 60
SSSSSSSSSS GPFGHEPDLV KDELQLYGDA PGEVVPSEGS GLRRRGSDDPA SGEVEASQLR 120
RLNIKKDEF FHFVLLCFAI GALLVCYHYW ADWFMSLGVG LLTFASLETV GIYFGLVYRI 180
HSVLQGFPL FQKRLTGFR KTD

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35 Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 243..896

40
45
50
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60
65
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1 11 21 31 41 51
ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
CCTTCTCTCG TCCGCACCTG GCCCCGCGCG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC 120
TGGCGGCTCG GGTGGCGCGG GTTCGGGCGG CCGCCTGGCT GCTCCTCGGG GCGGCGACGG 180
GGCTCAGCGG CGGGCCCGCG ACGGCCCTCA CCGCGCGCGG CTCTGACGCC GGCATAAGGG 240
CCATGTGTTT TGAAATTATT TTGAGGCAAG AAGTTTGTAA AGATGGTTTC CACAGAGACC 300
TTTAAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
TTAAACAGGA CATTCCTGCA GGACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG 420
AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAATTG TGATATAGAG GCCCCTAACT 480
ATTTGTCCAA GGAGTCTGAA GTTCTCATTT ATGCCAGAGC AGATTACAG TGCACTGACT 540
GTTTTCAAGC TTTTTGCTT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG 600
AAGCCTCGAT CTGTGTCAT AACCAGATT TGTGTATGTT TTGTGACCAA GAGTTCCTGA 660
TTTGAATG CTGGGCTCAC TCAGAGTGG CAGCCCTTGG TGGCTTGGAT AATGAGGATA 720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGTCT ATTACAATCC 840
TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAATATGAG CCATTTTCTC CTATAAGTTT 900
TATGTAGTTA AATGCTTCTT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
TTCTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
TAGAGGAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT 1080
CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTTCTG TAAATTAATG 1140
TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCAATT TAAGTACAAA ATTGAGAAAA 1260
CGGTTATAAA TAAGAATAAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCAGCAC 1320
TTTGGGAGCG CGAGGTGGGC GGTACACAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCTGTCTCT TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
GAGCCAGAT CGCACCACTG CACTACAGCC TGGGCGACAG AACGAGACCC TGCTCCAAA 1560
GGAAAAACAA AAAAGAAGAA TAAATAAATT TGGATGAAAA TCATGTTTAT TTAATAGTA 1620
ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTCAATGA AAATCATTAA AGTAGGACAG 1680
CTAAGAAATT AATATTAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATCTCTTA 1740
ACGCACTCCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
GGACTTGATG AAAGTGAAGT CTAAGATTG GTACAGAGTA TGTGAGGAG ACAACTCAGA 1860
TTGCCATTTT AAATAAGATT GTACATGAAC AAAAAAATAA AAAAAA

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75 Seq ID NO: 124 Protein sequence:
Protein Accession #: AAH22542

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1 11 21 31 41 51
MCSEILRQE VLKDGPHRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60
RNITEAVMVS ENFDIEAPNY LSKSEVLIY ARRDSQCIDC FQAFIPVHCR YHRPHSEEDGE 120
ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLLITILCS KKKKK

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85 Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

1	11	21	31	41	51	
AGACACCTCT	GGCCCTCACCA	TGAGCCTCTG	GCAGCCCTCTG	GTCCTGGTGC	TCCTGGTGTCT	60
GGGCTGCTGC	TTTGCTGCCC	CCAGACAGCG	CCAGTCCACC	CTTGTGCTCT	TCCCTGGAGA	120
CCTGAGAAC	AATCTCACCG	ACAGGCAGCT	GGCAGAGGAA	TACCTGTACC	GCTATGGTTA	180
CACCTGGGTG	GCAGAGATGC	GTGGAGAGTC	GAATCTCTCTG	GGGCTGTGCG	TGCTGCTTCT	240
CCAGAAGCAA	CTGTCCCTGC	CCGAGACCGG	TGAGCTGGAT	AGCGCCACGC	TGAAGGCCAT	300
GCGAACCCCA	CGGTGCGGGG	TCCAGACCT	GGGAGATTTC	CAAACCTTTG	AGGGCGACCT	360
CAAGTGGCAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGGCCGCG	420
GGCGGTGATT	GACGACGCGT	TTGCCGCGCG	CTTCGCACTG	TGGAGCGCGG	TGACGCGCGT	480
CACCTTCACT	CGCGTGTACA	GCCGGGACGC	AGACATCGTC	ATCCAGTTTG	GTGTGCGCGA	540
GCACGGAGAC	GGGTATTCCTT	TGCACGGGAA	GGACGGGCTC	CTGGCACACG	CCTTTCCTCC	600
TGGCCCCGGC	ATTGAGGGAG	ACGCCCATTT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660
GGGCGTCTGT	GTTCCAATCT	GGTTTGAAA	CGCAGATGGC	GCGGCTGCGC	ACTTCCCTCT	720
CATCTTCAG	GGCCGCTCCT	ACTCTGCTTG	CACCACCGAC	GGTCTGCTCG	ACGGCTTGCC	780
CTGGTGCAGT	ACCAACGCGC	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGCGA	840
GAGACTCTAC	ACCCGGGACG	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTCACTCT	900
CCAAGGCCAA	TCCTACTCCG	CCTGCACAC	GGACGGTCTG	TCCAGCGGCT	ACCGCTGGTG	960
CGCCACCAAC	GCCAACCTAC	ACCGGACAA	GCTCTTCGGC	TTCTGCCCGA	CCCGAGCTGA	1020
CTCGACGGTG	ATGGGGGGCA	ACTCGGCGGG	GGAGCTGTGC	GTCTTCCCCT	TCACTTTCCT	1080
GGGTAAAGAG	TACTCGACCT	GTACACGCGA	GGGCCGCGGA	GATGGGCGCC	TCTGGTGC	1140
TACCACCTCG	AACCTTGACA	GCCACAAGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
TTTGTTCCTC	GTGGCGGCGC	ATGAGTTCGG	CCACGCGCTG	GGCTTAGATC	ATTCTCTAGT	1260
GCCGAGGCG	CTCATGTACC	CTATGTACCG	CTTCACTGAG	GGGCCCTCTG	TGCTATAAGGA	1320
CGACGTGAAT	GTCATCCGCG	ACCTCTATGG	TCCTCGCCCT	GAACCTGAGC	CACGGCTCTC	1380
AACCACCAAC	ACACCGCAGC	CCACGGCTCC	CCGACGGTCT	TGCCCCACCG	GACCCCCAC	1440
TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTCAG	CTGGCCCCAC	1500
AGGTCCCCCG	ACTGCTGGCC	CTTCTACGGC	CACTACTGTG	CCTTTGAGTC	CGGTGGACGA	1560
TGCTTGCAAC	TGAACATCT	TCGACGCCAT	CGCGGAGATT	GGGAACCAAG	TGTATTTGTT	1620
CAAGGATGGG	AAGTACTGGC	GATTCTCTGA	GGGCAGGGGG	AGCCGCGCCG	AGGGCCCTCT	1680
CCTTATCGCC	GACAAGTGGC	CGCGCTGCGC	CGCAAGCTG	GACTCGGTCT	TTGAGGAGCC	1740
GCTCTCCAAG	AAGCTTTTCT	TCTTCTCTGG	GCGCCAGGTG	TGGGTGTACA	CAGGCGCGTC	1800
GGTGTCTGGC	CCGAGGCGTC	TGACAAAGCT	GGCCCTGGGA	GCCGACGTGG	CCGAGGTGAC	1860
CGGGGCCCTC	CGGAGTGGCA	GGGGGAAGAT	GCTGCTGTTT	AGCGGGCGCG	GCCTCTGGAG	1920
GTTCGACGTG	AAGGCGCAGA	TGGTGGATCC	CCGAGGCGCC	AGCGAGGTGG	ACCGGATGTT	1980
CCCCGGGGTG	CCTTTGGACA	CGCACGACGT	CTTCCAGTAC	CGAGAGAAAG	CCTATTTCTG	2040
CCAGGACCGC	TTCTACTGGC	GCGTGAAGTC	CCGAGTGGAG	TTGAACCAAG	TGGACCAAGT	2100
GGGCTACGTG	ACCTATGACA	TCCTGCAGTG	CCCTGAGGAC	TAGGGCTCCC	GTCTGCTCTT	2160
GCAGTGCCAT	GTAATATCCC	ACTGGGACCA	ACCCTGGGGA	AGGAGCCAGT	TTGCCGGATA	2220
CAAACTGTA	TTCTGTCTTG	GAGGAAAGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC	2280
TCACCTTTGT	TTTTTTTGG	AGTGTCTCTA	ATAAACTTGG	ATTCTCTAAC	CTTT	

Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_004985.1

1	11	21	31	41	51	
MSLWQPLVLV	LLVLGCCFAA	PRQRQSTLVL	FPGDLRLNLT	DRQLAEEVLY	RYGYTRVAEM	60
RGESKSLGPA	LLLLQKQLSL	PETGELDSAT	LKAMRTPRCG	VPLDGRFQTF	EGDLKWHHNN	120
ITYWIQNYSE	DLPRVIDDA	FARAFALWSA	VTPLTFTRVY	SRDADIVIQF	GVAEHGDGYP	180
FDGKDGLLAH	AFPPGPGIQG	DAHFDDELW	SLGKGVVVPT	RFGNADGAAC	HFPPFIFEGRS	240
YSACTTDGRS	DGLFWCSTTA	NYTDDRFGF	CPSERLYTRD	GNADGKPCQF	PFIFQGQSYS	300
ACTTDRSDG	YRWCAATTANY	DRDKLFGFCP	TRADSTVMGG	NSAGELCVFP	FTPLGKEYST	360
CTSEGRGDGR	LWCATTSNFD	SDKKWGFCPD	QGYSLFLVAA	HEFGHALGLD	HSSVPEALMY	420
PMYRFTGEP	LHKDDVNGIR	HLYGPRPEPE	PRPPTTTTPQ	PTAPPTVCPT	GPPTVHPSER	480
PTAGPTGPPS	AGPTGPPTAG	PSTATTVPLS	PVDDACNVNI	FDIAIEIGNQ	LYLPKDGKYW	540
RFSEGRGSRP	QGPFLLADKW	PALPRKLDV	FEEPLSKKLF	FFSGRQVWVY	TGASVLGPRR	600
LDKLGGLADV	AQVTGALRS	RGKMLLFSGR	RLWRFDVKAQ	MVDPRSASEV	DRMFPVPLD	660
THDVFQYREK	AYVFQDRFYV	RVSRSSELNQ	VDQVGYVTYD	ILQCPED		

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_004181
Coding sequence: 32-670

1	11	21	31	41	51	
GCAGAAATAG	CCTAGGGAGA	TCAACCCCGA	GATGCTGAAC	AAAGTGCTGT	CCCGGCTGGG	60
GGTCGCGGCG	CAGTGGGCGT	TCGTGGACGT	GCTGGGGCTG	GAAGAGGAGT	CTCTGGGCTC	120
GGTGCCAGCG	CCTGCCTGCG	CGCTGCTGCT	GCTGTTTCCC	CTCACGGCCC	AGCATGAGAA	180
CTTCAGGAAA	AAGCAGATTG	AAGAGCTGAA	GGGACAAGAA	GTTAGTCCTA	AAGTGTACTT	240
CATGAAGCAG	ACCATTTGGG	ATTCTGTGG	CACAATCGGA	CTTATTCACG	CAGTGGCCAA	300
TAATCAAGAC	AAACTGGGAT	TTGAGGATGG	ATCAGTTCTG	AAACAGTTTC	TTTCTGAAAC	360
AGAGAAAATG	TCCCTGAAG	ACAGAGCAAA	ATGCTTTGAA	AAGAATGAGG	CCATACAGGC	420
AGCCCATGAT	GCCGTGGCAC	AGGAAGGCCA	ATGTCGGGTA	GATGACAAGG	TGAATTTCCA	480
TTTTATTCTG	TTTAACAACG	TGATGGGCCA	CCTCTATGAA	CTTGATGGAC	GAATGCCTTT	540
TCCGTGAAC	CATGGCGCCA	GTTGAGGGA	CACCTGCTG	AAGGACGCTG	CCAAGGTGTG	600
CAGAGAATTG	ACCGAGCGTG	AGCAAGGAGA	AGTCCGCTTC	TCTGCCGTGG	CTCTCTGCAA	660
GGCAGCCTAA	TGCTCTGTGG	GAGGGACTTT	GCTGATTTCC	CCTCTTCCCT	TCAACATGAA	720
AATATATACC	CCCATGACG	TCTAAAATGC	TTCACTACTT	GTGAAACACA	GCTGTTCTTC	780
TGTTCTGCAG	ACCGGCTTTC	CCCTCAGCCA	CACCCAGGCA	CTTAAGCACA	AGCAGAGTGC	840
ACAGCTGTCC	ACTGGGCCAT	TGTGGTGTGA	GCTTCAGATG	GTGAAGCATT	CTCCCCAGTG	900
TATGTCTTGT	ATCCGATATC	TAACGCTTTA	AATGGCTACT	TTGGTTTCTG	TCTGTAAATT	960
AAGACCTTGG	ATGTGGTTAT	GTGTCTCTAA	AGAATAAATT	TTGCTGATAG	TAGC	

Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_004172

1	11	21	31	41	51	
MLNKVLSRLG	VAGQWRFDV	LGLEESLGS	VPAPACALLL	LPPLTAQHEN	FRKKQIEELK	60
GQEVSPKVPYF	MKQITIGNSCG	TIGLIHAVAN	NQDKLGFEDG	SVLKQFLSET	EKMSPEDRAK	120
CFEKNEAIIQA	AHDAVAQEGQ	CRVDDKVNFI	FILENNVDGH	LYELDGRMPF	PVNHGASSED	180
TLLKDAAKVC	REFTEREQGE	VRFSAVALCK	AA			

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 127-5385

1	11	21	31	41	51	
CGCCCGCGCG	CTGCAGCCCC	ATCTCCTAGC	GGCAGCCAG	GCGCGGAGGG	AGCGAGTCCG	60
CCCCGAGGTA	GGTCCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	GAGAGGGAGG	120
AAGAGGATGG	CAGGSCCAGC	CCCAGGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
AGCGTCAGCG	TCTCTGGGAC	CTTGGCAAA	CGCTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
ACGGAGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTTCAAGGAC	300
CGCGCGCTGA	ACACCCAGGC	GGAGCTGCTG	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
GTCATGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGGCGC	420
AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	GCGGCATTTT	480
GAGCTGGAGG	TGTTTGAGCC	ACTGGAGAGC	CCCGTGGACC	TGTACATCCT	CATGGACTTC	540
TCCAACCTCA	TGTCGATGA	TCTGGACAAC	CTCAAGAAGA	TGGGCGAGAA	CCTGGCTCGG	600
GTCCCTGAGCC	AGCTCACCAG	CGACTACACT	ATTGGATTGT	GCAAGTTTGT	GGACAAAGTC	660
AGCGTCCCGC	AGACGGACAT	GAGGCCTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
CCCCCTTCT	CCTTCAAGAA	CGTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCCGGAAT	780
AAACTGCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATGCC	840
ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCCGGACAG	CACCCACCTG	900
CTGGTCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	CGTCTGGCT	960
GGCATCATGA	GCCGCAACGA	TGAACGGTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
TACAGGACAC	AGGACTACCC	GTCCGTGCC	ACCCTGGTGC	GCCTGCTCGC	CAAGCACAA	1080
ATCATCCCCA	TCTTTGTGTG	CACCAACTAC	TCTATAGCT	ACTACGAGAA	GCTTCAACAC	1140
TATTTCCCTG	TCTCTTACT	GGGGGTGCTG	CAGGAGGACT	CGTCCAACAT	CGTGGAGCTG	1200
CTGGAGGAGG	CCTTCAATCG	GATCCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCC	1260
CGAGGCCTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCCTTT	1320
CACATCCGGC	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
GATGGGACGC	ACGTGTGCCA	GCTGCCGGAG	GACCAGAAGG	GCAACATCCA	TCTGAAACCT	1440
TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
CTGCAAAAAG	AGGTGCGTGC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
TGTGTGTGCA	GCGAGGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
GACATTGAGC	CCTGCCTGCG	GGAGGGCGAG	GACAAGCCGT	GCTCCGGCCG	TGGGGAGTGC	1680
CAGTGCGGGC	ACTGTGTGCG	CTACGGCGAA	GGCCGCTACG	AGGGTCAGTT	TGCGGAGTAT	1740
GACAACTTCC	AGTGTCCCGG	CACITCCGGG	TTCCTCTGCA	ATGACCGAGG	ACGCTGCTCC	1800
ATGGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTTCAGC	1860
AATGCCACCT	ACATGCGCAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
GGCCGCTGCC	ACTGCCACCA	GCAGTCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
TCCGCGATCC	ACCCGGGCGT	CTGCGAGGAC	CTACGCTCCT	GCGTGCACTG	CCAGGCGTGG	2040
GGCACCGGGC	AGAACGAAGG	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
GACGAGCTTA	AGAGAGCCGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
CTGGTGACA	AGAAAGAAAG	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
CTCCTCTCC	TGCCCTCTCT	GGCCTGCTA	CTGCTGCTAT	GCTGGAAGTA	CTGTGCTGCT	2340
TGCAAGGCCT	GCCTGGCACT	TCTCCCGTGC	TGCAACCGAG	GTCACATGGT	GGGCTTTAAG	2400
GAAGACCACT	ACATGCTCGG	GGAGAACCTG	ATGGCCTCTG	ACCACTTGGG	CACGCCCATG	2460
CTGCGCAGCG	GGAACTCAA	GGGCGGTGAC	GTGGTCCGCT	GGAAGGTCAC	CAACACATG	2520
CAGCGGCCTG	GCTTTGCCAC	TCATGCCGCC	AGCATCAACC	CCACAGAGCT	GGTGCCCTAC	2580
GGGCTGTCTC	TGGCGCTGGC	CCGCCTTTGC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
GAGTGCGCC	AGCTGCGCCA	GGAGGTGGAG	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
TCGGGTGTAC	ACAAGCTCCA	GCAGACCAAG	TTCCGGCAGC	AGCCCAATGC	CGGGAAAAAG	2760
CAAGACCACA	CAATTGTGGA	CACAGTGCTG	ATGGCGCCCC	GCTCGGCCAA	GCGCGCCGTC	2820
CTGAAGCTTA	CAGAGAAGCA	GGTGGAACAG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
GGCTACTACA	CCCTCACTGC	AGACCAGGAC	GCCCGGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
GTGGAAGCTG	TGGAGCTAGC	GGTGCCCTCT	TTTATCCGGC	CTAGGATGAA	CGACGAGAAG	3000
CAGCTGCTGG	TGGAGGCCAT	CGAGTGCCCC	GCAGGCACTG	CCACCTCTCG	CCGCGCCCTG	3060
GTAAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCCTTTGA	GCAGCTGAG	3120
TTCTCGGTCA	GCCGCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCCTGGAC	3180
GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
TACATCCCGG	TGGAGGGTGA	GCTGCTGTTT	CAGCCTGGGG	AGGCCCTGGA	AGAGCTGCAG	3300
GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCCGT	3360
TTCCAGCTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
ACCATCATCA	TCAGGACCCC	AGATGAACTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
TCACAGCCAC	CCCCTCAGCG	CGACCTGGGC	GCCCCGAGCA	ACCCCAATGC	TAAGGCCCGT	3540
GGGTCCAGGA	AGATCCATT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
GTAAAGTACT	GGATTCAAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
CCCTCAGTGG	CCTGACCCAA	CCTGATCCCG	TATGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
TACGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGGTGT	CCTGCGGCAC	CCACCAAGGA	3780
GTGCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTCGTCT	CCTCCACGGT	GACCCAGCTG	3840
AGCTGGGCTG	AGCCAGCGGT	GACCAACGGT	GAGATCACAG	CTACGAGGT	TGCTATGGC	3900
CTGGTCAACG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGTGGT	TGACAACCTT	3960
AAGAACCCGA	TGCTGCTTAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
AAGGCGCGCA	ACGGGGCCGG	CTGGGGCCCT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
CAGCCCAAGA	GGCCCATGTC	CATCCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCACG	4140
AGCGGGGAGG	ACTACGACAG	CTTCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
GGCAGCCAGA	GCCAGCAGGT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
TTTGCCCTTC	CGGGCAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGCTGCC	4320
TATGGCACCC	ACCTGAGCCC	ACAGTGCCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380

ACACGGGACT ACAACTCACT GACCCGCTCA GAACACTCAC ACTCGACCAC ACTGCCGAGG 4440
 GACTACTCCA CCTCACTCCT CGTCTCCTCC CACGACTCTC GCCTGACTGC TGGTGTGCC 4500
 GACACGCCCC CCCGCTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG 4560
 CAGGAGCCCG GGTGCATGAG GCGCTGACAG GGCTACAGTG TGGAGTACCA GCTGCTGAAC 4620
 5 GCGGTGAGC TGCATCGGCT CAACATCCCC AACCTGCCCC AGACCTCGGT GGTGGTGGAA 4680
 GACCTCTGC CCAACCACTC CTACGTGTTT CCGCTGCGGG CCCAGAGCCA GGAAGGCTGG 4740
 GGCCGAGAGC GTACGGGTGT CATCACCATT GAATCCAGG TGCAACCGCA GAGCCCACTG 4800
 TGTCCCTGCG CAGGCTCCGC CTTCACTTTG AGCACTCCCA GTGCCCCAGG CCGCTGCTGG 4860
 10 TTCACTGCCC TGAGCCAGCA CTCGCTGCAG CTGAGCTGGG AGCGGCCACG GAGGCCCAAT 4920
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 GCATTCCGGG TGGATGGAGA CAGCCCCGAG AGCCGGCTGA CCGTGCCGGG CCTCAGCGAG 5040
 AACGTGCCCT ACAAGTTCAA GGTGCAGGCC AGGACCACTG AGGGCTTCGG GCCAGAGCGC 5100
 GAGGGCATCA TCACCATGCA GTCCCAGGAT GGAGGACCTT TCCCGCAGCT GGGCAGCCGT 5160
 15 GCGGGCTCTT TCCAGCACCC GCTGCAAAAG GAGTACAGCA GCATCACCCAC CACCCACACC 5220
 AGCGCCACCC AGCCCTTCTT AGTGGATGGG CCGACCTTGG GGGCCAGCA CCTGGAGGCA 5280
 GCGCGCTCCC TCCAGCCGCA TGTGACCCAG GAGTTTGTGA GCGGCACTG GACCCACAGC 5340
 GGAACCTCTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTTGACCGCA CCTGCCCCA 5400
 CCCCCGCAAT GTCCCACTAG GCGTCTCTCC GACTCCTCTC CCGGAGCCTC CTCAGTACT 5460
 20 CCATCCTTGC ACCTCTGGG GCCACGCCCA CCCGCATGCA CAGAGCAGGG GCTAGGTGTC 5520
 TCCTGGGAGG CATGAAGGGG GCAAGGTCCG TCCTCTGTGG GCCCAACCT ATTGTAAACC 5580
 AAAGAGCTGG GAGCAGCACA AGGACCCAGC CTTTGTCTCG CACTTAATAA ATGGTTTTCG 5640
 ACTG

Seq ID NO: 130 Protein sequence:
 Protein Accession #: NP_000204

1 11 21 31 41 51
 30 | | | | |
 MAGPRPSPWA RLLAALISV SLSTLANRC KKAPVKSCTE CVRVKDKCAY CTDEMFRDRR 60
 CNTQAEALLAA GQQRRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL 120
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SQLTSDYTIG FGKFDVKVSV 180
 PQTDMRPEKL KEPWNSDPP FSFKNVISLT EDVDFRNKL QGERISGNLD APEGGFDAIL 240
 QTAICTRDIG RKPWDSHLLV FSTESAFHYE ADGANVLAGE MSRNDERCHL DTTGTYTQYR 300
 35 TDYPSVPTL VRLAKHNII PIFAVTNYSY SYEKLHTYF PVSSLGLVQE DSSNIVELLE 360
 EAFNRIRSNL DTRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGEVGYQV QLRALHVDG 420
 THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN 540
 40 FQCPRTSGFL CNDRCRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600
 CHCQQLSLYT DTICEINYSY IHPGLCEDLR SCVQCQAWGT GEKKGRTECE CNFKVMVDE 660
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDG APGNSTVLV HKKKDCPPGS FWWLIPLLL 720
 LLLPLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKEH HYMLRENLM A SDHLDTPMLR 780
 SGNLKGDRVV RKNVNNMQSR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840
 45 AQLRQEVEEN LNEVYRQISG VHKLQQTFR QPNAGKKQD HTIVDTVLMA PRSAKPALLK 900
 LTKQVEQRA FHDLLVAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDEKQL 960
 LVEAIDVPAQ TATLGRVLVN ITIKEQARD VVSFEQPEFS VSRGDQVARI PVIRVLDGG 1020
 KSQVSRYTQD GTAQGNRYI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
 VQLSNPKFPA HLGQPHSTTI IIRDPDELDR SFTSMLSSQ PPPHGDLAG QNPNKAAGS 1140
 50 RKIHFNWLPF SKKPMGYRVK YWIGLDSSESE AHLDSKVPS VELTNLYPYC DYEMKVCAYG 1200
 AQGEGPYSSL VSCRTHQEVV SEPGRFAFNV VSSTVTQLSW AEPATNGEI TAYEVCYGLV 1260
 NDDNRPIGPM KVLVDNPKN RMLLIENLRE SQPYRYTVKA RAGAGWGPER EAIINLATQP 1320
 KRPMSEIPII DPIPVDNAAG EDDYDFLMYS DDVLRSPSGS QRPVSDDTE HLVNRMDF 1380
 FPGSTNSLHR MTTTAAAYG THLSPHVPHR VLSTSTLTR DYNLSLRESE SHSTTLPRDY 1440
 55 STLTSSVSHD SRLTAGVPDT PTRLVFSALG PTLRVSQWE PRCEPLQGY SVEYQLLNGG 1500
 ELHRLNIPNP AGTSVVDL LPHNSYVFRV RAQSQEGWGR EREGVITIE QVHPQSLPLC 1560
 LPGAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM AQGGGPATF 1620
 RVDGDSPEER LTVPLGSENV PYKFKVQART TEGFPEREG IITIESQDGG PFPQLGSRA 1680
 LFQHPQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEF VSRTLTSTGT 1740
 60 LSTHMDQQFF QT

Seq ID NO: 131 DNA sequence
 Nucleic Acid Accession #: BC004372
 Coding sequence: 132..2231

1 11 21 31 41 51
 65 | | | | |
 CCTCGTCCCG CGGACCCAG CCTCTGCCAG GTTCGGTCCG CCATCCTCGT CCGCTCCTCC 60
 GCCGGCCCCCT GCCCGCGGCC CAGGGATCCT CAGCTCCTT TCGCCCGCGC CTTCCGTTCC 120
 70 CTCGGACAC CATGACAAG TTTTGGTGGC ACGCAGCTG GGAAGCTGCT CTCGTGCCGC 180
 TGAGCCTGGC GCAGATCGAT TTGAATATAA CCGCGCTT TGCAGGTGTA TTCCAGTGG 240
 AGAAAAATGG TCGCTACAGC ATCTCTCGGA CGGAGGCCGC TGACCTCTGC AAGGCTTTCA 300
 ATAGCACCTT GCCCAACTG GCCCAGATGG AGAAAGCTCT GAGCATCGGA TTTGAGACCT 360
 GCAGGTATGG GTTCTAGAA GGGCATGTGG TGATTCCTCG GATCCACCCC AACTCCATCT 420
 75 GTGCAGAAA CAACACAGGG GTGTACATCC TCACATCCAA CACCTCCAG TATGACACAT 480
 ATTGCTTCAA TGCTTCAGCT CCACCTGAAG AAGATTGTAC ATCAGTCACA GACCTGCCCA 540
 ATGCTTTTGA TGGACCAATT ACCTAACCTA TTGTTAACCG TGATGGCACC CGCTATGTCC 600
 AGAAAGGAGA ATACAGAAGC AATCCTGAAG ACATCTACCC CAGCAACCCT ACTGATGATG 660
 ACGTGAGCAG CGGCTCCTCC AGTGAAAGGA GCAGCACTTC AGGAGGTAC ATCTTTTACA 720
 80 CCTTTTCTAC GTTACACCCC ATCCAGACG AAGACAGTCC CTGATCACC GACAGCAGAG 780
 ACAGAATCCC TGCTACCACT ACGTCTTCAA ATACCATCTC AGCAGGCTGG GAGCCAAATG 840
 AAGAAAAATGA AGATGAAAGC GACAGACACC TCAGTTTTC TGGATCAGGC ATTGATGATG 900
 ATGAAGATT TATCTCCAGC ACCATTTCAA CCACACACG GGTCTTTGAC CACACAAAC 960
 AGAACCCAGG CTGAGCCAG TGAACCCAA GCCATTCAA TCCGGAAGTG CTACTTCAGA 1020
 85 CAACCAACAG GATGACTAGT TAGACAGAA ATGGCACCAC TGCTTATGAA GGAACCTGGA 1080
 ACCCAGAAGC ACACCTCCC CTCATTACC ATGAGCATCA TGAGGAAGAA GAGACCCAC 1140
 ATTCTACAAG CACAATCCAG GCAACTCCTA GTAGTACAAC GGAAGAAACA GCTACCCAGA 1200
 AGGAACAGTG GTTTGGCAAC AGATGGCATG AGGATATCG CCAACACACC AGAGAAGACT 1260

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CCCATTCGAC AACAGGGACA GCTGCAGCCT CAGCTCATAC CAGCCATCCA ATGCAAGGAA 1320
GGACAACACC AAGCCCAGAG GACAGTTCCT GGACTGATTT CTTCACCCCA ATCTCACACC 1380
CCATGGGACG AGGTTCATCA GATGGAAGAA GGATGGATAT GGACTCCAGT CATAGTACAA 1440
CGCTTCAGCC TACTGCAAAAT CCAAAACACAG GTTTGGTGGG AGATTGGAC AGGACAGGAC 1500
CTCTTTCAAT GACAACGAG CAGAGTAATT CTCAGAGCTT CTCTACATCA CATGAAGGCT 1560
TGGAAGAAGA TAAAGACCAT CCAACAACCT CTACTCTGAC ATCAAGCAAT AGGAATGATG 1620
TCACAGGTGG AAGAAGAGAC CCAATCATT CTGAAGGCTC AACTACTTTA CTGGAAGGTT 1680
ATACCTCTCA TTACCCACAC ACGAAGGAAA GCAGGACCTT CATCCCAAGT ACCTCAGCTA 1740
AGACTGGGTC CTTTGGAGTT ACTGCAGTTA CTGTGGAGA TTCCAACCTT AATGTCAATC 1800
GTTCTTTATC AGGAGACCAA GACACATTCC ACCCCAGTGG GGGGTCCCAT ACCACTCATG 1860
GATCTGAATC AGATGGACAC TCACATGGGA GTCAAGAAGG TGGAGCAAAC ACAACCTCTG 1920
GTCCTATAAG GACACCCCAA ATTCCAGAAT GGCTGATCAT CTTGGCATCC CTCTTGGCCT 1980
TGGCTTTGAT TCTTGCAGTT TGCATTGCG TCAACAGTCG AAGAAGGTGT GGGCAGAAGA 2040
AAAAGCTAGT GATCAACAGT GGCAATGGAG CTGTGGAGGA CAGAAAGCCA AGTGGACTCA 2100
ACGGAGAGGC CAGCAAGTCT CAGGAAATGG TGCATTGGT GAACAAGGAG TCGTCAGAAA 2160
CTCCAGACCA GTTTATGACA GCTGATGAGA CAAGGAACCT GCAGATGTG GACATGAAGA 2220
TTGGGGTGTA ACACCTACAC CATTATCTTG GAAAGAAACA ACCGTGGAA ACATAACCAT 2280
TACAGGGAGC TGGGACACTT AACAGATGCA ATGTGCTACT GATTGTTTCA TTGCGAATCT 2340
TTTTTAGCAT AAAATTTTCT ACTCTTAAAA AAAAAA AAAA

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Seq ID NO: 132 Protein sequence:
Protein Accession #: AAH04372

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1 11 21 31 41 51
| | | | |
MDKFWNHAAM GLCLVPLSLA QIDLNITCRF AGVFHVEKNG RYISIRTEAA DLCKAFNSTL 60
PTMAQMEKAL SIGFETCRYG PIEGHVVIPIR IHPNSICAAN NTGVYILTSN TSQYDITYCFN 120
ASAPPEEDCT SVTDLPNADF GPITITIVNR DGTRYVQKGE YRNPEDIYP SNPTDDDVSS 180
GSSERSSTS GGYIFYTFTST VHPIDEDSP WITDSTRIP ATSTSSNTIS AGWEPNEENE 240
DERDRHLSFS GSGIDDDDEF ISSTISTTFR AFDHTKQND WTQWNPSSHN PEVLLQTTR 300
MTDVRNGTT AYEGRWNPEA HPPLIHHEHH EEEETPHSTS TIQATPSSTT EETATQKEQW 360
FGRNWHGYSR QTPREDSSHST TGTAASAHT SHPMQGRTPP SPEDSSWTF FNPISHPMGR 420
GHQAGRMDM DSSHSTTLQP TANPNTGLVE DLDRTGPLSM TTQSNQSQSF STSHGLEED 480
KDHPFTSTLT SSNRNDVTGG RRDPNHSEGS TTLLEGYTSY YPHTKESRTF IPVTSAKTGS 540
FGTAVTVGD SMSNVRNRLS GDQDTFHPSG GSHTHGSES DGHSHGSQEG GANTTSGPIR 600
TPQIPWELII LASLLALALI LAVCIAVNSR RRCGQKKLV INSGNGAVED RKPISGLNGEA 660
SKSQEMVHLV NKESSETPDQ FMTADETRNL QNVDMKIGV

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Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_002882
Coding sequence: 150-755

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1 11 21 31 41 51
| | | | |
CGAGGTCGCG GTCCGTGGGCG GGAGGGAAGA GCGGGCGGGC GGGAGGCGCC GCGCCAGAC 60
GCGGAGGGAAG GGAGCTACGA GTAGCCGCCG AGAGGCCGCG GAGCCAGCGA CGACCGACCC 120
AGCCGAGCCG CCGCCGCCGC CGCGCCCCCA TGGCGGCCGC CAAGGACACT CATGAGGACC 180
ATGATACTTC CACTGAGAAT ACAGACGAGT CCAACCATGA CCCTCAGTTT GAGCCAATAG 240
TTTCTCTTCC TGAGCAAGAA ATTAACAAC TGGAAGAAGA TGAAGAGGAA CTTTTTAAAA 300
TGCGGGCAAA ACTGTTCGA TTTGCCTCTG AGAACGATCT CCCAGAATGG AAGGAGCGAG 360
GCACTGGTGA CGTCAAGCTC CTGAAGCACA AGGAGAAAGG GGCCATCCGC CTCCTCATGC 420
GGAGGGACAA GACCCTGAAG ATCTGTGCCA ACCACTACAT CACGCCGATG ATGGAGCTGA 480
AGCCCAACGC AGGTAGCGAC CGTGCCTGGG TCTGGAACAC CCACGCTGAC TTCGCCGACG 540
AGTGCACCAA GCCAGAGCTG CTGGCCATCC GCTTCCTGAA TGCTGAGAAT GCACAGAAAT 600
TCAAAACAAA GTTTGAAGAA TGCAGGAAAG AGATCGAAGA GAGAGAAAAG AAAGCAGGAT 660
CAGGCAAAAA TGATCATGCC GAAAAAGTGG CGGAAAAGCT AGAAGCTCTC TCGGTGAAGG 720
AGGAGACCAA GGAGGATGCT GAGGAGAAGC AATAAATCGT CTTATTTTAT TTTCTTTTCC 780
TCTCTTTCTT TTTCTTTTCT TAAAAAATTT TACCCTGCCC CTCTTTTTCG GTTTGTTTTT 840
ATTCTTTTCT TTTTACAAGG GACGTTATAT AAAGAAGTGA ACTC

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Seq ID NO: 134 Protein sequence:
Protein Accession #: NP_002873

65

70

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1 11 21 31 41 51
| | | | |
MAAAKDTHED HDTSTENTDE SNHDPQFEPI VSLPEQEIKT LEEDEEELFK MRKLFRFAS 60
ENDLPEWKER GTGDVKLLKH KEKGAIIRLLM RRDRTLKICA NHYITPMEL KPNAGSDRAW 120
VMNTHADPAD ECPKPELLAI RFLNAENAQK PKTKFEERK EIEEREKAG SGKNDHAEKV 180
AEKLEALSVK EETKEDAEK Q

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Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_000077.2
Coding sequence: 277-742

75

80

85

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1 11 21 31 41 51
| | | | |
CCCAACCTGG GCGCACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
TCCTCCGAGC ACTCGCTCAC GGCCTCCCTT TGCTGGAAA GATACCGCG TCCCTCCAGA 120
GGATTGTAGG GACAGGTCAG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
GGGCTGGCTG GTCACCAGAG GGTGGGGCGG ACCGCGTGG CTCGGCGGCT GCGGAGAGGG 240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
GCCTTGGCTG GACTGGCTGG CCACGGCGCG GGCCTGGGGT CGGGTAGAGG AGGTGCGGGC 360
GCTGCTGGAG GCGGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA 420
GGTCATGATG ATGGGCAGCG CCCGAGTGGC GGAGCTGCTG CTGCTCCAGC GCGCGGAGCC 480

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CAACTGCGCC GACCCCGCCA CTCTCACCAG ACCCGTGCAC GACGCTGCCC GGGAGGGCTT 540
CCTGGACACG CTGGTGGTGC TGACACGGGC CGGGGCGCGG CTGGACGTGC GCGATGCCTG 600
GGGCGGTCTG CCCGTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTGC CACGTTACCT 660
GCGCGGGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
TCCCTCAGAC ATCCCGGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
GATCATCAGT CACCGAAGGT CCTACAGGGC CACAACGCC CCGCCACAA CCCACCCCGC 840
TTTCGTAGTT TTCATTAGA AAATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT 900
ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATCTTATATA 960
AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTTCAGTG TGTGGAGTT TTCTGGAGTG 1020
AGCACTCAGC CCCTAAGCGC ACATTTCATGT GGGCATTCTT TGCGAGCCTC GCAGCCTCCG 1080
GAAGCTGTGC ACTTCATGAC AAGCATTTTG TGAACAGGGG AAGCTCAGGG GGGTTACTCG 1140
CTTCTCTTGA GTCACACTGC TAGCAATGG CAGAACCAAA GCTCAATAA AAATAAAATA 1200
ATTTTCATTC ATTCATC

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Seq ID NO: 136 Protein sequence:
Protein Accession #: NP_000068.1

20

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1      11      21      31      41      51
|      |      |      |      |      |
MEPAAGSSME PSADWLATAA ARGVVEEVRA LLEAGALPNA PNSYGRRIQ VMMMGSRVA 60
ELLLLHGAEP NCADPATLTR PVHDAAREGP LDTLVVLHRA GARLDVRDAW GRLPVDLAE 120
LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

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25
Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: NM_058196.1
Coding sequence: 104-421

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1      11      21      31      41      51
|      |      |      |      |      |
TGTGTGGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCCTTTC CGTCATGCCG 60
GCCCCCACC TCCTGCTGAC CATCTGTGTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
CCGAGTGGCG GAGCTGCTGC TGCTCCACGG CGCGGAGCCC AACTGCGCCG ACCCGCCAC 180
TCTCACCCGA CCCGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
GCACCGGGCC GGGGCGCGGC TGGACGTGCG CGATGCCCTGG GCGCGTCTGC CCGTGGACCT 300
GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACCTG CGCGCGGCTG CCGGGGGCAC 360
CAGAGGCAGT AACCATGCCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCCGATTG 420
AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAAACTTAG ATCATCAGTC ACCGAAGGTC 480
CTACAGGGCC ACAACTGCCC CCGCCACAAC CCACCCCGCT TTCTAGTTT TCATTTAGAA 540
AATAGAGCTT TAAAAATGT CCTGCCCTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
TAAATGTCCA TTTATATCAT TTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
CGCTTCTGCC TTTTCTGCT GTTGGAGTTT TCTGGAGTGA GCACTCACGC CTAAGCGCA 720
CATTTCATGT GGCATTTCTT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTTCATGACA 780
AGCATTTTGT GAACTAGGGA AGCTCAGGGG GGTACTGGC TTCTCTTGG TCACTCTGCT 840
AGCAATGGC AGAACCAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCATCT

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50
Seq ID NO: 138 Protein sequence:
Protein Accession #: NP_478103.1

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1      11      21      31      41      51
|      |      |      |      |      |
MMMGSRVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG 60
RLPVDLAEEL GHRDVARYLR AAGGTRGSN HARIDAEGB SDIPD

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60
Seq ID NO: 139 DNA sequence
Nucleic Acid Accession #: NM_058197.1
Coding sequence: 272-684

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80
85

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1      11      21      31      41      51
|      |      |      |      |      |
CCCAACCTGG GCGGACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC 60
TCCTCCGAGC ACTCGCTCAC GCGTCCCCT TGCTGGAAA GATACCGCG TCCCTCCAGA 120
GGATTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
GGGCTGGCTG GTCACAGAG GGTGGGGCGG ACCCGTGGC CTGGCGGCT GCGGAGAGGG 240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
GCCGCGCGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCCCG 360
GGGTGCGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA 420
TAGTTACGGT CGGAGGCCGA TCCAGGTGGG TAGAAGTCT GCAGCGGAG CAGGGGATGG 480
CGGGCGACTC TGGAGGACGA AGTTTGACAG GGAATTGGAA TCAGGTAGCG CTTTCGATTCT 540
CCGAAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAAAGG GTTTGTAATC ACAGACCTCC 600
TCCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTTGTAT TAGATGGAAG 720
TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGCG GCGGAGCCCA 780
ACTGCGCGGA CCGGCCACT CTCACCGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC 840
TGGACACGCT GGTGGTGTG CACCGGGCGG GGGCGCGGCT GGACGTGCGC GATGCCTGGG 900
GCCGTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTCGCA CGGTACCTCG 960
GCGCGGCTGC GGGGGGCCAC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
CCTCAGACAT CCCCGATTGA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
CATCAGTCA CAAAGGCTCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 1140
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTTAA CGTAGATATA 1200
TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1260
TGTAATAAAG AAAAACACCG CTTCTGCCTT TCACTGTGT TGGAGTTTTC TGGAGTGAGC 1320
ACTCAGCCCC TAACGCGACA TTCATGTGGG CATTCTTGC GAGCCTCGCA GCCTCCGGAA 1380
GCTGTGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTAAGTGGCT 1440
CTCTTGAGTC ACACGTCTAG CAAATGGCAG AACCAAGGCT CAAATAAAAA TAAATAAATT 1500

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Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

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1      11      21      31      41      51
|      |      |      |      |      |
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVALL BAGALPNAPN SYGRRPIQVG 60
RRSAAGAGDG GRLWRKFAG ELESSESIL RKGRLPGEF SEGVNHRPP PGDALGAWET 120
KEEE

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Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

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1      11      21      31      41      51
|      |      |      |      |      |
CCTCCCTACG GCGCCTCCG GCAGCCCTTC CCGCGTGGC AGGGCTCAGA GCCGTTCCGA 60
GATCTTGGAG GTCCGGGTGG GAGTGGGGT GGGGTGGGG TGGGGTGAA GGTGGGGGGC 120
GGGCGCGCTC AGGGAAGCGG GGTGCGCGCC TGGGGGGCG AGATGGGCAG GGGCGCGTGC 180
GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG 240
GGCGGCGCAG CGGTGCCGA GCTCGGCCCT GGAGGCGCG AGACATGGT GCGCAGGTTC 300
TTGGTGACCC TCCGATTTCG GCGCGCGTGC GGGCGCGCG GAGTGAGGT TTTCTGGTT 360
CACATCCCGC GGCTCAGGGG GGAGTGGGCA GCGCCAGGGG CGCCCGCCGC TGTGGCCCTC 420
GTGCTGATGC TACTGAGGAG CCAGCCTCTA GGGCAGCAGC CGTTCCTAG AAGACCAGGT 480
CATGATGATG GGCAGCGCCC GAGTGGCGGA GCTGCTGCTG CTCCACGGCG CGGAGCCCAA 540
TGTGCGCCGAC CCGCCACTTC TCACCCGACC CGTGACGAC GCTGCCCGGG AGGGCTTCCT 600
GGACAGCTG GTGGTGTCTG ACCGGGCGG GCGCGGCTG GACGTGCGCG ATGCTGGGG 660
CCGTCTGCCC GTGACCTTGG CTGAGGAGCT GGGCCATGCG GATGTCGCAC GGTACCTGCG 720
CGCGGCTGCG GGGGGCACC GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC 780
CTCAGACATC CCGATTGAA AGAACACAG AGGCTCTGAG AACCTCGGG AAACCTAGAT 840
CATCAGTCAC CGAAGTCTCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCCGCTTT 900
CGTAGTTTTT ATTAGAAAA TAGAGCTTTT AAAAATGTCC TGCTTTTAA CGTAGATATA 960
TGCTTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1020
TGTAAAAAAG AAAAACACCG CTCTGCTTCT TTTACTGTGT TGGAGTTTTC TGGAGTGAGC 1080
ACTCAGCCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCTCGCA GCCTCCGGAA 1140
GCTGTGAGCT TCATGACAAG CATTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT 1200
CTCTTGAGTC AACTGCTAG CAAATGGCAG AACCAAGCT CAAATAAAAA TAAATAAATT 1260
TTCATTCACT CACTC

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Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

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1      11      21      31      41      51
|      |      |      |      |      |
MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AALGPGGGE NMVRRFLVTL RIRRACGPPR 60
VRVFFVHIPP LTGEWAAPGA PAAVALVLM LRSQRLGQQP LPRRPGHDDG QRPSSGAAAA 120
PRRGAQLRRP RHSHPTRARR CPGGLPGHAG GAAPGRGAAG RARCLGPSAR GPG

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Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

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1      11      21      31      41      51
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GAAATTGCAC ACTTAAGAC ATCAGTGGAT GAAATCACA GTGGGAAAGG AAAGCTGACT 60
GATAAAGAGA GACAGAGACT TTTGGAGAAA ATTCGAGTCC TTGAGGCTGA GAAGGAGAAG 120
AATGCTTATC AACTCAGACA GAAGGACAAA GAAATACAGC GACTGAGAGA CCAACTGAAG 180
GCCAGATATA GTACTACCGC ATTGCTTGAA CAGCTGGAAG AGACAACGAG AGAAGGAGAA 240
AGGAGGGAGC AGGTGTGTAA AGCCTTATCT GAAGAGAAAG ACGTATTGAA ACAACAGTTG 300
TCTGCTGCAA CCTCAGCAAT TGCTGAACTT GAAAGCAAAA CCAATACACT CCGTTTATCA 360
CAGACTGTGG CTCCAACCTG CTTCAACTCA TCAATAAATA ATATTCATGA AATGGAAATA 420
CAGCTGAAAG ATGCTCTGGA GAAAAATCAG CAGTGGCTCG TGTATGATCA GCAGCGGGAA 480
GTCTATGTAA AAGGACTTTT AGCAAAGATC TTTGAGTTGG AAAAGAAAAA GGAACAGCT 540
GCTCATTAC TCCACAGCA GACAAAAAAG CCTGAATCAG AAGGTTATCT TCAAGAAGAG 600
AAGCAGAAAT GTTACACGA TCTCTTGGCA AGTGCAAAAA AAGATCTTGA GGTGAAACGA 660
CAAAACATAA CTCAGCTGAG TTTTGAACCT AGTGAATTTC GAAGAAAAATA TGAAGAAACC 720
CAAAAAGAAG TTCACAAATT AAATCAGCTG TTGTATTAC AAAGAAGGGC AGATGTGCAA 780
CATCTGGAAG ATGATAGGCA TAAAACAGAG AAGATACAAA AACTCAGGGA AGAGAATGAT 840
ATTGCTAGGG GAAAACTTGA AGAAGAGAAG AAGAGATCCG AAGAGCTCTT ATCTCAGGTC 900
CAGTCTCTTT ACACATCTCT GCTAAAGCAG CAAGAAGAAC AAACAAGGCT AGCTCTGTTG 960
GAACAACAGA TGCAGGCATG TACTTTAGAC TTTGAAAATG AAAAAGCTCGA CCGTCAACAT 1020
GTGCAGCATC AATTGCTATG AATTCTTAAG GAGCTCCGAA AAGCAAGAAA AAATAACACA 1080
GTTGGAATCC TTGAAACAGC TTCATGAGTT TGCCATCACA GAGCCATTAG TCACTTTCCA 1140
AGGAGAGACT GAAAAACAGAG AAAAAGTTGC CGCCTCACCA AAAAGTCCCA CTGCTGCACT 1200
CAATGGAAGC CTGGTGAATG GTCCCAAGTG CAATATACAG TATCCAGCCA CTGAGCATCG 1260
CGATCTGCTT GTCCATGTGG AATACTGTTT AAAGTAGCAA AATAAGTATT TGTTTTGATA 1320
TTAAAAGATT CAATATGTGA TTTTCTGTTA GCTTGTGGGC ATTTTGAATT ATATATTTCA 1380
CAATTTGCTT AAAACTGCTT ATCTACCTTT GACACTCCAG CATGCTAGTG AATCATGTAT 1440
CTTTTAGGCT GCTGTGCAAT TCTCTTGGCA GTGATACCTC CCTGACATGG TTTATCATCA 1500
GGCTGCAATG ACAGAAATGTG GTGAGCAGCG TCTACTGAGA TACTAACATT TTGCACTGTC 1560
AAAACTACTG GTGAGGAAAA GATAGCTCAG GTTATTGCTA ATGGGTTAAT GCACCAGCAA 1620
GCAAAATATT TTATGTTTTG GGGGTTTTGA AAAATCAAAG ATAATTAACC AAGGATCTTA 1680
ACTGTGTTCC CATTTTTTAT CCAAGCACTT AGAAAACCTA CAATCCTAAT TTTGATGTCC 1740
ATTGTTAAGA GGTGGTGATA GATACATTTT TTTTTCATA TTGTATAGCG GTTATTAGAA 1800

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AAGTTGGGGA TTTTCTTGAT CTTTATTGCT GCTTACCATT GAAACTTAAC CCAGCTGTGT 1860
 TCCCAACTC TGTTCTGCGC ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA 1920
 CACACAATGT TTCTCTTAT GTTATCTGGC AGTAACTGTA ACTTGAATTA CATTAGCACA 1980
 TTCTGCTTAG TTAATAATGT TAAATAAAC CCAATGTAGCC CTCTCATTTG 2040
 ATTGACAGTA TTTTAGTTAT TTTTGGCATT CTAAAGCTG GGCAATGTAA TGATCAGATC 2100
 TTTGTTTGTC TGAACAGGTA TTTTATACA TGCTTTTGT AAACCAAAAA CTTTAAAT 2160
 TCTTCAGGTT TCTAACATG CTTACCACGT GGCTACTGTA AATGAGAAAA GAATAAAATT 2220
 ATTTAATGTT TT

Seq ID NO: 144 Protein sequence:
 Protein Accession #: NP_060601

1 11 21 31 41 51
 | | | | |
 MEIQLKDALE KNQQLVLYDQ QREVVYKGLL AKIFELEKKT ETAHSLPQQ TKKPESEGYL 60
 QEEKQKCYND LLASAAKDLK VERQTITQLS FELSEFRKRY EETQKEVHNL NQLLYSQRRR 120
 DVQHLEDDRH KTEKIQLKRE ENDIARGKLE EEKKRSEELL SQVQSLYTSL LKQEEQTRV 180
 ALLEQQMQAC TLDPENEKLD RQHVQQLHV ILKELRKARK NNTVGILETA S

Seq ID NO: 145 DNA sequence
 Nucleic Acid Accession #: NM_001168
 Coding sequence: 50..478

1 11 21 31 41 51
 | | | | |
 CCGCCAGATT TGAATCGCGG GACCCGTTGG CAGAGGTGGC GCGGCGGCA TGGGTGCCCC 60
 GACGTTGCCC CTGCTCTGGC AGCCCTTTCT CAAGGACCAC CGCATCTCTA CATTCAAGAA 120
 CTGGCCCTTC TTGGAGGGCT GGCCTGCAC CCCGGAGCGG ATGGCCGAGG CTGGCTTCAT 180
 CCACTGCCCC ACTGAGAACG AGCCAGACTT GGCCAGTGT TTCTTCTGCT TCAAGGAGCT 240
 GGAAGGCTGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGGTTG 300
 CGCTTTCTCT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTTGGTGAAT TTTTGAAACT 360
 GGACAGAGAA AGAGCCAAGA ACAAATTGCG AAAGGAAACC AACATAAGA AGAAAGAATT 420
 TGAGGAAACT GCGAAGAAAG TGCGCCGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG 480
 CCTCTGGCCG GAGCTGCCTG GTCCAGAGT GGCTGCACCA CTTCCAGGGT TTATTCCTCG 540
 GTGCCACCAG CCTTCTGTGT GGCCCTTAG CAATGTCTTA GGAAAGGAGA TCAACATTTT 600
 CAAATTAGAT GTTCAACTG TGCTCCTGTT TTGCTTGTAA AGTGGCACC GAGGTGCTTC 660
 TGCTGTGCA GCGGGTGGCT CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTTTT 720
 GGGGGCTCAT TTTTGTGTTT TTGATTCCCG GGCTTACCAG GTGAGAAGTG AGGGAGGAAG 780
 AAGGCAGTGT CCTTTTGTCT AGAGCTGACA GCTTTGTTCG CGTGGGCAGA GCCTTCCACA 840
 GTGAATGTGT CTGGACTCTA TGTGTTGAG GCTGTACAG TCCTGAGTGT GGACTTGGCA 900
 GGTGCTGTGT GAATCTGAGC TGCAGGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG 960
 ACAGTTTTTT TGTGTTGTGT TTTTGTGTT TTTTGTGTT GGTAGATGCA TGACTTGTGT 1020
 CTGATGAGAG AATGGAGACA GATCCCTGG CTCCTCTACT GTTAAACAAC ATGGCTTTCT 1080
 TATTTTGTGT GAATTGTGTA TTCACAGAAT AGCACAACCT ACAATTAAAA CTAAGCACAA 1140
 AGCCATTCTA AGTCATTGGG GAAACGGGGT GAACTTCAGG TGGATGAGGA GACAGAATAG 1200
 AGTAGAGGA AGCGTCTGGC AGATACTCCT TTGCGCACTG CTGTGTGATT AGACAGGCC 1260
 AGTAGAGCCG GGGGCACATG CTGGCCGCTC CTCCTCAGA AAAAGGCAGT GGCCTAAATC 1320
 CTTTTTAAAT GACTTGGCTC GATGCTGTGG GGGACTGGCT GGGCTGCTGC AGGCCGTGTG 1380
 TCTGTACGCC CAACCTTCAC ATCTGTACG TTCTCCACAC GGGGGAGAGA CGCAGTCCCG 1440
 CCAGGTCCCC GCTTCTTTG GAGGCAGCAG CTCGCGCAGG GCTGAAGTCT GGCCTAAGAT 1500
 GATGGAATTT ATTCGCCCTC CTCCTGTCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC 1560
 GCTGGAACCC TCTGGAGTCT ATCTCGGCTG TTCCTGAGAA ATAAAAAGCC TGTCATTTT

Seq ID NO: 146 Protein sequence:
 Protein Accession #: NP_001159

1 11 21 31 41 51
 | | | | |
 MGAPTLPPAW QPFLKDHRS TFKNWPPLEG CACTPERMAE AGFIHCPTEN EPDLAQCFPC 60
 FKELEGWEPD DDPIEHHKH SSGCAFLSVK KQFEBELTGE FLKLDREKAK NKIAKETNNK 120
 KKEFEETAKK VRRAIQDLAA MD

Seq ID NO: 147 DNA sequence
 Nucleic Acid Accession #: NM_014176.1
 Coding sequence: 127-720

1 11 21 31 41 51
 | | | | |
 GCGCGCAGCG CTGGTACCCC GTTGGTCCGC GCGTTGCTGC GTTGTGAGGG GTGTGAGTCT 60
 AGTGCATCCC AGGCAGCTCT TAGTGTGGAG CAGTGAACCT TGTGTGGTTC CTCTACTTTG 120
 GGGATCATGC AGAGAGCTTC ACGTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA 180
 CCCCAGGCA TCACATGTTG GCAAGATAAA GACCAATGG ATGACCTGCG AGCTCAAATA 240
 TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT 300
 GAGAGGTACC CATTGGAACC TCCTCAGATC CGATTCTCA CTCCAATTTA TCATCCAAAC 360
 ATTGATTCTG CTGGAAGGAT TGTCTGGAT GTTCTCAAAT TGCCACCAAA AGGTGCTTGG 420
 AGACCATCCC TCAACATCGC AACTGTGTTG ACCTCTATTC AGCTGCTCAT GTCAGAACCC 480
 AACCTGTATG ACCCGCTCAT GGCTGACATA TCCTCAGAAT TTAATATATA TAAGCCAGCC 540
 TTCTCAAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA GACAGAAACA AAAGGCTGAT 600
 GAGGAAGAGA TGCTTGATAA TCTACCAGAG GCTGGTGACT CCAGAGTACA CAACTCAACA 660
 CAGAAAAGGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTTTCATCC TGATGTTTGT 720
 GGGACTTGTC CTGGTTCATC TTAGTTAATG TGTCTTTGTC CAAGGTGATC TAAGTTGCCCT 780
 ACCTTGAATT TTTTTTAAAT TATATTTGAT GACATAATTT TTGTGTAGTT TATTTATCTT 840
 GTACATATGT ATTTTGAAAT CTTTAAACC TGAAAAATAA ATAGTCATTT AATGTTGAAA 900

Seq ID NO: 148 Protein sequence:
 Protein Accession #: NP_054895.1

1	11	21	31	41	51	
MQRASRLKRE	LHMLATEPPP	GITCWQDKDQ	MDDLRAQILG	GANTPYEKGV	FKLEVIIPER	60
YFPFPPQIRF	LTPIYHPNID	SAGRICLDVL	KLPPKGAWRP	SLNIATVLTS	IQLLMSEPNP	120
DDPLMADISS	EPFKYNKPAFL	KNARQWTEKH	ARQKQKADEE	EMLDNLPEAG	DSRVHNSTQK	180
RKASQLVGIE	KKFHPDV					

Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_003812
 Coding sequence: 224-2722

1	11	21	31	41	51	
TCCTCTGCGT	CCCGCCCCGG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
GCCCAGCCCC	GAGCCCCCGG	CCCCGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGCGGCA	120
CCATGCGCGC	CGAGCCGGCG	TGACCGGCTC	CGCCCGCGGC	CGCCCCGCGC	CTAGCCCGGC	180
GCTCTCGCGC	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGCGAG	240
CAGCTCGCGG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCTT	GCGGCCCCCA	300
ACGCGGCCCC	GCCGGCTCGG	TGCCTGCCAG	CGCCCCGGCC	CGCACGCGCG	CCTGCCCGCT	360
GCTTCTGCTC	CTTCTCTCTG	TGCCTCCGCT	CGCCGCGCTG	TCCGCGCCCC	GCGCCTGGGG	420
GGCTGCTGCG	CCCAGCGCTC	CGCATTGGAA	TGAAACTGCA	GAAAAAAATT	TGGGAGTCCT	480
GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600
AAGCCCTTAT	CACGTCTTGT	ACACAAAGGC	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTCA	TTCTTGACCT	720
CATACGTAAC	AATGTTTGTG	TGTCTTCTGA	TTATGTGGAG	ATTCAGTACG	AAAATGGGAA	780
ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAAGCATCA	GAGGCGTCAA	840
AGACTCCAAG	GTGGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
CTTCGTGTAT	GTAGATAGAG	CACATAGAGT	GGTTCATGAT	GAGAAAAGCA	CAGGTCGACC	960
ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAAAATGAAGA	ATCTCACTAT	1020
GGAAAGAGGT	GACCACTGGC	CCTTCTCTCT	TGAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
AGCAGTGAAT	GCATACAGCT	GTATATTGGA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
TAATGATCAC	AAAACGTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACCTTGC	1200
AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
CCTGTGGCTG	GTAGAGACCT	GGACTGAGAA	GGATCAGATT	GACATCACCA	CCAACCTCTG	1320
GCAGATGCTC	CATGAGTTCT	CAAAATACCG	GCAGCGCATT	AAGCAGCATG	CTGATGCTGT	1380
GCACCTCATC	TCGCGGGTGA	CATTTCACTA	TAAGAGAAGC	AGTCTGAGTT	ACTTTGGAGG	1440
TGTCGTCTCT	CGCACAAAGG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500
ACAAGTATTA	TCGCAGAGCC	TGGCTCAAAA	CCTTGGAAATC	CAATGGGAAC	CTTCTAGCAG	1560
AAAGCCAAAA	TGTGACTGCA	CAGAAATCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
GTCCATTCTT	CGAAAATTTT	CAAAAGTGCA	CATTTTGGAG	TATAGAGACT	TTTACAGAG	1680
AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
AAATGGATAC	GTGGAAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCATGTGG	AATGCTATGG	1800
ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGACG	GGCCCTGCTG	1860
TAACAATACC	TCATGTCTTT	TTCAGCCACG	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
GTGTGATATT	ACTGAATATT	GTACTGGAGA	CTCTGGTCAG	TGCCCCACCA	ATCTTCATAA	1980
GCAAGACGGA	TATGCATGCA	ATCAAAATCA	GGGCGCTGTC	TACAATGGCG	AGTGCAAGAC	2040
CAGAGACAAC	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
CTATGAAAAG	CTGAATACAG	AAGGCACTGA	GAAGGGAAGC	TGCCGGGAAG	ATGGAGACCG	2160
GTGGATTTCG	TGCAGCAAA	ATGATGTGTT	CTGTGGATTG	TTACTCTGTA	CCAATCTTAC	2220
TCGAGCTCCA	CGTATTGGTC	AACCTCAGGG	TGAGATCATT	CCAACCTCCT	TCTACCATCA	2280
AGGCCGGGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTGA	GATGATGATA	CGGATGTGGG	2340
CTATGTAGAA	GATGGAACGC	CATGTGGCCC	GTCTATGATG	TGTTTAGATC	GGAAAGTCCCT	2400
ACAAATTCAA	GGCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTGTG	GATTTCACCT	GGGCAGGGAC	2520
AGATTGCGAG	ATCCGGGATC	CAGTTAGGAA	CCTTCACCCC	CCCAAGGATG	AAGGACCCAA	2580
GGTCTCTAGT	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
TATTGTCTCT	GGGGGACAGC	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTCGATCC	2700
TACTCAGCAA	GGCCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCACTTTTGG	2760
ATTCTGGGTA	TGACATACTC	GCAGCAGTGT	TACTGGAACT	ATTAAGTTTG	TAAACAAAAC	2820
CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TGGGGGTGAC	AAGGATGGGG	TAAAGAAAAA	2880
CTGTCTCTTT	TGGAATAAAT	ACCTTTACCC	ACCTGTGAGT	AAACGGGGGA		2940
GGGGGCAAAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTTTTT	TCCCTAATGG	3000
ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GGAATCATTG	AAAA	

Seq ID NO: 150 Protein sequence:
 Protein Accession #: NP_003803

1	11	21	31	41	51	
MKPPGSSSRQ	PPLAGCSLAG	ASCGPQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPLLAASS	60
RPRWGAAP	SAPHWNETAE	KNLGLVADED	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
INQDESYPH	VLDTKARHQ	KHNKAVHLAQ	ASFQIEAFGS	KFILDLLNN	GLLSSDYVEI	180
HYENGKPYQS	KGGEHCYHYH	SIRGVKDSKV	ALSTCNGLHG	MFEDDTFVYM	IEPLELVHDE	240
KSTGRPHIQ	KTLAGQYSKQ	MKNLTMERGD	QWPFSELQW	LKRRKRAVNP	SRGIFEEMKY	300
LELMIVNDHK	TYKHRSSHA	HTNFAKSVV	NLVDISIYKEQ	LNTRVVLVAV	ETWTEKDQID	360
ITTNPVQMLH	EPISKYQRIK	QHADAHLIS	RVTFFHYKRSS	LSYFVGVCSS	TRGVGVNEYG	420
LPMAVAQVLS	QSLAQNGLGQ	WEPSSRKPKC	DCTESWGGCI	MEETGVSHSR	KFSKCSILEY	480
RDPLQRGGGA	CLFNRPTKLF	EPTECGNGYV	EAGEECDGCF	HVECYGLGCK	KCSLSNGAHC	540
SDGPCCNNTS	CLFQPRGYEC	RDVNECDIT	EYCTGDSGQC	PPNLHKQDGY	ACNQNGRCRY	600
NGECKTRDNQ	CQYIWTGKAA	GSDKFCYEKL	NTEGTEKGNC	GKGDWRWICQ	SKHDVFCGFL	660

LCTNLTRAPR IGQLQGEIIP TSFYHQGRVI DCSGARHVLD DDTDVGYVED GTPCGPSMMC 720
 LDRKCLQIQA LNMSSCPLDS KGVKCSGHGV CSNEATCICD FTWAGTDCSI RDPVRNLHPP 780
 KDEGPKGPSA TNLIIGSIAG AILVAAIVLG GTGWGFKNVK KRRFDPTQQG PI

5 Seq ID NO: 151 DNA sequence
 Nucleic Acid Accession #: NM_023915
 Coding sequence: 250-1326

10 1 11 21 31 41 51
 | | | | | |
 GGCACGAGGG TTTCGTTTTC ATGCTTTACC AGAAAATCCA CTTCCTGCC GACCTTAGTT 60
 TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 15 CCCACGCTCT AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC 240
 AACTGAAGAA TGGGGTTCAA CTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 CAAGAGAGT CCAATTGAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC 360
 AATGAATTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480
 20 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTTCTCTG CAGATACACT 600
 TCAGTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
 GATCGCTATC TGAAGTGTG CAAGCCATT GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGGTTT TATCTGTTTG TGTTCGGTG ATCATGGCTG TTTTGTCTTT GCCAACATC 780
 ATCTCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAAGT 840
 25 CCTTTGGGGG TCAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
 AGGCAATTCA TAAGTCAGT AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
 30 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAGAA 1140
 ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCTGGATC CAATAATTTA CTTTTCATG 1200
 TGTAGGTCAT TTTCAAGTAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAAGC 1260
 ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380
 35 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 152 Protein sequence:
 Protein Accession #: NP_076404

40 1 11 21 31 41 51
 | | | | | |
 MGFNLTAKL PNNELHQGES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFPHI RNKTSIFLYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL 120
 45 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTFTKV LSVCVWVIMA VLSLPNIILT 180
 NQOFTEDNIH DCSKLSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKXH NQSIKRVVAV FPTCFLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
 FLSACNVCLD PIYFFMCRS PSRRLPKXSN IRTRESIRS LQSVRRSEVR IYYDYTDV

50 Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: D80008.1
 Coding sequence: 149-739

55 1 11 21 31 41 51
 | | | | | |
 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCGCGCG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAT CGGCGGCCCG AAGGCCAACT GCCTGCCCTC AACGAGGATG GACTCAGACA 240
 60 AGTTCTGGAG GAGATGAAAG CTTTGTATGA ACAAACCAG TCTGATGTGA ATGAAGCAAA 300
 GTCAAGTGGG CGAAGTGATT TGATACCAAC TATCAAATT CGACACTGTT CTCTGTAAAG 360
 AAATCGACGC TGCACTGTAG CATACCTGTA TGACCGCTG CTTGGATCA GAGCACTCAG 420
 ATGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATT CACATGGCTG CTGAAGAAAT 480
 GGAGTGGTTT AATAATTATA AAAGATCTCT TGCTACTTAT ATGAGGTAC TGGGAGGAGA 540
 TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGTCCG 600
 65 GTGTCTAAAA GACTATGGAG AATTTGAAGT TGATGATGGC ACTTCAGTCC TATTAATAAA 660
 AAATAGCCAG CACTTTTAC CTCGATGGAA ATGTGAGCAG CTGATCAGAC AAGGAGTCCCT 720
 GGAGCACATC CTGTCATGAC CATGCGCGGA GGCACCTCCA GGCCTCACTC AACTCATGGA 780
 CTCCTCTGTA CTCACTCTCT CCACCACTCC CTTCACTCC CTCTTTGATT TTAGAAGCTA 840
 TAGACATTGT TTAAGATAAC TAAGAATACT TGGCTAAGAA GTATAATTG CTAACATTA 900
 70 AGGACTTTCT TTTTCTAATG TTGTACACTA TTCTTCCTAC TCTTTTGGG TTTTGGTTT 960
 GTTTGTAGA GACTGTCTCA CTATGTTGCC CAAGCTGGTC TCAAACCTCT GGCCTCAAGC 1020
 AGTCCTCCCA CCTTAGCTTC TCAAAGTGT GAGATCACAG GCGTGAGCCA CTGACCCCG 1080
 CCCCTACTCC TTTTCTAAT AAGCTGTATC TGTAATCACA GCATTCCTAC AGTTGTGACA 1140
 75 GTGTGTTTTT TAAATGAAAG TAAACATGGT TACATTGAA TCTCTTAAAT AAGCAGTCAC 1200
 TTGGCTGGAC AGGAAGAAGG TAGATCCTGT GTGTCTTGT TCTGGTCAT GTGTATTGTA 1260
 CAAGCTAGAG AGCTGAATT CTGAGATACA CATTTTCAAA TCACATGCAA GTGAAGATGA 1320
 TGGTCTGTAG AAATTTTCAG TATATATAAT GTTTAATGAC ATACTAATT ATCATCTGGC 1380
 TATTTGGGAA GGAAGGACAC ACATGGATT TGACATTTC CACCATGGTG GCTGGTGTG 1440
 CTTGTGGCTA TGGGGGTATC ACCAGTATCA CCACCTTGA AGGGGACAGT GAAATTGGGG 1500
 80 CTAGAGAAGG AACTTTGTAC AGTTTCCCT GAGATTGAGA TTGACTGAAA AGTCACATGA 1560
 AGAGTGTATT GTCTTTAAT GGTATGTTT AAACAGCTGA CATTTTAAAT TTTGATGAAA 1620
 TCCAGTTTAT TCGTTTGTTC TTTTATGCTT TGGGTGTTG ATCCGAGAAA TCTTTTCCCA 1680
 TCCCAAGATC ACAAATTTT TCTCTTTTTA CTTCTAGAAG TGTATATAAT TTAAGCTTTA 1740
 TACTTTGGTC TATGACCCGT TTTTCTTTT GTTTTGTGTT GTTTTTCGT TTTTCTTT 1800
 85 GTTTTGTAGT GGAGTCTGT TCTGTACCC AGGCTGGGGT GCAGTGGCGT GATCTTGGCT 1860
 CACTGCAATC TCTATCCCT GGGTCAAGT GATTCTCTTG TCTCAGCCTC CCAAGTAGCT 1920
 GGGATTACAG GCACAGGCCG CCACGCTCG CTAATTTTGT TATTTTGTAGT AGAGACAGAG 1980

TTTTACCATG TTGGCCAGGC TGGTTTCAAA CTCCTGACCT CAAGTGACCC ACCTTGGCCT 2040
 CCCAAGTTT TGGGATTACA AGTGTGGGCC ACCGCGGCCA GCCTATGATC CATTTTGAAT 2100
 GAATTTTATA TATGGTCAA GGTGTCAATC CACCTTCACT TTTTCTTGGG AATATAGATA 2160
 TCCAGCTGTT TCACTACCAT TTTTGAAGG GACTGCCCTT TGCTCTATCA CCTTTGCATT 2220
 TTTGTAAAA AGTAGTTGTC AATGTATATG TGGGTTTATT TCAGGACTCT GTTTTGTTC 2280
 ATTGACCTGT TTTTCTCTCC TGAATGCCAA TACCATATTT GTATGTAGTG TATGTAATTT 2340
 TCTAATAATT CTGAAACAG ATAGTATTAA TGTGTCAAT TTTTGTCTGT GTTTGTATTT 2400
 TTTGTAGAGA TGGGGTTTCA CCGTGTGGC CAGGCTGTGT TGAACCTCTG AGCTAAAGCA 2460
 ATACACTTGC CTCGTCTCTC CCATGTGCTG GGATTACAGG CGTGAGCCTT GGTGCTGGCC 2520
 CAGTGTACCA CATTTCTTTT TGAGATTGTT TTTGGCTATG TTAAGTCCTT TGCTTTTGAT 2580
 GTGAAATTG GGAACAGGCA GGGTGTGGTG GCTTATGCCT GTAATCCTAG AACTTTGGGA 2640
 GGCCTAGATG GGTGGATCAC TTGAGCTCAG GAGTTCAGA CCAGCCGGG CCTATGGCAA 2700
 AACTCCGTCT CTACAAAAA TAGAAAAAAT TAGCCAGGTG TGGTGGTGCA TGCTGTAGT 2760
 CACAGTTACA CGGCAGGCTG AGGTGGGAGG ATCACTTGAA CCCAGAGGT CAAGACTGCA 2820
 GTGAGCTGAG ATCACACCAC TGTACTCCAG CCTGGGTGAC AAAGTGAGAC TCTATCTCAA 2880
 AAAGAAATTA GGATCAATTT GTCAATTTCT ACAACAACAA CAACAAAAAC CCTGTGTGGG 2940
 CACCTTGATT GAGATTGCAT TGAATTTATA TAAACCTGTT GGGAGAATTG ACATCTTAAT 3000
 AATATTGAGT CTTCTGGCCT ATAAACAAGG TCTGTCTTCC TAGGTATTAA TGTTTTGTCT 3060
 TCTATTCTCT TTAATATCTT TTTGTAGTTT TCAGTGATCA GGTCTACCAT GTCAGCATT 3120
 CATAGTTTGT ATGCTAAATG GTATTTTAAA ATTTCAAATT CTAACCACTT GTTGCTAGTA 3180
 AATAGAAATA CAATTGATGT TGAACCTGTA TCCTTCAGCC TTGCTAAACT GTGAGTTCTC 3240
 ATGGTGTGTT TGTAAATTAC ATCAACAGTC ATGTGTTCTA TGAATAAAGA GTTTTACTCC 3300
 TTC

Seq ID NO: 154 Protein sequence:
 Protein Accession #: BAA11503.1

1 11 21 31 41 51
 MFCEKAMELI RELHRAPEQ LPAFNEGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLEP ALRFHMAAEE MEWFNNYKRS 120
 LATYMRSLGG DEGLDITQDM KPPKSLYIEV RCLKDYGEFE VDDGTSVLLK KNSQHPLPRW 180
 KCEQLIRQGV LEHILS

Seq ID NO: 155 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 149-709

1 11 21 31 41 51
 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCCGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCCAA AAAGCCATGG AACTGATCGC 180
 CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGACA 240
 AGTTCTGGAG GAGATGAAAG CTTGTATGTA ACAAACCCAG TCTGATGTGA ATGAAGCAAA 300
 GTCAGGTGGA CGAAGTGATT TGATACCAAC TATCAAAATT CGACACTGTT CTCTGTTAAG 360
 AAATCGACGC TGCACGTAG CATACCTGTA TGACCGCTTG CTTGGATCA GAGCACTCAG 420
 ATGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATTT CACATGGCTG CTGAAGAAAT 480
 GGAGTGGTTT AATAATTATA AAAGATCTCT TGCTACTTAT ATGAGGTCAC TGGGAGGAGA 540
 TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGCTGG 600
 ATGCAGTGGC GCGATCTCGG CTCACCTGCA AACCTCCACC TCCCAGGTTT ACCTCAACTG 660
 CAACCTCCAC TCCACAGTTA CAGTGTCTAA AAGACTATGG AGAATTTGAA GTTGATGATG 720
 GCACTTCAGT CCTATTAATA AAAAATAGCC AGCACTTTTT ACCTCGATGG AAATGTGAGC 780
 AGCTGATCAG ACAAGGAGTG CTGGAGCACA TCCTGTGATG ACCATGCGCC GAGGCACTTC 840
 CAGGCTTCAC TCAACTCATG GACTCCTCTG TACTCACTCT CTCACCACT CCCTTCACTT 900
 CCCTCTTTGA TTTTAGAAGC TATAGACATT GTTTAAGATA ACTAAGAATA CTTGGCTAAG 960
 AAGTATAATT TGCTAACTAT TAAGGACTTT CTTTTTTTAA TGTGTATAC TATTCTTCCT 1020
 ACTCTTTTTT GTGTTTGTGT TGTGTTTGTG GAGACTGTCT CACTATGTTG CCCAAGCTGG 1080
 TCTCAAACCT CTGGCCTCAA GCAGTCTCTC CACCTTAGCT TCTCAAAGTG TTGAGATCAC 1140
 AGGCGTGAGC CACTGCACCC GGCCCTTACT CCTTTTCTTA ATAAGCTGTA TCTGTAATCA 1200
 CAGCATTCCT ACAGTTTGGC CAGTGTGTTT TTTAAATGAA AGTAACATG GTTACATTTG 1260
 AATCTCTTAA ATAAGCAGTC ACTTGGCTGG ACAGGAAGAA GGTAGATCCT GTGTGTCTTG 1320
 TTTTCTGGTC ATGTGTATTG TACAAGCTAG AGAGCTGAAT TTCTGAGATA CACATTTTCA 1380
 AATCACATGC AAGTGAAGAT GATGGTCTGT AGAATTTTCT AGTATATATA ATGTTTAATG 1440
 ACATACTAAT TTATCATCTG GCTATTTGGG AAGGAAGGAC ACACATGGAT TTTGCACATT 1500
 TCCACCATGG TGGCTGGTGT GGCTGTGGC TATGGGGTGA TCACCAGTAT CACCACCTTG 1560
 GAAGGGGACA GTGAAATTGG GGCTAGAGAA GGAACCTTGT ACAGTTTTCCT CTGAGATTCA 1620
 GATTGACTGA AAAGTCACAT GAAGAGTTGA TTGTCTTTTA ATGGTATGTT TTAACAGCT 1680
 GACATTTTAA ATTTTGTATG AATCCAGTTT ATTCGTTTGT TCTTTTATGC TTTGGGTGTT 1740
 GCATCCGAGA AATCTTTTCC CATCCCAAGA TCACAATTTT TTTTCTTTT TACTTCTAGA 1800
 AGTGTATAAA TTTTAAGCTT TATACTTTGG TCTATGACCC GTTTTTTTTT TTGTTTGTGTT 1860
 TTGTTTTTCT GTTTGTCTCT TGTGTTTGGG ATGGAGTCTT GTTCTGTGAC CCAGGCTGGG 1920
 GTGCAGTGGC GTGATCTTGG CTCACCTGCA TCTCTATCCC CTGGGTTCAA GTGATTCTCT 1980
 TGTCTCAGCC TCCCAAGTAG CTGGGATTAC AGGCACAGGC CGCCACGCCT GGCTAATTTT 2040
 TGTATTTTAA GTAGAGACAG AGTTTATCCA TGTGGGCCAG GCTGGTTTCA AACTCCTGAC 2100
 CTCAAGTGAC CCACCTTGGC TCCCCAAAGT TTTGGGATTA CAAGTGTGGG CCACCGCGGC 2160
 CAGCCTATGA TCCATTTTGA ATGAATTTT TATATGGTGC AAGGTGTCAA TCCACCTTCA 2220
 CTTTTTCTTG GGAATATAGA TATCCAGCTG TTTCACTACC ATTTTGTGAA AGGACTGCCC 2280
 TTTGCTCTAT CACCTTTTGA TTTTGTGTA AAGTGTATG TCAATGTATA TGTGGGTTTA 2340
 TTTCAGGACT CTGTTTGTGT CCATTGACCT GTTTTCTCT CCTGAATGCC AATACCATAT 2400
 TTGTATGTAG TGTATGTAAT TTTCTAATAA TTCTTGAAAC AGATAGTATT AATGTGTCAT 2460
 ATTTTGTCTG TTGTTGTGAT TTTTGTAGA GATGGGGTTT CACCGTGTG GCCAGGCTGT 2520
 GTTGAACCTC TGAGCTAAAG CAATACACTT GCCTCGTCTT CCCCATGTGC TGGGATTACA 2580
 GGCCTGAGCC TTGGTGTCTG CCCAGTGTAC CACATTTCTT TTTGAGATT GTTTTGGCTA 2640
 GTTAAAGTCC TTTAGCTTTT ATGCGAAATT TGGGAACAGG CAGGGTGTGG TGGCTATGTC 2700
 CTGTAATCCT AGAATCTTGG GAGGCCTAGA TGGGTGGATC ACTTGAGCTC AGGAGTTCCA 2760
 GACCAGCCCG GGCCTATGSC AAAATCTCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG 2820

TGTGGTGGTG CATGCCCTGTA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG 2880
 AACCCAGAG GTCAAGACTG CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG 2940
 ACAAAGTAG ACTCTATCTC AAAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC 3000
 AACACAACAAA ACCCTGTGTG GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAACTG 3060
 TTGGGAGAAT TGACATCTTA ATAATATTGA GTCTTCTGGC CTATAAACAA GGTCTGTCTT 3120
 CCTAGGTATT AATGTTTTGT CTCTATTTC TCTTAATAAT CTTTGTAGT TTTCACTGTA 3180
 CAGGTCTACC ATGTGAGCAT TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAAA 3240
 TTCTAACAC TTGTGTCTAG TAAATAGAAA TACAATTGAT GTTGAACCTG TATCCTTCAG 3300
 CCTTGCTAAA CTGTGAGTTT TCATGGTGT TTTGTAAATT ACATCAACAG TCATGTGTTT 3360
 TATGAATAAA GAGTTTACT CCTTC

Seq ID NO: 156 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MFCEKAMELI RELHRAPEQG LPAFNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRTVAVYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS 120
 LATYMRSLGG DEGLDITQDM KPPKSLYIEA GCSGAISAQP ATSTSQVHLN CNLHLPGPVS 180
 KRLWRI

Seq ID NO: 157 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-621

1 11 21 31 41 51
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 GAAAGGAGTG AGCGCGCGAG AGCCAGAGATA CCATTTTGGC GTGAGAGCTG GTGGTTGGCA 120
 AGCGCGCGGG AGTGGGAAGC GTCCGCCATG TTCTGCGAAA AAGCCATGGA ACTGATCCGC 180
 GAGCTGCATC GCGCGCCCGA AGGGCAACTG CCTGCCTTCA ACGAGGATGG ACTCAGACAA 240
 GTTCTGGAGG AGATGAAAGC TTTGTATGAA CAAAACCACT CTGATGTGAA TGAAGCAAAG 300
 TCAGGTGGAC GAAGTGATTT GATACCAACT ATCAAATTTT GACACTGTTC TCTGTTAAGA 360
 AATCGACGCT GCACTGTAGC ATACCTGTAT GACCGCTTGC TTCGGATCAG AGCACTCAGA 420
 TGGGAATATG GTAGCGTCTT GCCAAATGCA TTACGATTTC ACATGGCTGC TGAAGAAGTC 480
 CGGTGTCTAA AAGACTATGG AGAATTTGAA GTTGATGATG GCACCTTCAGT CCTATTAAAA 540
 AAAAAATAGCC AGCACTTTTT ACCTCGATGG AAATGTGAGC AGCTGATCAG ACAAGGAGTC 600
 CTGGAGCACA TCCTGTCATG ACCATGCGCC GAGGCACTTC CAGGCTTCAC TCAACTCATG 660
 GACTCCTCTG TACTCACTCT CTCCACCACT CCCTTCACCT CCCTCITTGA TTTTAGAAGC 720
 TATAGACATT GTTCAAGATA ACTAAGAATA CTTGGCTAAG AAGTATAAAT TGCTAACTAT 780
 TAAGGACATT CTTTTTTTAA TGTGTACAC TATTCTTCCT ACTCTTTTTT GGTTTTGGTT 840
 TTGTTTTGTA GAGACTGTCT CACTATGTTG CCCAAGCTGG TCTCAAACTC CTGGCCTCAA 900
 GCAGTCTCC CAGCTCAGCT TCTCAAGTGT TTGAGATCAC AGGCGTGAGC CACTGCACCC 960
 GGCCCTACT CTTTTTTCTA ATAAGCTGTA TCTGTAATCA CAGCATTCCT ACAGTTGTTA 1020
 CAGTGTGTTT TTTAATGAA AGTAAACATG GTTACATTG AATCTCTTAA ATAAGCAGTC 1080
 ACTTGGCTGG ACAGGAAGAA GGTAGATCCT GTGTGCTTGG TTTTCTGGTC ATGTGTATTG 1140
 TACAAGCTAG AGAGCTGAAT TTCTGAGATA CACATTTTCA AATCACATGC AAGTGAAGAT 1200
 GATGGTCTGT AGAAATTTTC AGTATATATA ATGTTTAAAT ACATACATAAT TTATCATCTG 1260
 GCTATTGTTG AGGGAAGGAC ACACATGGAT TTTGCACATT TCCACCATGG TGGCTGGTGT 1320
 GGCTTGTGGC TATGGGGTGA TCACCACTAT CACCACCTTG GAAGGGGACA GTGAAATTGG 1380
 GGCTAGAGAA GGAACTTTGT ACAGTTTTC CTGAGATTCA GATTGACTGA AAAGTCACAT 1440
 GAAGAGTTGA TTGTCTTTTA ATGGTATGTT TTAACAGCT GACATTTTAA ATTTTGATGA 1500
 AATCCAGTTT ATTCGTTTGT TCTTTTATGC TTTGGGTGTT GCATCCGAGA AATCTTTTCC 1560
 CATCCCAAGA TCACAAATTTT TTTTCTTTT TACTTCTAGA AGTGTATATA TTTTAAAGCTT 1620
 TATACTTTGG TCTATGACCC GTTTTTTTTT TTGTTTTGTT TTGTTTTTTC GTTTGTTTCT 1680
 TTGTTTTGAG ATGGAGTCTT GTTCTGTAC CCAGGCTGGG GTGCAGTGGC GTGATCTTGG 1740
 CTCACTGCAA TCTCTATCCC CTGGGTCAA GTGATTCTCT TGTCTCAGCC TCCCAAGTAG 1800
 CTGGGATTAC AGGCAGAGC GGCACGCTT GGCTAATTTT TGATTTTITA GTAGAGACAG 1860
 AGTTTTACCA TGTGGCCAG GCTGGTTTCA AACTCCTGAC CTCAAGTGAC CCACCTTGGC 1920
 CTCCCAAAGT TTTGGGATTA CAAGTGTGGG CCACGCGGCG CAGCCTATGA TCCATTTTGA 1980
 ATGAATTTT TATATGGTGC AAGTGTCAA TCCACCTTCA CTTTTTCTTG GGAATATAGA 2040
 TATCCAGCTG TTTCACTACC ATTTTGTGAA AGGACTGCCC TTTGCTCTAT CACCTTTGCA 2100
 TTTTGTGTA AAGTAGTTG TCAATGTATA TGTGGGTTTA TTTGAGGACT CTGTTTGTGT 2160
 CCATTGACCT GTTTTCTCT CTTGAATGCC AATACCATAT TTGTATGTAG TGTATGTAAT 2220
 TTTCTAATAA TTCTTGAAC AGATAGTATT AATGTGTCTAT ATTTTGTCTG TGTGTTGTAT 2280
 TTTTGTGTA GATGGGGTTT CACCGTGTG GCCAGGCTGT GTTGAACCTC TGAGCTAAAG 2340
 CAATACACTT GCCTCGTCTT CCCCATGTGC TGGGATTACA GGCGTGAGCC TTTGTTGCTG 2400
 CCCAGTGTAC CACATTTCTT TTTGAGATT GTTTTGGCTA TGTAAAGTCC TTTGCTTTTG 2460
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 GAGGCCTAGA TGGTGGATC ACTTGAGCTC AGGAGTTCCA GACCAGCCCG GGCCTATGGC 2580
 AAAACTCCGT CTCTACAAA AATAGAAAA ATTAGCCAGG TGTGGTGGTG CATGCCGTGA 2640
 GTCACAGTTA CACGGCAGCG TGAGGTGGGA GGATCACTTG AACCCAGAG GTCAAGACTG 2700
 CAGTGAGCTG AGATCAACCC ACTGTACTCC AGCCTGGGTG ACAGAGTGAG ACTCTATCTC 2760
 AAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC AACACAACAAA ACCCTGTGTT 2820
 GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAACTG TTGGGAGAAT TGACATCTTA 2880
 ATAAATATGA GTCTTCTGGC CTATAACAA GGTCTGTCTT CTTAGGTATT AATGTTTTGT 2940
 CTCTATTTC TCTTAATAAT CTTTGTAGT TTTCACTGTA CAGGTCTACC ATGTGAGCAT 3000
 TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAAA TTCTAACAC TTGTTGCTAG 3060
 TAAATAGAAA TACAATTGAT GTTGAACCTG TATCCTTCAG CCTTGCTAAA CTGTGAGTTC 3120
 TCATGGTGT TTTGTAAATT ACATCAACAG TCATGTGTTT TATGAATAAA GAGTTTACT 3180
 CCTTC

Seq ID NO: 158 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |

MFCEKAMELI RELHRAPEGO LPAFNEGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRTVAYL YDRLLRIRAL RWEYGSVLPN ALRPHMAAEE VRCLKDYGEF 120
 EVDGTSVLL KNSQHLPLR WKCEQLIRQG VLEHILS

5

Seq ID NO: 159 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 149-229

10 1 11 21 31 41 51
 | | | | | |
 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACAAATTAGC TGGGTGTGGT 240
 15 GGCACACACC TGTAGTCCCA GCAACTTAGG AGGCTGAAAT GAGAGGATTG CATGGCTCCA 300
 GGAAGTTGAA ACTGCAGTGA ACTGTGGTCA CGCTATTACA CTCCAGCCTG GGTGACAGAC 360
 TGAATCCCTG TCTCAAAAAG GAAAAGGAGG ATGGACTCAG ACAAGTTCTG GAGGAGATGA 420
 AAGCTTTGTA TGAACAAAAC CAGTCTGATG TGTCTCTGT TAAGAAATCG ACGCTGCACT 480
 20 GTAGCATACC TGTATGACCG CTGCTTCGG ATCAGAGCAC TCAGATGG

Seq ID NO: 160 Protein sequence:
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51
 | | | | | |
 ATGTTCTGCG AAAAAGCCAT GGAAGTATC CGCGAGCTGC ATCGCGCGCC CGAAGGGCAA 60
 CTGCCTGCCT TCAACAATTA G

30

Seq ID NO: 161 DNA sequence
 Nucleic Acid Accession #: U10694
 Coding sequence: 1333-2280

35 1 11 21 31 41 51
 | | | | | |
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 ACAGGGAGGC CTGTGTTTCG ACAGACACAG TGGTCCCAGG ATTGGAGAGC AGTCCAGGTG 120
 AGGAACCTAA GGGAGGATCG AGGGTACCTC CAGGCCAGAG AAATCTCTAG ATCAAGAGAG 180
 TTTGGCCCTGC CCTACTGTC ACCCCAGAGA GCCCGGGCAG GGCTGTCTGC TGAGGTGCTC 240
 CCTTTATCCT GGGATCACTG GTGTGCGGGA GGGCTGGCCT TGGTCTGAGG GGGCTGCACT 300
 40 CAGCTCAGCA GAGGGAGGGT CCCAGGCCCT GCCAGGAGTC CAGGTGCAGA CTGAGGGGAC 360
 CCCACTCACC AAACACAGAG GACCTAGCCC CACCCTGCCC CTTGTGTGTA CTGAGGGGAG 420
 CCGCTGGGTG GATGGAATCC CTTCACTTCC TCTTCAGGTG TCTCTGGAG ATAGGGCCTC 480
 AGGTCAACAG AGGGAGGGTT CCAGACCTCG CAGGCATCAA GATGAGGACC AGGCAGTATC 540
 CTACCCCCAG GACACATGGA CCCATTGAA TTTAGACATC TCTTACTGTA CTTCCGAGGA 600
 45 AACCTGGGCG AGGTGTGGGC AGATGTTGGT TGGGGCATGT CCTTCTGTTC CATATCAGGG 660
 ATGTGAGCTC CTGATCTGAG AGACTCTCAG GCAAGTAGAG GAGTAGAGTC CAGTCCCTGC 720
 CAGGAGAAAG GTGAGGGCCC TGAGTGAGCG CAGAGGGGAC CATCCACCCC AAAAGTGTGT 780
 AGAACTCAAG AGTGTCCAGC CCGCCCTCTT GACAGCACTG AGGGACCGGG GCTCTGCCTG 840
 CAGTCTCAGC CTTAAGGGCC CTTGATTCCT TCTTCCAGGA GCTCCAGGAA GCAGGCAGGC 900
 50 CTTGGTCTGA GACAGTGTCC TCAGGTGCGA GAGCAGAGGA GACCCAGGCA GTGTGAGCAG 960
 TGAAGGTGAA GTGTTACACC TGAATGTGCA CCAAGGGCCC CACCTGCCCC AGCACACATG 1020
 GGACCCCATG GCACCTGGCC CCATTCCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC 1080
 AGGCTAGCTG CACGCTGAGT AGCCCTCTCA CTTCTCTCCT CAGGTTCTCG GGACAGGCTA 1140
 ACCAGGAGGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAAGTCA 1200
 55 GCCTTTGTTA GAACCTCCAA GGTTCGGTTC TCAGCTGAAG TCTCTCACAC ACTCCCTCTC 1260
 TCCCGAGGCC TGTGGGTCTC CATCGCCAG CTCCTGCCCA CGCTCTGAC TGCTGCCCTG 1320
 ACCAGAGTCA TCATGTCTCT CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT 1380
 GAAGCCCAAG GAGAGGACTT GGGCCTGATG GGTGCACAGG AACCCACAGG CGAGGAGGAG 1440
 60 GAGACTACCT CCTCTCTGA CAGCAAGGAG GAGGAGGTGT CTGCTGCTGG GTCATCAAGT 1500
 CCTCCCCAGA GTCTCAGGG AGGCGCTTCC TCCTCCATTT CCGTCTACTA CACTTTATGG 1560
 AGCCAAATTC ATGAGGGCTC CAGCAGTCAA GAAGAGGAAG AGCCAAAGCTC CTGGTTCGAC 1620
 CCAAGTCAAG TGGAGTTTAT GTTCCAAGAA GCACTGAAAT TGAAGGTGGC TGAGTTGGTT 1680
 CATTTCTGTC TCCACAAATA TCGAGTCAAG GAGCCGGTCA CAAAGGCAGA AATGCTGGAG 1740
 AGCGTCATCA AAAATTACAA GCGCTACTTT CCTGTGATCT TCGGCAAGAG CTCGAGTTTC 1800
 65 ATGCAGGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGACC CCGCCGGCCA CTCCTACATC 1860
 CTTGTCACTG CTCTGGCCT CTCGTGCGAT AGCATGCTGG GTGATGGTCA TAGCATGCCC 1920
 AAGGCCGCC TCTGTATCAT TGTCTGGGT GTGATCCTAA CCAAGAGCAA CTGCGCCCCT 1980
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 70 TTCTACGGGG AGCCAGGAA GCTGCTCACC CAAGATTGGG TGCAGGAAAA CTACCTGGAG 2100
 TACCGGCAGG TGCCCGCAG TGATCCTCGC CACTACGAGT TCCTGTGGGG TTCCAAGGCC 2160
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 CCCATCTGCT ACCATCTCCT TTATGAAGAG GTTTTGGGAG AGGAGCAGA GGGAGTCTGA 2280
 GCACAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTGAGG CCCCATCCAG CAGCTGCCTT 2340
 75 GCCCATGTG ACATGAGGCC CATCTCTCGC TCTGTGTTTG AAGAGAGCAA TCAGTGTCTT 2400
 CAGTGGCAGT GGGTGAAGT GAGCACACTG TATGTCTCT CTGGGTTCCT TGTCTATTGG 2460
 GTGATTTGGA GATTTATCCT TGCTCCCTTT TGAATTTGTT CAAATGTTCT TTTAATGGTC 2520
 AGTTTAAATGA ACTTCACCAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATTGCTGTTT 2580
 ATGTTATTTA GGAGTAAGAT TCTTGCTTTT GAGTCACATG GGGAAATCCC TGTATTTTT 2640
 TGAATTTGGA CAGATAAACA TAGCAGAGGA ATTAATAATT TTTTGAAGAA TTGAAGTTAG 2700
 80 CAGCAAAATA CAGCTATATA AGAAATAGTG AAATGAAAT GTAGTTAATT CTGCTCTTAT 2760
 ACCCTCTTCT CTCTCCTGTA AAATTAAGAC ATATACATGT ATACCTGGAT TTGCTTGGCT 2820
 TCTTTGAGCA TGAAGAGGAA ATAAATATG AAAGAATAAT TTTTCTGTT CACTGGCTCA 2880
 85 TTTTCTTCTC AGACACGCAC TGAACATCTG TTATTCGGAA CACCCTGGGT T

Seq ID NO: 162 Protein sequence:
 Protein Accession #: AAA68877.1

1	11	21	31	41	51	
MSLEQRSPHC	KPDEDLEAQQ	EDLGLMGAQE	PTGEEEBETTS	SSDSKEEEVS	AAGSSSPPOS	60
PQGGASSSIS	VYYTLWSQFD	EGSSSQEEEE	PSSSVDPQAL	EFMFQEALKL	KVAELVHFL	120
HKYRVKEPVT	KAEMLESVIK	NYKRYFPVIF	GKASEFMQVI	FGTDVKEVDP	AGHSYILVTA	180
LGLSCDSMLG	DGHSMFKAAL	LIIVLGVILT	KONCAPEEVI	WEALSVMGVY	VGKEHMFYGE	240
PRKLLTQDWW	QENYLEYRQV	PGSDPAHYEF	LWGSKAHAET	SYEKVINYL	MLNAREPICY	300
PSLYEEVLGE	EQEGV					

Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: AF292100
Coding sequence: 30-809

1	11	21	31	41	51	
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AAGTTCGTCA	GTTTATGATC	TTACACAAT	CTAGTGAAAA	AACAGCAGTA	AGTTGTCTTT	120
CTCAAAATGA	CTGGAAGTTA	GATGTTGCAA	CAGATAATTT	TTTCCAAAT	CCTGAACTTT	180
ATATACGAGA	GAGTGTAATA	GGATCATTTG	ACAGGAAGAA	GTTAGAACAG	CTGTACAATA	240
GATACAAAGA	CCCTCAAGAT	GAGAATAAAA	TTGGAATAGA	TGGCATAACG	CAGTTCTGTG	300
ATGACCTGGC	ACTCGATCCA	GCCAGCATT	GTGTGTTGAT	TATTGCGTGG	AAGTTCAGAG	360
CAGCAACACA	GTGCGAGTTC	TCCAAACAGG	AGTTCATGGA	TGGCATGACA	GAATTAGGAT	420
GTGACAGCAT	AGAACAACCT	AAGGCCCAGA	TACCCAAGAT	GGAACAAGAA	TTGAAAGAAC	480
CAGGACGATT	TAAAGATTTT	TACCAGTTTA	CTTTTAATTT	TGCAAGAAT	CCAGGACAAA	540
AAGGATTAGA	TCTAGAAATG	GCCATTGCCT	ACTGGAACCT	AGTGCTTAAT	GGAAGATTTA	600
AATTCTTAGA	CTTATGGAAT	AAATTTTGT	TGGAACATCA	TAAACGATCA	ATACCAAAAG	660
ACACTTGGA	TCTTCTTTTA	GACTTCAGTA	CGATGATTGC	AGATGACATG	TCTAATTATG	720
ATGAAGAAGG	AGCATGGCCT	GTCTTATTG	ATGACTTTGT	GGAATTGCA	CGCCCTCAAA	780
TTGCTGGGAC	AAAAGTACA	ACAGTGTAGC	ACTAAAGGAA	CCTTTTAGAA	TGTACATAGT	840
CTGTACAATA	AATACAACAG	AAAATTGCAC	AGTCAATTTT	TGCTGGCTGG	ACTGAACTGA	900
AGATCAATCC	TACAAGTTCA	GACTGAGGGT	TGAGACAAAA	CTTTAAGGAT	ACATCTTGGA	960
CCATATCGTA	TTTCATTCTT	CTAATGGTGG	TTTGGGCTTG	TCTTCTAGTC	TGGGCGCGTC	1020
TAAACATTTA	TAATTCACAC	ATTGTGGATT	TCATCTTATA	TCGTGGGACC	ATCCTAGTTT	1080
ATTCTCCCAT	AAGTCTTAGA	AGCTTTATGG	TGATTATTTT	GAGGTTTTCA	TCTCGCATA	1140
AAGCACAATG	CTGTCTTCAT	CAGAAAACAG	TTGGCATAAG	AATTAAACAT	ATGAACATCA	1200
CAAAACAATT	TATAAAAAT	TCTTAAATAT	ACGCTTTGGG	CTAGTTGCAA	AGACTATGCT	1260
AATAGCACTT	CCAGTGAGAG	TGATATATTT	AAGTGTACTG	GATCTGGAAT	GGTGTTTTGG	1320
TTTGGGGGGA	ATTTTTTTTT	TTTCTCGCA	AATCACATAT	GTGTGTGATG	TGAGTATCTG	1380
ATGAAAAAAC	AATGTCAGAA	TAACCGACAT	GAAAAATTTT	TAGGATAACT	TGGTGCCCTAC	1440
CTGAAAAATG	TATTGTGTTT	TAGACTCTTG	ATTTCAAAAG	GTTCACAGAG	ACTAGTCTGC	1500
GCTTACCTTA	CCCATGTTTA	TATATAGCTG	TCCTACAGGG	AGCTTTTATT	TAGAAAAATG	1560
CTGCATAATG	TTAGATTCTT	CTCCTGTCTA	CATTATGCAC	TACATAATTG	GACTTCATTA	1620
TGCTTTTGAA	ATGCTTATCT	GCCTGTACAC	TAAGTTAAAC	TATTTAATTT	GTTTGAATG	1680
TTTTGGATTG	CTACACAATA	CAATATTCTA	AATTTAGGCA	TGAGGGTTTT	TTTGTTTTAT	1740
TTTTACTTTT	TTTTGTTCAT	TGCACTATGG	AACACAAATG	AAATCTCTTT	AATTTATAAG	1800
AAGATAGTAG	GAGTTAATGG	TTGAAATGGG	TTGTGATGAG	CCACGAAAT	CAATCTTTAT	1860
AATATAGGTA	CTGCTCTTTC	AGACAAACAG	TCCATTTTAA	ATGACTTCTT	ATTTGTGTGA	1920
AATTACTTTA	ACTGCTAATC	ACTGTGGTTG	CCAAATATTT	ACTTCAGAA	CAAAGATTTT	1980
CAAAACAAGCA	TACACATGAC	AAAATACCAG	TCTGGCTTCT	AGTCTATTTA	CTGTTTGTGT	2040
TCACTCAGAT	TAGCTCAGTT	TTCTCATCAA	AGCAGAAATG	TATCTTGCGT	GTGTGTGTGT	2100
GTGTGTGTGT	GTGTGTGTGT	GTATGTGTGT	ATATATATAT	ATATATATAT	ATATATATTT	2160
TTTTTTTTTT	TTTTTTTTTA	ATACAAAAAG	CCATGAGCTG	CTTTTATGCT	GAAAAATGGT	2220
ATTTCCCTGT	TCACCTACTG	ACATGTGAAG	AAGGGTTTCT	TGCTTCTCTA	AACATTTCCG	2280
TAAGGCAGCG	TAGAAATGTA	ATACTTCAAA	TGTTTGATGA	TTATGGTCTT	TTGATAGGAA	2340
TAGATTCTGC	TTGGGATATA	TATCCAGGCA	CTCTCTAAGG	TCTAGGGTTG	ATATTAACAA	2400
AGGAATGTAC	TTAGAATAGC	AGTACATTTT	ATGCAAAAT	GGAATTAATT	TTAAGAAACA	2460
ATGACATATC	AAAACGTGCT	TTTACATGAT	TTTGAATAG	ACTAGAAAGC	TTTCCCTATA	2520
GACATATTAA	TATTTCAACT	ATAACTTTAA	TTCAAGAAATG	CAGTTTACC	AAAAGAAAAA	2580
TTTGAAAAAT	TCTATTTCAG	CTACTGGAAT	TGGTTATTAA	AAGAAAAAGG	AAAAAGAGA	2640
ATCTTGCTGC	TTTCAGTATT	TCCTGATTTT	TTTGAAATA	TAAAGAGGAA	CTTCAATTAT	2700
GAAAAATTTT	TAAAGATAT	ATATATCTAT	ATATCTATAT	ATATGTACTG	TTTGTTTTCC	2760
TGTCTTGAAG	ATTTGAGTT	ATGGTTATTG	GTTTCAGATT	GATTAATTCA	CATATGCTGT	2820
GTTTCTTTTA	AAAGTCATAT	GGGTTCTGTTG	CCTAATGCCT	TGGATTTTAC	ATATTTTCT	2880
TTTTAAATGC	AAAACCTTTT	CAACAAAAATA	GTGTTTGTCA	TCAGGTGGT	ACTAAACATT	2940
TATAAATACT	GTGTAATTAT	AAACAAAAAT	ACATAAAGCT	TTGAATATAA	TTATGTAGCA	3000
TAAAAGTTAA	GGTTGTTTAC	TATGATGGCA	TCTTAGAATT	AAACAAAACT	TTTACTAGGG	3060
CTGAAAAGAG	AAGACTGATT	TAATGTGGTG	TGATTATTCT	GAAGATAAAT	GTCTGGCTAC	3120
AGGGAATATT	TTGTAATAAA	AAATGATTAC	ACATATGGCT	GTGTGTGTTT	GAGTCTGTGT	3180
CTGTGAGAGA	GCCAGAGAGA	GTGAGAGAGA	TTGACAGAGA	AAGGGAGAGA	CACACACACG	3240
CCCCTGAAT	TGCTTTAACT	CCTAAGTGT	TCAGTCTCTA	TTCCGGTAAA	CTCCCATGTC	3300
TGATTCTTTG	TTTTAAACTG	AACCATAGGT	ACAGTTTCCT	TTTTGCCAAA	TGTCAAAAACA	3360
GGTACAAATT	TTAAATGTGA	ATGCTTTTTA	AATAGAAAAA	TGTATAAAAT	TAGAAGTGCC	3420
CACATATAAA	AAATACTTTG	GATGAAGATT	ATCTTTAGTG	AATATCATCT	GCATATCTCT	3480
GTAAGTTCAA	TTGTGTTTCT	TACAGTCCCT	GTCATATTAC	CAACAGAGGC	AATAAAGCT	3540
GCAGTGAAT	TG					

Seq ID NO: 164 Protein sequence:
Protein Accession #: AAG00606

1	11	21	31	41	51	
MNKLKSSQKD	KVRQFMIFTO	SSEKTAVSCL	SQNDWKLDVA	TDNFFQNP	YIRESVKGSL	60
DRKKLEQLYN	RYKDPQDENK	IGIDGIQQFC	DDLALDPASI	SVLIIAWKFR	AATQCEPSKQ	120
EFMDGMTLGL	CDSIEQLKAQ	IPKMEQELKE	PGRPKDFYQF	TFNFAKNPQ	KGLDLEMAIA	180
YWNVLNLRGF	KFLDLWNKFL	LEHMKRSIPK	DTWNLLDLFS	TMIAADMSNY	DEEGAWPVLI	240
DDFVEFARPO	IAGTKSTTV					

Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

5	1	11	21	31	41	51	
	CTCCAGTCCG	CATGCTCAGT	AGCTGCTGCC	GGCCGGGGCTG	GGGGGGGGCG	TCCGCTGCGC	60
10	GCCTACGGGC	TGCGGTGGCG	GCCGCCCGCG	CACCCGGCAG	GGCCCGCCAG	TCCCCGCTTC	120
	CCTGCTCCAG	AGCCGCCGCC	TGGGCCGGGG	CAGGGCGGGC	CCGGGGCTCC	TCCATGCTGC	180
	CAGCCGCCGG	GCTGCGGAGC	CGACCAAGTG	GCTCCTGCGA	TGGCGGCGGA	AGAGGAGGCT	240
	GCGGCGGGAG	GTAAAGTGTT	GAGAGAGGAG	AACCAAGTGA	TTGCTCTCTG	GGTTTCCAGC	300
	CGGTGAGTC	CAGGGACAAG	ACCAACAGCT	ATGGGGTCTT	TCAGCTCACA	CATGACAGAG	360
15	TTTCCACGAA	AACGCAAAAG	AAGTGATTCA	GACCCATCCC	AAGTGAAGA	TGGTGAACAC	420
	CAAGTTAAAA	TGAAGGCCTT	CAGAGAAGCT	CATAGCCAAA	CTGAAAAGCG	GAGGAGAGAT	480
	AAAATGAATA	ACCTGATTGA	AGAACTGTCT	GCAATGATCC	CTCAGTGCAA	CCCCATGGCG	540
	CGTAAACTGG	ACAAACTTAC	AGTTTAAAGA	ATGGCTGTTC	AACACTTGAG	ATCTTTAAAA	600
	GGCTTGACAA	ATTCTTATGT	GGGAAGTAAT	TATAGACCAT	CATTCTTCTA	GGATAATGAG	660
20	CTCAGACATT	TAATCTTAA	GACTGCAGAA	GGCTTCTTAT	TTGTGGTTGG	ATGTGAAAGA	720
	GGAAAAATTC	TCTTCGTTTC	TAAGTCAGTC	TCCAAAATAC	TTAATTATGA	TCAGGCTAGT	780
	TTGACTGGAG	AAAGCTTATT	TGACTTCTTA	CATCCAAAAG	ATGTTGCCAA	AGTAAAGGAA	840
	CAACTTCTCT	CTTTTGATAT	TTCACCAAGA	GAAAAGCTAA	TAGATGCCAA	AAGTGGTTTG	900
	CAAGTTCACA	GTAATCTCCA	CGCTGGAAGG	ACACGTGTGT	ATTCTGGCTC	AAGACGATCT	960
25	TTTTTCTGTC	GGATAAAGAG	TTGTAATAATC	TCTGTCAAAG	AAGAGCATGG	ATGCTTACCC	1020
	AACTCAAAGA	AGAAAAGACA	CAGAAAATTC	TATACTATCC	ATTGCCTGGT	TTACTTGAGA	1080
	AGCTGGCCTC	CAAAATATTGT	TGGAATGGAA	GAAGAAAGGA	ACAGTAAGAA	AGACAACAGT	1140
	AATTTTACCT	GCCTTGTGGC	CATTGGAAGA	TTACAGCCAT	ATATTGTCTC	ACAGAACAGT	1200
	GGAGAGATTA	ATGTGAAACC	AACCTGAATT	ATAACCCGGT	TTGCAGTGAA	TGGAAAATTT	1260
30	GTCTATGTAG	ATCAAAGGGC	AACAGCGATT	TTAGGATATC	TGCCTCAGGA	ACTTTTGGGA	1320
	ACTTCTTGTT	ATGAATATTT	TCATCAAGAT	GACCACAATA	ATTTGACTGA	CAAGCACAAA	1380
	GCAGTTCTAC	AGAGTAAGGA	GAAAATACTT	ACAGATTCCCT	ACAAATTCAG	AGCAAAAGAT	1440
	GGCTCTTTTG	TAACCTTAAA	AAGCCAATGG	TTTAGTTTCA	CAAAATCCTG	GACAAAAGAA	1500
	CTGGAATATA	TTGTATCTGT	CAACACTTTA	GTTTGGGAC	ATAGTGAGCC	TGGAGAAGCA	1560
35	TCATTTTAC	CTTGAGCTC	TCAATCATCA	GAAGAATCCT	CTAGACAGTC	CTGTATGAGT	1620
	GTACCTGGAA	TGTTACTGCG	AACAGTACTT	GGTGCTGGTA	GTATTGGAAC	AGATATTGCA	1680
	AATGAAATTC	TGGATTATCA	GAGGTTACAG	TCTTCTTCAT	ACCTTGATGA	TTGAGTCCA	1740
	ACAGGTTTAA	TGAAGATAC	TCATACTGTA	AACCTGCAGG	GTATGTCAAA	TAAGGAGTTG	1800
40	TTTCCACCAA	GTCTTCTGA	AATGGGGGAG	CTAGAGGCTA	CCAGGCAAAA	CCAGAGTACT	1860
	GTTGCTGTCC	ACAGCCATGA	GCCACTCTCT	AGTGATGGTG	CACAGTTGGA	TTTCGATGCC	1920
	CTATGTGACA	ATGATGACAC	AGCCATGGCT	GCAATTTATGA	ATTACTTAGA	AGCAGAGGGG	1980
	GGCTTGGGAG	ACCTTGGGGA	CTTCAGTGAC	ATCCAGTGGG	CCCTCTAGCC	TTTGATTTTT	2040
	AACTCCAAAA	ATGAGAAAAC	TTTTAAAGCA	TTATTACGA	AAAAACTGTC	TCAACTATTTC	2100
	TTAAGTACTG	TATGTATATT	GTTTGTATCT	TTTATTAATG	TTCTACCACT	TTTTATAGAT	2160
45	TTGCATCTTC	CTGTACACAG	GATGTGGGGA	AATACGTTTT	CCTCCCAAGA	GAACCAAGTT	2220
	TATTATAGAC	TCCTTTATTC	AGTGAAATGG	CTTATAATCC	ACTAGTTGCC	ATATTTTTCG	2280
	TAAATATTT	CTAACCAAGA	ATACTACTTA	CATATTGTTT	TGGCTTTGTT	TTATTTTGA	2340
	TGCAGTTTTT	TTTAGTTGAG	GTAATGTAAT	ATATTGATGT	TTTCTTTTGT	GTCTAAGATT	2400
	GATTATATAAT	AGTAGGTTTG	TATAATTTGG	AACATTTTCC	ATGCCCTTGG	AAATTCCTTA	2460
50	ATTGAGGATA	GGGCTTACAC	ACTTTAAGAA	AACAGTGAGT	ACTTGAACAT	TTAAAGGGAC	2520
	AGTGCAATTT	ATAGTCATAA	TCACATTGAA	TACTGTATTT	GATCTTTGGA	GACTTAGGCA	2580
	AGCACAGAGC	TGGGATATTT	ATGCTCAGTT	GAGCACTTTA	AGATGAATTT	TAAGTGAGAT	2640
	GATTTCTTGC	TTAAACTCAG	GAAAGTCAAA	AGAGTTTCAG	CTTTCTTAC	AGAAAAGGAA	2700
	GGATCTTGGG	CCCTAGATCT	TGGGGATTAA	CCTCTGCATA	TAAGATTTAC	TCTTAATAGG	2760
55	CCAGACGTGG	TGCTCACGCC	TGTAATCCCA	GTACTTTGGG	AGGCTGAGAC	GGGCAGATCA	2820
	CTTGAGGTCA	GGAGTTCAAG	ACCAGCCTGG	CCAATATGGT	GAAACCCCGT	TTCTACTAAA	2880
	AATACAAAAA	AAATTTACCA	GGCACTCACT	CTTGAGGTAA	CTAACCAACT	CCCACGATAA	2940
	TGACAGTCCA	TTCATGAGCG	CAAGGCCCTC	ATGACCTAAT	GGCACACACC	TGTAATCCCA	3000
	ACTGCTTGGG	AGGCTGAGGC	GAGAGGATTG	CTTGAACCTG	GGAGGCAGAG	GTTGCACTGA	3060
60	GCGGAGATCG	CACCACTGCA	CTCCAGTCTG	GGCAACAGAG	TGAGACTTCA	TCTCAAAAAA	3120
	AGTAAAAAAA	AAGATTATAT	ATAATCACTG	AAGATCTCTA	TTATAGATAG	ATTAGGTTTT	3180
	TGACATTGGA	AACATACTTA	GGGATAGATT	TGTCCTAAAG	GAAAAAAGTA	GGCCCGGCA	3240
	GATTAAATGT	CTTGTGTAAA	GTCACACATT	AAATTCAGTC	ACACATTAAA	TTCTAGAGAT	3300
	TTTAAATGTT	TAATGTATAT	AAACCAAGTT	CTTTATACAC	ATTTGGGAAA	ACATTGGTCT	3360
	CACAGATTAA	ATGATTAACT	AACTGACCCA	GGAAGTAGTT	GTAGCTTTCT	AAGTAATTAG	3420
65	GCAATTACAG	TTATTGCCCT	TAACCAAGGG	TAATAAAACA	AAATGACAAG	TACATGTTTA	3480
	AAATTATGAG	GCAATGAGAA	ATAATTAAAA	AACCAATTTT	CTAGTTATAA	TTTAAATTTT	3540
	GGAGAGCATT	TTTACAGTGA	ATTAATCCAG	AGGTGGCTCA	AATTGAGTAT	AAGAAATTAAG	3600
	ATTATTAAAA	ATACTGCATG	TCTACCTTCT	CGGGGATCAT	ACTTTATAAC	ACTTTCTGCT	3660
70	TCAGTAGCTC	TTCATAGCTT	GCCAAGTATG	CTCCCATATT	TTCTCTCTCG	TGCCTCGCAA	3720
	ATGAAAGTCA	GATAGGCTGG	GAACCTATGG	GGCAGCCCTC	AGACTTCAAT	GTGGGCTTCA	3780
	AATCCAGTTT	CCTGTTCTAT	ATGGTGCTAC	ATCTTTCCAG	AAAATTTCCC	TCAGAGCCCC	3840
	TCGCCAAAAA	AAAGCATTAT	TTTGACCCCTG	CATGCTATTT	CTTTAGCTGT	AGGTGATAGA	3900
	TTAGAACTTC	TGTCAGACAT	GTTAATGACA	AACATACCAG	CAGACAATAA	CCAAAGCAAA	3960
75	TGTTTCTCTC	AAGTGTGAAA	TGTGCAAGGG	CTCGTGGGCA	AGGATGTATT	GGCACACTGT	4020
	CCTCTTGAAC	TGATAGTGTC	CCAGCAATGT	TGGAGGTTGG	CACCATTCCT	GGTCCGACAC	4080
	TTGAGGACCT	GAGAGACATC	AGGTTTAGAA	TGAGCCAAAG	AAATCCTTACA	AGATGGGGAG	4140
	AATTGGTGTG	CAGCAGCCTA	AGTGTATAG	TTAAGTCTAA	AGAAGTATGA	AAGATCCCCCT	4200
	GTGTTCTCTA	AATTGAGCAG	AGGGGCCTGC	CTACCAATAT	CACTTTTATG	GGGACTGAAC	4260
	CATTGCAGGT	TAGACTTGGC	TTCCAAAGAG	TCTGCCTAAG	CCAGGGGTGG	CAGGGTAGCG	4320
80	CATCATAGCT	GGATGGCCCT	AAAAGCAGAT	GGGGGCAGAC	TTGCCCTCGT	GATGCCAGGA	4380
	TTTGAGAGGC	AGAGTTTCTA	GAGGGAGACC	AGTGCTGCCT	CTCACAGTGG	CAGTTTTCCT	4440
	TCTTTGCAAG	AGGAGGGGCT	GTTCAATTCC	ATAGACCAGT	GGGCAGATAG	CCAGTTGAAT	4500
	ACTCTGTGCA	TGGTTTGATG	CTTTATTAGT	TCGCTCTAAT	ATTTTCTCTG	AGATCTCTTT	4560
	GTCTCTGACT	CAAAATCTAA	TCCATGCATT	GTATGATACC	GTAGCTCTCC	TAAGGTTTGT	4620
85	GTTTCTCTCA	AAATGTTTTA	GTTTTCTTCA	ACTAAATTTG	ATTTTGTGCT	TTAGAAGTGA	4680
	CATATTTTTA	TGGTATACAC	TATGTTCTCT	TTTCTACTG	CGAGTCAATT	TTTTGAATTT	4740
	TCGTGAGAAA	GAATATATCT	ACAAATTGCA	CGAAAGTATC	ATAAAAAACG	TACTCTAGAG	4800

	CAGCGCTGTC	CAATAGAAAT	ATAATCTGAG	CCACATGTAT	AATTTTATTT	TCTTCTAGCC	4860
	ACATTAAAGA	AGTAAAAAGA	TACAAGTAGA	ACTAATTTTA	ATGTTTTAAT	TCAGTATATC	4920
	CAAAAATATCA	TTTGAACATG	TAATTAATAT	AAAATTATTA	ATGTGATATT	TTACATTCTT	4980
5	TTGGTAATAC	TAGTCTTCAA	AATCTGGTAT	GTATCTTACA	TTGATAGCAC	ATCTCACTTT	5040
	GTACTAGCCA	CATTGCAAGT	GCTCAGTAGC	CACATGTGGC	TAGTGGCTAC	TGCACTGGAC	5100
	AGCACAGTTC	TAGGTTCCAC	CCTAACACCC	AAGTCTGTG	GATTAGAATC	CCAGAATCAG	5160
	AGCTGGAAGT	AAACATAGAG	ATCAAACTTC	CTTTTAAAAA	TGAGGACGCT	GAGGCACAGA	5220
	GTTTAAATGG	CTTGCAATGAG	GTACATACAGC	TAAATTCAGC	CTCAACAGGG	TCTTCTGATT	5280
10	CCAGGCACTC	TTCCCACTCC	ACTACATTAC	TGTAGTGGTA	ATTCTTAGGG	TTAAAAAAG	5340
	TGTAGAGTAG	GCCGGGCGCA	GTGGCTCATG	CCTGTAATCC	CAGCACTTTG	GGAGGCCGAA	5400
	GTGGGCGGAT	CACGAGGTCA	GGAGATCGAG	ACCATCCTGG	CCAACATGGT	GAAACCCCGT	5460
	CTCTACTGAA	AATACAAAGC	AAAATTAGCC	AGGTGTGGTG	GCGGGCGCCT	GTGGTCCCAG	5520
	CTGCTCTGGA	GGCTGAGGAG	GAATGGCGTG	AACCCAGGAG	GCAGAGATGG	CAGTGAGCCA	5580
15	AGATCGCGCC	ACTGCACCCC	AGCCTGGGCG	ACAGAGCGAG	ACTCCATCTC	AAAAAAGAAA	5640
	AAAAAAGAAA	AAGAAAAGAA	AAGAAAAGTC	TAGAGAACAT	TATATTAAGT	GGTTATTATT	5700
	GAAGTAGACC	AAAGTTTATA	CCATAAGGAT	ATTTTTCCTT	AAATACCATG	TTTGAAGAAC	5760
	AATTATTATT	TGATCTTGTA	ATCTGTAAGA	TCAAATAACA	AGTCTCTATC	CATGTTACCA	5820
	AAITTTAACCT	TTTGAATAA	ATAAACTTTA	AAATATCAGA	TGTGTTATTA	CAGGATGATA	5880
20	CTTGGAATCA	AGTGAATGA	GTTATATGGT	CATCACTAAA	TTTAGAAATC	TATTGTGAAA	5940
	CAAGACAAA	CAGGAAAGTA	CAGAATAGAG	ACTTTTAGTA	AATAAATGGA	ATTTAAAGA	6000
	AAGTGTATT	TTACAGTGTG	ACGACAGAAA	AGGATGTCTT	TGTTGTGATA	GTCTTTGAGG	6060
	GATCTCCGTA	AAATCTGGGG	CACAGGTACA	AGAAATAGCC	AATATTAGT	TCCAGACCA	6120
	TGTTTAGTAG	TGTCTAGTTC	CAGATCATGC	TGCCAAGAGG	TATCTCCCCC	TCAGGTGGGT	6180
25	CATCACTGAG	CCCTGGAATT	GGAGACTCAT	ACTTGCCGAG	CACAATGTTA	CGGGCAGACA	6240
	GGCCGACATC	TATGATTAGC	TAGAAGCCAT	AAAGAAAAGC	TGCTAAGTGG	CCACTAGGTG	6300
	CCACTTTTCT	GTTTTGTGTA	TGCTTTCATT	AGCAGATCTT	TTTTTTCCAA	GCTCCATGGG	6360
	GCCTATGAGA	GGCATTTATG	ATTTTGTGTC	CTACAATAAG	TCAGCCTGTC	TGGTGTGAGT	6420
	TGTTTATGA	GAAATGCTTT	CCAAGGGAGG	TCTAGGAAGA	TCCTGACACA	TAAGAACTTT	6480
30	GGCTTAGAGA	GCTTTCCAGG	TGTAGTGCCA	ATAAAACTG	ACCTGGAAG	AAAACTGCC	6540
	CAGCAGGAA	CATGCTTTCT	GAATCACTT	GAGAGTGAT	GGTGTATGTC	ACTTCTCATA	6600
	TATTCTTGAG	TTTAGATTG	TCTTTTATAC	AATTTTATAGC	TCTTTTCCAG	TTCACTTGTG	6660
	CTCGTCTGTA	TATTGCTTAT	TTTAAATTTT	TGTGGTAAAT	AATGAAAGA	GTGAAATTAT	6720
	ATTTTATAAT	TACTCATTG	TAGTTTTTTT	TTTTAATTTA	ATAAACTTCC	TCCAAAAGT	6780
35	GCCTCCCTAA	AA					

Seq ID NO: 166 Protein sequence:
Protein Accession #: AAG34652

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	QVEDGEHQVK	MKAFAREHSQ	TEKRRRDKNM	NLIEELSAMI	PQCNPMARKL	DKLTVLRMAV	120
	QHLRSKGLT	NSYVGSNYRP	SPLQDNELRH	LILKTAEGFL	FVVGCEGRKI	LFVSKSVSKI	180
45	LNVDQASLTG	QSLFDFLHPK	DVAKVKEQLS	SFDISPREKL	IDAKTGLQVH	SNLHAGTRTV	240
	YSGSRRSFFC	RIKSKISIVK	EEHGCLPNSK	KKEHRKFYTI	HCTGYLRSWP	PNIVGMEEER	300
	NSKKNNSNFT	CLVATIGRLQ	YIVPQNSGEI	NVKPTEFITR	FAVNGKFVYV	DQRATAILGY	360
	LPQELLGTSC	YEFYHQDDHN	NLTDKHKAVL	QSKEKILTDS	YKFRKADGSP	VTLKSQWFSF	420
50	TNPWTKELEY	IVSVNLTVLG	HSEPEGEASF	PCSSQSSEES	SRQSCMSVPG	MSTGTVLGAG	480
	SIGTDIANEI	LIDLRLQSSS	YLDDSSPTGL	MKDTHTVNCR	SMSNKELFPP	SPSEMGELEA	540
	TRQNQSTVAV	HSHEPILLSG	AQLDFDALCD	NDDTAMAAFM	NYLEAEGGLG	DPGDFSDIQW	600
	TL						

Seq ID NO: 167 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

60	1	11	21	31	41	51	
	GGTTACTCAT	CCTGGGCTCA	GGTAAGAGGG	CCCGAGCTCG	GAGGCGGCAC	ACCCAGGGGG	60
	GACGCCAAGG	GAGCAGGAGC	GAGCCATGGA	CCCCGCCAGG	AAAGCAGGTG	CCCGAGGCCAT	120
	GATCTGGACT	GCAGGCTGCG	TGCTGCTGCT	GCTGCTTCGC	GGAGGAGCGC	AGGCCCTGGA	180
	GTGCTACAGC	TGCGTGACAG	AAGCAGATGA	CGGATGCTCC	CCGAACAAGA	TGAAGACAGT	240
	GAAAGTGCGG	CCGGGCGTGG	ACGTCTGCAC	CGAGGCCGTG	GGGGCGGTGG	AGACCATCCA	300
65	CGGACAATTC	TCCGTGGCAG	TGCSGGGTG	CGGTTCCGGA	CTCCCCGGCA	AGAATGACCG	360
	CGGCCTGGAT	CTTCAGGGGC	TTCTGGCGTT	CATCCAGCTG	CAGCAATGCG	CTCAGGATCG	420
	CTGCAACGCC	AAGCTCAACC	TCACTCGCG	GGCGCTCGAC	CCGGCAGGTA	ATGAGAGTGC	480
	ATACCCGCCC	AACGGCGTGG	AGTGCTACAG	CTGTGTGGGC	CTGAGCCGGG	AGGCGTGCCA	540
	GGGTACATCG	CGCCCGGTGG	TGAGCTGCTA	CAACGCCAGC	GATCATGTCT	ACAAGGGCTG	600
70	CTTCGACGGC	AACGTCAACT	TGACGGCAGC	TAATGTGACT	GTGTCCTTGC	CTGTCCGGGG	660
	CTGTGTCCAG	GATGAATTTCT	GCACCTCGGA	TGGAGTAACA	GGCCCAAGGT	TACGCTCAG	720
	TGGCTCTCTG	TGCCAGGGGT	CCCGCTGTAA	CTCTGACCTC	CGCAACAAGA	CCTACTTCTC	780
	CCCTCGAATC	CCACCCCTTG	TCCGGCTGCC	CCCTCCAGAG	CCCACGACTG	TGGCCTCAAC	840
	CACATCTGTC	CACACTTCTA	CCTCGGCCCC	AGTGAGACCC	ACATCCACCA	CCAAACCCAT	900
75	GCCAGCGCCA	ACCAGTCAGA	CTCCGAGACA	GGGAGTAGAA	CACGAGGCCT	CCCGGATGA	960
	GGAGCCCAGG	TTGACTGGAG	GCGCCGCTGG	CCACCAGGAC	CGCAGCAATT	CAGGGCAGTA	1020
	TCCGTCAAAA	GGGGGGCCCC	AGCAGCCCCA	TAATAAAGGC	TGTTGGCTC	CCACAGCTGG	1080
	ATTGGCAGCC	CTTCTGTTGG	CCGTGGCTGC	TGGTGTCTTA	CTGTGAGCTT	CTCCACCTGG	1140
80	AAATTTCCCT	CTCACCTACT	TCTCTGGCCC	TGGGTACCCC	TCTTCTCATC	ACTTCTCTGT	1200
	CCCACTACTG	GACTGGGCTG	GCCAGCCCCC	TGTTTTTCCA	ACATTCCTCA	GTATCCCCAG	1260
	CTTCTGCTGC	GCTGGTTTGC	GGCTTTGGGA	AATAAATAC	CGTTGTATAT	ATTCTGGCAG	1320
	GGGTGTTCTA	GCTTTTGTAG	GACAGCTCCT	GTATCCTTCT	CATCCTTGTC	TCTCCGCTTG	1380
	TCCTCTTGTG	ATGTTAGGAG	AGAGTGAGAG	AAGTCAGCTG	TCACGGGGAA	GGTGAGAGAG	1440
	AGGATGCTAA	GCTTCTTACT	CACTTTCTCC	TAGCCAGCCT	GGACTTTTGA	GCGTGGGGTG	1500
85	GGTGGGACAA	TGGTCCCCCA	CTCTAAGCAC	TGCCTCCCCC	ACTCCCCGCA	TCTTTGGGGA	1560
	ATCGGTTCCC	CATAGTCTCT	CCTTACTAGA	CTGTGAGCTC	CTCAGGGGCA	GGGACCGTGC	1620
	CTTATGTCTG	TGTGTGATCA	GTTTCTGGCA	CATAAATGCC	TCAATAAAGA	TTTAATTACT	1680

TTGTATAGTG AAAAAAAA

Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

1	11	21	31	41	51	
MDPARKAGAG	AMIWTAGWLL	LLLLRGGAAQ	LECYSCVQKA	DDGCSFNKMK	TVKCAPGV DV	60
CTEAVGAVET	IHQQFSLAVX	GGGSLGPKGN	DRGLDLHGLL	AFIQLQQCAQ	DRCNALNLT	120
SRALDPAGNE	SAVPPNGVEC	YSCVGLSREA	CQGTSPFVVS	CYNASDHVYK	GCFDGNVTLT	180
AANVTVSLPV	RGCVDQDEFCT	RDGVTGPGFT	LSGSCCQGSR	CNSDLRNKTY	FSPRIPLVR	240
LPPPEPTTVA	STTSVTITST	APVRPTSTTK	PMPAPTSQTP	RQGVHEHESR	DEEPRLTGGA	300
AGHQDRNSNG	QYPAKGGPQQ	PHNKGCVAPT	AGLAALLLAV	AAGVLL		

Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

1	11	21	31	41	51	
GAATTCGGCA	CGAGCGCGCG	GCGAATCTCA	ACGCTGCGCC	GTCTGCGGGC	GCTTCCGGGC	60
CACCAGTTTC	TCTGCTTTCC	ACCCTGGCGC	CCCCCAGCCC	TGGCTCCCCA	GCTGCGCTGC	120
CCCGGGCGTC	CACGCCCTGC	GGGCTTAGCG	GGTTCAGTGG	GCTCAATCTG	CGCAGCGCCA	180
CCTCCATGTT	GACCAAGCCT	CTACAGGGGC	CTCCGCGGCC	CCCGGGGACC	CCCACGCGCG	240
CGCCAGGAGG	CAAGGATCGG	GAAGCGTTCC	AGGCCGAGTA	TGACTCGGC	CCCCTCCTGG	300
GTAAAGGGGG	CTTTGGCACC	GTCTTCGCAG	GACACCGCCT	CACAGATCGA	CTCCAGGTGG	360
CCATCAAAGT	GATTCGCCCG	AATCGTGTGC	TGGGCTGGTC	CCCCTGTGCA	GACTCAGTCA	420
CATGCCCACT	CGAAGTCGCA	CTGCTATGGA	AAGTGGGTGC	AGGTGGTGGG	CACCCTGGCG	480
TGATCCGCGT	GCTTGACTGG	TTTGAGACAC	AGGAAGGCTT	CATGCTGGTC	CTCGAGCGGC	540
CTTTGCCCGC	CCAGGATCTC	TTTGACTATA	TCACAGAGAA	GGGCCCACTG	GGTGAAGGCC	600
CAAGCCGCTG	CTTCTTTGGC	CAAGTAGTGG	CAGCCATCCA	GCAGTCCCAT	TCCCGTGGAG	660
TTGTCCATCG	TGACATCAAG	GATGAGAACA	TCCTGATAGA	CCTACGCGGT	GGCTGTGCCA	720
AACTCATTGA	TTTTGGTTCT	GGTGCCCTGC	TTTATGATGA	ACCCTACACT	GACTTTGATG	780
GGACAAGGGT	GTACAGCCCC	CCAGAGTGGA	TCTCTCGACA	CCAGTACCAT	GCACTCCCGG	840
CCACTGTCTG	GTCACCTGGC	ATCCTCCTCT	ATGACATGGT	GTGTGGGGAC	ATTCCCTTTG	900
AGAGGGACCA	GGAGATTCTG	GAAGCTGAGC	TCCACTTCCC	AGCCCATGTC	TCCCCAGACT	960
GCTGTGCCCT	AATCCGCGCG	TGCCTGGCCC	CCAAACCTTC	TTCCCGACCC	TCACTGGAAG	1020
AGATCCTGCT	GGACCCCTGG	ATGCAAAAC	CAGCCGAGGA	TGTTACCCCT	CAACCCCTCC	1080
AAAGGAGGCC	CTGCCCTTTT	GGCCTGGTCC	TTGCTACCCT	AAGCCTGGCC	TGGCCTGGCC	1140
TGGCCCCCAA	TGGTCAGAAG	AGCCATCCCA	TGGCCATGTC	ACAGGGATAG	ATGGACATTT	1200
GTGCACTTGG	TTTTACAGGT	CATTACCACT	CATTAAAGTC	CAGTATTACT	AAGGTAAGGG	1260
ATTGAGGATC	AGGGGTAGTA	AGACATAAAC	CAAGTTTGCC	CAGTTCCTCT	CCCAATCTTA	1320
CAAAGGAGCC	TTCTCTCCAG	AACCTGTGGT	CCCTGATTTT	GGAGGGGGAA	CTTCTTGCTT	1380
CTCATTTTGC	TAAAGGAAGT	TATTTTGGTG	AAGTTGTTCC	CATTITGAGC	CTCGGGACTC	1440
TTATTTTGAT	GATGTGTGAC	CCACATTTGG	CACCTCCTAC	TACCACCACA	CAAACTTAGT	1500
TCATATGCTT	TTACTTGGGC	AAGGGTGCTT	TCCTTCCAAT	ACCCAGTAG	CTTTTATTTT	1560
AGTAAAGGGA	CCCTTTCCCG	TAGCCTAGGG	TCCCATATTG	GGTCAAGCTG	CTTACCTGCC	1620
TCAGCCCAAG	ATTTTATTAT	TTGGGGGAGG	TAATGCCCTG	TTGTTACCCC	AAGGCTTCTT	1680
TTTTTTTTTT	TTTTTTTTTG	GGTGAGGGGA	CCCTACTTTG	TTATCCCAAG	TGCTCTTATT	1740
CTGGTGAGAA	GAACCTTAAT	TCCATAATTT	GGGAAGGAAT	GGAAGATGGA	CACCACCGGA	1800
CACCACAGAG	CAATAGGATG	GGATGGATGG	TTTTTTGGGG	GATGGGCTAG	GGGAAATAAG	1860
GCTTGCTGTT	TGTTTTCCTG	GGGCGCTCCC	TCCAATTTTG	CAGATTTTGG	CAACCTCCTC	1920
CTGAGCCGGG	ATTGTCCAAT	TACTAAATG	TAAATAATCA	CGTATTGTGG	GGAGGGGAGT	1980
TCCAAGTGTG	CCCTCCTTTT	TTTTCTCTGC	TGGATTATTT	AAAAAGCCAT	GTGTGGAAAC	2040
CCCATATTTA	ATAAAGTAA	TAGAATCAGA	AAAAAATAAA	AAAAAATAAA		

Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

1	11	21	31	41	51	
MLTKPLQGP	APPGTPTPPP	GKNDREAFEA	EYRLGPLLKG	GGFGTVFAGH	RLTDLRLQVAI	60
KVIPRNRVLG	WSPLSDSVTC	PLEVALLWKV	GAGGGHPGVI	RLLDFWETQE	GFMLVLERPL	120
PAQDLFDYIT	EKGPLGEGPS	RCFFGQVVA	IQHCHSRGVV	HRDIKDENIL	IDLRRGCAKL	180
IDFGSALLH	DEPYTFDGT	RVYSPPPEWIS	RHQYHALPAT	VWSLGILLYD	MVCGDIPFER	240
DQEILEAEHL	FPAHVSPDCC	ALIRRLAPK	PSSRPSLEBI	LLDPWMQTPA	EDVTPQLQR	300
RPCPFGLVLA	TLSLANPGLA	PNGQKSHPM	MSQG			

Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

1	11	21	31	41	51	
GCGGCGGGGA	GCGGGCGTGC	TGAGCCCCCG	CGGCCGGCCC	GGCATGGGCG	TCTCCCGCGG	60
GCCTTCGCGC	GGCCCGGGCT	AGGGCCGGAT	GGAGCCGCGG	GACCGTAGCC	CCGAGGCCCC	120
GAGCAGCGAC	TCCGAGTCGG	CTTCCGCCTC	GTCCAGCGGC	TCCGAGCGCG	ACGCGGCTCC	180
CGAGCCGGAC	AAGGCGCGCG	GGCGACTCAA	CAAGCGGCGC	TTCCCGGGGC	TGCGGCTCTT	240
CGGGCACAGG	AAAGCATATC	CCAAGTCGGG	CCTCCAGCAC	CTGGCCCCCC	CTCCGCCCCC	300
CCCTGGGGCC	CCGTGCAGCG	AGTCAGAGCG	GCAGATCCGG	AGTACAGTGG	ACTGGAGCGA	360
GTCAGCGACA	TATGGGGAGC	ACATCTGGTT	CGAGACCAAC	GTGTCCGGGG	ACTTCTGCTA	420
CGTTGGGGAG	CAGTACTGTG	TAGCCAGGAT	GCTGAAGTCA	GTGTCTCGAA	GAAAGTGCGC	480
AGCTTGCAAG	ATTGTGGTGC	ACACGCCCTG	CATCGAGCAG	CTGGAGAAGA	TAAATTTCCG	540
CTGTAAGCCG	TCCTTCGGTG	AATCAGGCTC	CAGGAATGTC	CGCGAGCCAA	CCTTTGTACG	600
GCACCACTGG	GTACACAGAC	GACGCCAGGA	CGGCAAGTGT	CGGCACTGTG	GGAAGGGATT	660
CCAGCAGAAG	TTCACTTCC	ACAGCAAGGA	GATTGTGGCC	ATCAGCTGCT	CGTGGTGCAA	720

	GCAGGCATAC	CACAGCAAGG	TGTCCTGCTT	CATGCTGCAG	CAGATCGAGG	AGCCGTGCTC	780
	GCTGGGGGTC	CACGCAGCCG	TGGTCATCCC	GCCCACTGGG	ATCCTCCGGG	CCCGAGGGCC	840
	CCAGAATACT	CTGAAGACAA	GCAAGAAGAA	GAAGAGGGCA	TCCTTCAAGA	GGAAAGTCCAG	900
5	CAAGAAAGGG	CTCTAGGAGG	GCCGCTGGAG	ACCCCTTCATC	ATCAGGCCCC	CCCCCTCCCC	960
	GCTCATGAAG	CCCCTGCTGG	TGTTTGTGAA	CCCCAAGAGT	GGGGGCAACC	AGGGTGCAAA	1020
	GATCATCCAG	TCTTCTCTCT	GGTATCTCAA	TCCCAGACAA	GTCTTCGACC	TGAGCCAGGG	1080
	AGGGCCCAAG	GAGGCGCTGG	AGATGTACCG	CAAAGTGCAC	AACTCGGGGA	TCCTGGCGTG	1140
	CGGGGGCGAC	GGCACGGTGG	GCTGGATCCT	CTCCACCTTG	GACCAGCTAC	GCCTGAAGCC	1200
10	GCCACCCCTT	GTTCGCATCC	TGCCCTGGG	TACTGGCAAC	GACTTGGCCC	GAACCTCTAA	1260
	CTGGGGTGGG	GGCTACACAG	ATGAGCCTGT	GTCCAAGATC	CTCTCCACAG	TGGAGGAGGG	1320
	GAACGTGGTA	CAGCTGGACC	GCTGGGACCT	CCACGCTGAG	CCCAACCCCG	AGGCAGGGCC	1380
	TGAGGACCGA	GATGAAGGCG	CCACCGACCG	GTTCGCCCTG	GATGTCTTCA	ACAACCTACT	1440
	CAGCTTGGGG	TTTGACGCCC	AGGTCAACCT	GGAGTTCCAC	GAGTCTCGAG	AGGCCAACCC	1500
15	AGAGAAATTC	AACAGCCGCT	TTCCGAATAA	GATGTTCTAC	GCCGGGACAG	CTTCTCTCTGA	1560
	CTTCCTGATG	GGCAGCTCCA	AGGACCTGGC	CAAGCACATC	CGAGTGGTGT	GTGATGGAAT	1620
	GGACTTGACT	CCCAAGATCC	AGGACCTGAA	ACCCAGTGTG	GTGTGTTTCC	TGAACATCCC	1680
	CAGGTACTGT	GCGGGCACCA	TGCCCTGGGG	CCACCTGGGG	GAGCACCACG	ACTTTGAGCC	1740
	CCAGCGGCAT	GACGACGGCT	ACCTCGAGGT	CATTGGCTTC	ACCATGACGT	CGTTGGCCGC	1800
20	GCTGCAGGTG	GGCGGACACG	GCGAGCGGCT	GACGACGTGT	GCGGAGGTGG	TGCTCACCAC	1860
	ATCCAAGGCC	ATCCCGGTGC	AGGTGGATGG	CGAGCCCTGC	AAGCTTGACG	CCTCAGGCAT	1920
	CCGCACTGCC	CTGCGCAACG	AGGCCACCAT	GGTGACAGAG	GCCCAAGCGG	GGAGCGCCGC	1980
	CCCCCTGCAC	AGCGGACACG	AGCCGGTGCC	AGAGCAGTTG	CGCATCCAGG	TGAGTCGCGT	2040
	CAGCATGCAC	GACTATGAGG	CCCTGCACCT	CGACAAGGAG	CAGCTCAAGG	AGGCCTCTGT	2100
	GCCGCTGGGC	ACTGTGGTGG	TCCAGGAGGA	CAGTGACCTA	GAGCTCTGCC	GTGCCCCACAT	2160
25	TGAGAGACTC	CAGCAGGAGG	CCGATGTTGC	TGGAGCCAAAG	TCCCGGACAT	GCCAGAAACT	2220
	GTCCCCCAAG	TGGTGCTTCC	TGGACGCCAC	CACCTGCCAGC	CGCTTCTACA	GGATCGACCG	2280
	AGCCCAAGG	CACCTCAACT	ATGTGACTGA	GATCGACAG	GATGAGATTT	ATATCTCTGA	2340
	CCCTGAGCTG	CTGGGGGCTG	CGGCCCGGCC	TGACCTCCCA	ACCCCACTT	CCCTCTCTCC	2400
30	CACCTCACCC	TGCTCACCCA	CGCCCGGTGC	ACTGCAAGGG	GATGCTGCAC	CCCCTCAAGG	2460
	TGAAGAGCTG	ATTGAGGCTG	CCAAGAGGAA	CGACTTCTGT	AAGCTCCAGG	AGCTGCACCG	2520
	AGCTGGGGGC	GACCTCATGC	ACCGAGACGA	GCAGAGTGGC	ACGCTCCTGC	ACCACGCACT	2580
	AGCACTGGC	AGCAAGGATG	TGGTCCGCTA	CCTGCTGGAC	CAGCCCCCCC	CAGAGATCCT	2640
	TGATGCGGTG	GAGGAAACAG	GGGAGACCTG	TTTGACACAA	GCAGCGGCCC	TGGGCCAGCG	2700
35	CACCATCTGC	CATCATATCT	TGGAGGCCGG	GGCCTCGCTC	ATGAAGACAG	ACCAGCAGGG	2760
	CGACACTCCC	CGGCAGCGGG	CTGAGAAAGG	TCAGGACACC	GAGCTGGCCG	CCTACTCTGA	2820
	GAACCGGCAG	CATACACAGA	TGATCCAGCG	GGAGGACCAG	GAGACGGCTG	TGTAGCGGGC	2880

Seq ID NO: 172 Protein sequence:
Protein Accession #: NP_003637

	1	11	21	31	41	51	
	MEPRDGSPEA	RSSDSESASA	SSSGSERDAG	PEPDKAPRRL	NKRRFPGLRL	FGHRKAITKS	60
	GLQHLAPPPP	TPGAPCSESE	RQIRSTVDWS	ESATYGEHIW	FETNVSGDFC	YVGEQYCVAR	120
45	MLKSVSRRCR	AACKIVVHTP	CIEQLEKINF	RCKPSFRESG	SRNVREPTFV	RHHVWHRRRQ	180
	DGKCRHCGKG	FQKQFTFSK	EIVAISSWC	KQAYHSKVSC	FMLQIEBPC	SLGVHAAVVI	240
	PPTWILRARR	PQNTLKAASK	KKRASFPRKS	SKKGPEEGRW	RPFIIRPTPS	PLMKPLLVFV	300
	NPKSGNQQA	KIQSFLWYL	NPRQVFDLSQ	GGPKAEALMY	RKVHNLRLA	CGDGTGVGWI	360
50	LSTLDQLRLK	PPPPVAILPL	GTGNDLARTL	NWGGGYTDEP	VSKILSHVEE	GNVVQLDRWD	420
	LHAEPNPEAG	PEDRDEGATD	RLPLDVFNHY	FSLGFDHVT	LEFHESREAN	PEKFNSRFRN	480
	KMFYAGTAFS	DPLMGSSKDL	AKHRRVVDG	MDLTPKIQDL	KPQCVVFLNI	PRYAGTMPW	540
	GHPGEHDFE	PQRHDDGYLE	VIGFTMTSLA	ALQVGGHGER	LTQCREVVL	TSKAIPVQVD	600
	GEPCKLAAAR	IRIALRNQAT	MVQAKRRSA	APLHSDQQPV	PEQLRIQVSR	VSMHDEYALH	660
55	YDKQQLKEAS	VPLGTVVVPG	DSBLELCRAH	IERLQQEPDG	AGAKSPTCQK	LSPKWCFLDA	720
	TTASRFYRID	RAQEHNLVYT	EIAQDEIYIL	DPELLGASAR	PDLPTPTSPL	PTSPCSPTPR	780
	SLQGDAAFPQ	GBELIEAAKR	NDFCKLQELH	RAGGDLMHRD	EQSRTLHHA	VSTGSKDVVR	840
	YLLDHAPPBI	LDAVEENGET	CLHQAAALGQ	RTICHYIVEA	GASLMKTDQ	GDTPRQRAEK	900
	AQDTLAAAYL	ENRQHYQMIQ	REDQETAV				

Seq ID NO: 173 DNA sequence
Nucleic Acid Accession #: AF232772
Coding sequence: 1-1662

	1	11	21	31	41	51	
65	ATGCCCGTGC	AGCTGACGAC	AGCCCTGCGT	GTGGTGGGCA	CCAGCCTGTT	TGCCCTGGCA	60
	GTGCTGGGTG	GCATCCTGGC	AGCCTATGTG	ACGGGCTACC	AGTTCATCCA	CACGGAAAAG	120
	CACCTACCTGT	CCTTCGGCCT	GTACGGCGCC	ATCCTGGGCC	TGCACCTGCT	CATTACAGAGC	180
70	CTTTTTCGCT	TCCTGGAGCA	CGGGCGCATG	CGAGCTGCCG	GCCAGGCCCT	GAAGCTGCCCC	240
	TCCCCCGCGC	GGGGCTCGGT	GGCACTGTGC	ATTGCCGCAT	ACCAGGAGGA	CCCTGACTAC	300
	TTGCGCAAGT	GCTGCGCTC	GGCCAGCGC	ATCTCCTTCC	CTGACCTCAA	GGTGGTCATG	360
	GTGGTGGATG	GCAACCGCCA	GGAGGACGCC	TACATGCTGG	ACATCTTCCA	CGAGGTGCTG	420
	GGCGGCACCG	AGCAGGCCGG	CTTCTTTGTG	TGGCGCAGCA	ACTTCCATGA	GGCAGGCGAG	480
75	GGTGAGACGG	AGGCCAGCTG	GCAGGAGGGC	ATGACCGGTG	TGCGGGATGT	GGTGCGGGCC	540
	AGCACCTTCT	CGTGATCAT	GCAGAAGTGG	GGAGGCAAGC	GCGAGGTCTA	GTACACGGCC	600
	TTCAAGGCC	TCGGCGATTC	GGTGGACTAC	ATCCAGGTGT	GCGACTCTGA	CACTGTGCTG	660
	GATCCAGCCT	GCACATCTGA	GATGCTTCGA	GTCTGGAGG	AGGATCCCCA	AGTAGGGGGA	720
	GTGCGGGGAG	ATGTCCAGAT	CCTCAACAAG	TACGACTCAT	GGATTTCCTT	CCTGAGCAGC	780
80	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCCTGCC	AGTCTACTTT	TGGCTGTGTG	840
	CAGTGATATTA	GTGGGCCCTT	GGGCATGTAC	CGCAACAGCC	TCCTCCAGCA	GTTCCTGGAG	900
	GACTGGTACC	ATCAGAAGTT	CCTAGGCAGC	AAGTGCAGCT	TGCGGGATGA	CCGGCACCTC	960
	ACCAACCGAG	TCCTGAGCCT	TGGCTACCGA	ACTAAGTATA	CCGCGCGCTC	CAAGTGCCTC	1020
	ACAGAGACCC	CACCTAAGTA	CCTCCGGTGG	CTCAACAGAG	AAACCCGCTG	GAGCAAGTCT	1080
	TACTCCGGG	AGTGCTCTA	CAACTCTCTG	TGGTTCATTA	AGCACCACCT	CTGGATGACC	1140
85	TACGAGTCAG	TGGTCACGGG	TTTCTTCCCC	TTCTTCTCTA	TTGCCACGGT	TATACAGCTT	1200
	TTTACCCGGG	CGGCATCTGG	GAACATTCTC	CTCTTCTCTG	TGACGGTGCA	GCTGGTGGGC	1260
	ATTATCAAGG	CCACCTACGC	CTGCTTCTCT	CGGGGCAATG	CAGAGATGAT	CTTCATGTCC	1320

	CTCTACTCCC	TCCTCTATAT	GTCCAGCCTT	CTGCCGGCCA	AGATCTTTGC	CATTGCTACC	1380
	ATCAACAAAT	CTGGCTGGGG	CACCTCTGGC	CGAAAAACCA	TTGTGGTGAA	CTTCATTGGC	1440
	CTCATTCCCTG	TGTCCATCTG	GGTGGCAGTT	CTCCTGGAGG	GGCTGGCCTA	CACAGCTTAT	1500
5	TGCCAGGACC	TGTTCACTGA	GACAGAGCTA	GCCTTCCTTG	TCTCTGGGGC	TATACTGTAT	1560
	GGCTGCTACT	GGGTGGCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG	1620
	AAGAAGCCGG	AGCAGTACAG	CTTGGCTTTT	GCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	CGGGTAAAGT	GCAATGGGTA	AGGGAGGGAA	GGGGAATGGA	AGAGAAAAGA	CAGGGTGGGA	1740
	GGGAGGAGGG	AGTGCTGTGT	TTTAGTCTCT	TAATGGTCCA	AAGGACAAAT	CTAAAAATGCA	1800
10	AAGAACGGTG	ATGTAGTATG	GCCTGACAGC	TCTGTTTAGA	GGAGGCAACA	CTGATCCCCC	1860
	AGATGCGAGG	CTGCAGGGGA	TTCTGTGTTT	TCAGACTGCC	TGTCTGCTTG	CATCTGCACA	1920
	TAGGCAGTAG	CCTCCTCCTG	GGCTCCAGAG	GGCACTCAGA	AGTTGTGCTA	AACCAAGTTA	1980
	AGTCCCATTC	AGTGGCAACT	TGTGATAGGT	ACCTGAGTGA	CGGCAACCTG	CGGAAGGAGG	2040
	TTCTCCCAGC	CCATCTGAAC	ACAACCAGAG	GTGGCAGGAG	AATTTCTACT	GAGCGAGGTG	2100
	GGCCGGTTAG	TGTATGTCTC	CCCCCCCCCA	CCCATAAGTA	GTCAATCAATG	CAATAAGATT	2160
15	GCCGCTGAGA	TACAAGGCC	AGAAAGCCTGA	TCTTTGGGCA	TCAGAAAACA	GGGTCCAGGA	2220
	ATGGTGCTTT	ATGTGAGATA	CCCCACTCCA	CATCAACATT	CCAGGGATGA	GCCAAACCAG	2280
	CAGGAGGTTA	GCACTGAAGT	GCTTTTAAAA	GTGCACATTA	AAAAGGAAAG	TTTGCCAGGA	2340
	GGAAACAAAGA	GATTGTGGTG	GTGCTAAAGG	AGGCCATAAG	CTACACAGAG	GCCTTGGGTG	2400
20	TTCCACCTGG	AAACTGCTCA	GACGTCTAGA	TGGGTTCTTA	GCTTGTCTGT	GATCTCTGCT	2460
	GGGGAGATAA	AAAGATTAA	CCCCAACATG	TTCAAGAAAG	AAGTGAAGTC	TTGGGTATTT	2520
	TAACCTGTAT	ACTCTTGAAT	TCCTCTCAAA	TTGAGGTAT	CACTGCAGTC	ACCTCTTCTA	2580
	CCCCACTTCA	CTTTCTTCAA	AGCCACATTT	TTTGGGTAT	CACTGCAGTC	ACCTCTTCTA	2640
	CCCTCATCAT	CATAGTAAAG	GTTTCAAGG	TGGCAATTGG	GGCGGAGCCC	CGGCTTCTTA	2700
25	TAGAAGCTTC	AGCAGGAGGC	AAGCGTGTTC	TCAGCACATA	TGGGAACAT	GAGGAGCCTC	2760
	TGATCAAAAT	GGCTACAATC	TTGGAGCTGC	TTGGACGGAT	TCCTTGGCAG	CCGGGTTAGC	2820
	ATGTGTGACT	TTGAGGCTAC	TGTTCTTGAC	AATCATCTCC	AATGGAAGC	TTTTCAGTGT	2880
	TCCCAAAGTG	AACCTCTCAA	TCCAAATGG	TTATCTTTGA	GACCATCCAT	TCTCCTCAGT	2940
	GGCTTCTCCA	GGGAATTTCT	ACAGCCAAGT	TGTGACAGTC	ACTGCATTTG	CCTGCTTCTT	3000
30	TTCCAGAAACC	AAAGTAGGAT	ATGAAACTGG	TTCTCATATC	CTAAGGTCTT	TGCTTTCTCT	3060
	CTCATGCCTC	CTGAGGCTGT	TTTTGGCTGT	TTTCCCTCTG	CTGCTTTTGG	GGAATGAGGG	3120
	GAAGCCATTT	TCCAAGTGAC	TTGCAATCCA	GGCTGTTCTC	AGCGTTTGA	GTTTAAACC	3180
	TGGGATCCTG	ACTAAGCCTT	GACTTAAAGG	GTGCTTGCT	TGCCCTCCAA	ATGTCCTTTC	3240
	TCAAAGGGGC	CAACTAACCC	GTGCAGAAC	AGCACTAAGG	TGGACAGCAG	ACAAGAGGGC	3300
35	AAGCCTCTAA	TGTACCAAGT	GCTTCTTACA	AAGACGCAAG	GTGTGCTCTC	AACCACAGAT	3360
	GGGCAAAACC	TGGTGCTTTC	CTTCATCTCC	CACGAACTCA	AGGGTTTCC	AAGTGTAGCT	3420
	AACAGTTGCC	ACATCACACA	GACCTCCAGT	TTCTGGTAAG	ACTGCTGTT	GACATCAGAC	3480
	CCAACCCATT	GAAGGCTGGA	AGGCAGCAGG	CATTTGTCTA	GGCAGCTGAT	CCAGGCAATC	3540
	GTTCTGCTGG	CCAAGAAAGT	AAACTATTTT	GAGCATTAGA	ATGGAGGAAA	TCCGGTCAGC	3600
40	CAAGTGACAG	GTTTCAAGTT	CGCTAAGGGC	TTGTTTTTCT	TCAGCATTTA	CTTGAAGATT	3660
	AATGTAGGAT	GACAGGCTCT	CCTGGCTGTC	CTACCATCAG	CTCTGCCCTG	CACGTGTGGT	3720
	GTCAACTTTC	CTCAAAATCAA	AAACAGGCAG	GTACAGGTAG	TGGGCTCACA	ACGTTTGACC	3780
	TCGACTGGTT	TTTCTAAGTT	ATTTTGTACA	TTTTTCAGCA	GCAAAACCAA	ACTGGGTCTT	3840
	CAGCTTTATC	CCCGTTTCTT	GCAAGGGGAG	AGCCTTTATA	CAATTGGACG	CATTTTGGTT	3900
45	TTTCTCTATT	WFKHHLWMT	YESVVTGFFP	FFLIATVIQL	FYRGRIRNII	LFLTLVQLVG	3960
	TTTATTTTAA	CCTGCTTTTT	TTTTTTTTTT	TAATTTTCAG	GTCAGTTT	TTATACTGCA	4020
	CTTATTTGTC	AAAATAAAGA	TTCTCACAT				

Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

50	1	11	21	31	41	51	
	MPVQLTALR	VVGTSFLFALA	VLGGILAAVY	TGYQFIHTEK	HYLSFGLYGA	ILGLHLLIQS	60
55	LFAPLEHRRM	RRAGQALKLP	SPRRGSVALC	IAAYQEDPDY	LRKCLRSAQR	ISFPDLKVVM	120
	VVDGNRQEDA	YMLDIFHEVL	GGTEQAGFFV	WRSNFHEAGE	GETEASLQEG	MDRVRDVVRA	180
	STFSIMQKW	GKGREVMYTA	FKALGDSVDY	IQVCDSDTVL	DPACTIEMLR	VLEEDPQVGG	240
	VGGDVQILNK	YDSWISFLSS	VRYWMAFNVE	RACQSYFGCV	QCISGFLGMY	RNSLLQGFLE	300
	DWYHQKPLGS	KCSFGDDRHL	TNRVLSLGYR	TKYTARSKCL	TETPTKYLRW	LNQOTRWSKS	360
60	YFREWLXNSL	WFKHHLWMT	YESVVTGFFP	FFLIATVIQL	FYRGRIRNII	LFLTLVQLVG	420
	IIKATYACFL	RGNAEMIFMS	LYSLLYMSSL	LPAKIFAIAT	INKSGWGTSG	RKTIVVNFIG	480
	LIPVSIWVAV	LLEGLAYTAY	CQDLFSETEL	AFLVSGAIIY	GCYVVALML	YLAIIRRCG	540
	KKPBQYSLAF	AEV					

Seq ID NO: 175 DNA sequence
Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

70	1	11	21	31	41	51	
	CCAGGAGCCC	CAGTTACCGG	GAGAGGCTGT	GTCAAAGGCG	CCATGAGCAA	GATCAGCGAG	60
	GCCGTGAAGC	GCGCCCGCGC	CGCCTTCAGC	TCGGGCAGGA	CCCGTCCGCT	GCAGTTCCGA	120
	TTCCAGCAGC	TGGAGGCGCT	GCAGCGCCTG	ATCCAGGAGC	AGGAGCAGGA	GCTGGTGGGC	180
75	GCGCTGGCCG	CAGACTCTGA	CAAGAAATGAA	TGGAACGSCCT	ACTATGAGGA	GGTGGTGTAC	240
	GTCCTAGAGG	AGATCGAGTA	CATGATCCAG	AAGCTCCCTG	AGTGGGCCCG	GGATGAGCCC	300
	GTGGAGAAGA	CGCCCCAGAC	TCAGCAGGAC	GAGCTCTACA	TCCACTCGGA	GCCACTGGGC	360
	GTGGTCTCTG	TCAATGGCAC	CTGGAACCTAC	CCCTTCAACC	TCACCATCCA	GCCCATGGTG	420
	GGCGCCATCG	CTGCAGGGAA	CGCAGTGGTC	CTCAAGCCCT	CGGAGCTGAG	TGAGAACATG	480
80	GCGAGCCTGC	TGGCTACCAT	CATCCCCCAG	TACCTGGACA	AGGATCTGTA	CCCAGTAATC	540
	AATGGGGGTG	TCCCTGAGAC	CACGGAGCTG	CTCAAGGAGA	GGTTCGACCA	TATCCTGTAC	600
	ACGGGCAGCA	CGGGGGTGGG	GAAGATCATC	ATGACGGCTG	CTGCCAAGCA	CCTGACCCCT	660
	GTACAGCTGG	AGCTGGGAGG	GAAGATGCCC	TGCTACGTGG	ACAAGAACTG	TGACCTGGAC	720
	GTGGCCTGCC	GACGCATCGC	CTGGGGGAAA	TTTATGAACA	GTGGCCAGAC	CTGCGTGGCC	780
85	CCAGACTACA	TCCTCTGTGA	CCCCTCGATC	CAGAAACCAA	TTGTGGAGAA	GCTCAAGAAG	840
	TCATGAAAG	AGTTCTACGG	GGAAGATGCT	AAGAAATCCC	GGGACTATGG	AAGAATCATT	900
	AGTGCCCGGC	ACTTCCAGAG	GGTGATGGGC	CTGATTGAGG	GCCAGAAGGT	GGCTTATGGG	960
	GGCACCCGGG	ATGCCGCCAC	TCGCTACATA	GCCCCACCA	TCCTCACGGA	CGTGGACCCC	1020

5
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CAGTCCCGG	TGATGCAAGA	GGAGATCTTC	GGGCTGTGTC	TGCCCATCGT	GTGCGTGCGC	1080
AGCCTGGAGG	AGGCCATCCA	GTTCATCAAC	CAGCGTGAGA	AGCCCCCTGC	CCTCTACATG	1140
TTCTCCAGCA	ACGACAAGGT	GATTAAGAAG	ATGATTGCAG	AGACATCCAG	TGGTGGGGTG	1200
GCGGCCAACG	ATGTCATCGT	CCACATCACC	TTGCACTCTC	TGCCCTTCGG	GGGCGTGGGG	1260
AACAGCGGCA	TGGGATCCGA	CCATGGCAAG	AAGAGCTTCG	AGACTTTCTC	TCACCGCGC	1320
TCTTGCTCGG	TGAGGCTCTC	GATGAATGAT	GAAGGCTTGA	AGGTCAAGATA	CCCCCGAGC	1380
CCGCCAAGA	TGACCCAGCA	CTGAGGAGGG	GTGCTCCGC	CTGGCCTGGC	CATACTGTGT	1440
CCCATCGGAG	TGCGGACCC	CCTCACTGGC	TCTCCTGGCC	CTGGAGAATC	GCTCCTGCAG	1500
CCCCAGCCCA	GCCCCACTCC	TCTGCTGACC	TGCTGACCTG	TGCACACCCC	ACTCCACAT	1560
GGGCCCAGGC	CTCACCATTG	CAAGTCTCCA	CCCCTTTCTA	GACCAATAAA	GAGACAATA	1620
CAATTTTCTA	ACTCGG					

Seq ID NO: 176 Protein sequence:
Protein Accession #: NP_000682

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1	11	21	31	41	51	
MSKISEAVKR	ARAAPSSGR	RPLQFRFQQL	EALQRLIQEQ	EQELVGALAA	DLHKNEWNAY	60
YEEVVVLEE	IEYMIQKLPE	WAADPEVEKT	PQTQQDELYI	HSEPLGVVLV	IGTWNYPFNL	120
TIQPMVGAIA	AGNAVVLKPS	ELSENMASLL	ATIIPQYLDK	DLYPVINGGV	PETTELLKER	180
FDHILYTGST	GVGKIIMTAA	AKHLTPVTLE	LGGKSPCYVD	KNCCLDVACR	RIANGKFMNS	240
GQTCVAPDYI	LCDPSIQNQI	VEKLKSLKE	FYGEDAKKSR	DYGRISARH	QVRVMGLIEG	300
QKVAYGGTGD	AATRYIAPTI	LTDVDPQSPV	MQEEIFGPVL	PIVCVRSLER	AIQFINQREK	360
PLALYMFSSN	DKVIKIMIAE	TSSGGVAAND	VIVHITLHSL	PFGVGNSGM	GSYHGKKSFE	420
TFSHRRSCLV	RPLMNDGLK	VRYPPSPAKM	TQH			

Seq ID NO: 177 DNA sequence
Nucleic Acid Accession #: NM_001067.1
Coding sequence: 108-4703

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CTGTTTAGTC	GCTTTACAGG	TTCTTGAGCC	CCTTCAAGAC	CGTCACCATG	GAAGTGTGCA	120
CATTGCAGCC	TGTAAATGAA	AATATGCAAG	TCAACAAAAT	AAAGAAAAAT	GAAGATGCTA	180
AGAAAAGACT	GTCTGTGAA	AGAATCTATC	AAAAGAAAAC	ACAATTGGAA	CATATTTTGC	240
TCCGCCAGCA	CACCTACATT	GGTCTGTGG	AATTAGTGAC	CCAGCAAATG	TGGGTTTACG	300
ATGAAGATGT	TGGCATTAAC	TATAGGGAAG	TCACTTTTGT	TCCTGGTTTG	TACAAAATCT	360
TTGATGAGAT	TCTAGTTAAT	GCTGCGGACA	ACAAACAAAG	GGACCCAAAA	ATGTCCTGTA	420
TTAGAGTCAC	AATTGATCCG	GAAAACAATT	TAATTAGTAT	ATGGAATAAT	GGAAAAAGTA	480
TTCTCTGTGT	TGAACACAAA	GTTGAAAAGA	TGTATGTCCC	AGCTCTCATA	TTTGGACAGC	540
TCCTAACTTC	TAGTAACAT	GATGATGATG	AAAAGAAAAG	GACAGGTGGT	CGAAATGGCT	600
ATGGAGCCAA	AATTGTGTAAC	ATATTCAGTA	CCAAATTTAC	TGTGGAACA	GCCAGTAGAG	660
AATCAAGAA	AATGTTCAAA	CAGACATGGA	TGGATAATAT	GGGAAGAGCT	GGTGAGATGG	720
AACTCAAGCC	CTTCAATGGA	GAAGATTATA	CATGTATCAC	CTTTCAGCCT	GATTGTCTA	780
AGTTTAAAT	GCAAGCGCTG	GACAAAGATA	TTGTTGCACT	AATGGTCAGA	AGAGCATATG	840
ATATTGCTGG	ATCCACCAAG	GATGTCAAAG	TCTTTCTTAA	TGGAATAAAA	CTGCCAGTAA	900
AAGGATTTTG	TAGTTATGTT	GACATGTATT	TGAAGGACAA	GTTGGATGAA	ACTGGTAACT	960
CCTTGAAAGT	AATACATGAA	CAGTAAACC	ACAGGTGGGA	AGTGTGTTTA	ACTATGAGTG	1020
AAAAGGCTTC	TGAGCAAAAT	AGCTTTGTCA	ACAGCATTGC	TACATCCAAG	GGTGGCAGAC	1080
ATGTTGATTA	TGTAGCTGAT	CAGATTGTGA	CTAAACTTGT	TGATGTTGTG	AAGAAGAAGA	1140
ACAAGGGTGG	TGTTGCAATG	AAAGCACATC	AGGTGAAAAA	TCACATGTGG	ATTTTGTGTA	1200
ATGCCCTTAAT	TGAAACCCCA	ACCCTTGACT	CTCAGACAAA	AGAAAACATG	ACTTTACAAC	1260
CCAAGAGCTT	TGGATCAACA	TGCCAATTGA	GTGAAAAATT	TATCAAAGCT	GCCATTGGCT	1320
GTGGTATTGT	AGAAAGCATA	CTAAACTGGG	TGAAGTTTAA	GGCCCAAGTC	CAGTTAAACA	1380
AGAAAGTGTCT	CAGCTGTAAA	CATAATAGAA	TCAAGGGAAT	TCCCAAACTC	GATGATGCCA	1440
ATGATGCAGG	GGGCCGAAAC	TCCACTGAGT	GTACGCTTAT	CCTGACTGAG	GGAGATTGAG	1500
CCAAAACCTT	GGCTGTTTCA	GGCCTTGGTG	TGTTTGGGAG	AGACAAATAT	GGGGTTTTCC	1560
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AAGATTCAAT	GAAGACGCTT	CGTTATGGGA	AGATAATGAT	TATGACAGAT	CAGGACCAAG	1740
ATGGTTCCCA	CATCAAGAGC	TTGCTGATTA	ATTTTATCCA	TCACAACCTG	CCCTCTCTTC	1800
TGCGACATCG	TTTTCTGGAG	GAATTTATCA	CTCCCATTTG	AAAGGTATCT	AAAAACAAGC	1860
AAGAAATGGC	ATTTTACAGC	CTTCCGTAAT	TTGAAGAGTG	GAAGAGTTCT	ACTCCAAATC	1920
ATAAAAAATG	GAAAGTCAAA	TATTACAAAG	GTTTGGGCAC	CAGCACATCA	AAGGAAGCTA	1980
AAGAATACTT	TGCAGATATG	AAAAGACATC	GTATCCAGTT	CAAATATTCT	GGTCTGAAG	2040
ATGATGCTGC	TATCAGCCTG	GCCTTTAGCA	AAAAACAGAT	AGATGATCGA	AAGGAATGGT	2100
TAACATAATT	TATGGAGGAT	AGAAGACAAC	GAAAGTTACT	TGGGCTTCCT	GAGGATTACT	2160
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TGTTCTCAAA	TTCTGATAAC	GAGAGATCTA	TCCCTTCTAT	GGTGGATGGT	TTGAAACCAG	2280
GTGAGAGAAA	GGTTTGTGTT	ACTTGCTTCA	AACGGAATGA	CAAGCGAGAA	GTAAGGTTTG	2340
CCCAATTAGC	TGGATCAGTG	GCTGAAATGT	CTTCTTATCA	TCATGGTGAG	ATGTCACTAA	2400
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AGCCCATTTG	TCAGTTTGGT	ACCAGGCTAC	ATGGTGGCAA	GGATTCTGCT	AGTCCAGGAT	2520
ACATCTTTAC	AATGCTCAGC	TCTTTGGCTC	GATTGTTATT	TCCACCAAAA	GATGATCACA	2580
CGTTGAAGTT	TTTATATGAT	GACAAACAGC	GTGTTGAGCC	TGAATGGTAC	ATTCCTATTA	2640
TTCCCATGGT	GCTGATGAAT	GGTGCTGAAG	GAATCGGTAC	TGGGTGGTCC	TGCAAAATCC	2700
CCAACCTTGA	TGTGCGTGAA	ATTGTAAATA	ACATCAGGCG	TTTGATGGAT	GGAGAAGAAC	2760
CTTTGCCAAT	GCTTCCAAGT	TACAAGAACT	TCAAGGGTAC	TATTGAAGAA	CTGGCTCCAA	2820
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CTGTGAAATT	TGTTGTGAAG	ATGACTGAAG	AAAACTGGC	AGAGGCAGAG	AGAGTTGGAC	3060
TACACAAAGT	CTTCAAACTC	CAAAGTAGTC	TCACATGCAA	CTCTATGGTG	CTTTTGGACC	3120
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TCAGACTTAA	ATATTATGGA	TTAAGAAAAG	AATGGCTCCT	AGGAATGCTT	GGTGCTGAAT	3240
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	TTGAAATATA	GCCTAAGAAA	GAATTAATTA	AAGTCTGTAT	TCAGAGGGGA	TATGATTCGG	3360
	ATCCTGTGAA	GGCCTGGAAA	GAAGCCCAGC	AAAAGGTTCC	AGATGAAGAA	GAAAATGAAG	3420
	AGAGTGACAA	CGAAAAGGAA	ACTGAAAAGA	GTGACTCCGT	AACAGATTCT	GGACCAACCT	3480
5	TCAACTATCT	TCTTGATATG	CCCCCTTGGT	ATTTAACCAA	GGAAAAGAAA	GATGAACCTCT	3540
	GCAGGCTAAG	AAATGAAAAA	GAACAAGAGC	TGGACACATT	AAAAAGAAAG	AGTCCATCAG	3600
	ATTTGTGGAA	AGAAGACTTG	GCTACATTTA	TTGAAGAATT	GGAGGCTGTT	GAAGCCCAAG	3660
	AAAAACAAGA	TGAACAAGTC	GGACTTCCTG	GGAAAGGGGG	GAAGGCCAAG	GGGAAAAAAA	3720
	CACAAATGGC	TGAAGTTTTC	CCTTCTCCGC	GTGGTCAAAG	AGTCATTCCA	CGAATAACCA	3780
10	TAGAAATGAA	AGCAGAGGCA	GAAAAGAAAA	ATAAAAGAAA	AATTAAGAAT	GAAAAACTAG	3840
	AAGGAAGCCC	TCAGAAGAT	GGTGTGGAAC	TAGAAGGCCT	AAAACAAGAA	TTAGAAAAGA	3900
	AACAGAAAAG	AGAACCAGGT	ACAAAGACAA	AGAAACAAAC	TACATTGGCA	TTTAAGCCAA	3960
	TCAAAAAAGG	AAAGAAAGAA	AATCCCTGGC	CTGATTGAGA	ATCAGATAGG	AGCAGTGACG	4020
	AAAGTAATTT	TGATGTCCCT	CCACGAGAAA	CAGAGCCACG	GAGAGCAGCA	ACAAAAACAA	4080
15	AATTCACAAT	GGATTGGAT	TCAGATGAAG	ATTTCTCAGA	TTTTGATGAA	AAAACCTGAT	4140
	ATGAAGATTT	TGTCCCATCA	GATGCTAGTC	CACCTAAGAC	CAAACTTCC	CCAAAACTTA	4200
	GTAACAAAGA	ACTGAAACCA	CAGAAAAGTG	TCGTGTCAGA	CCTTGAAGCT	GATGATGTTA	4260
	AGGGCAGTGT	ACCACTGTCT	TCAAGCCCTC	CTGCTACACA	TTTCCAGAT	GAAACTGAAA	4320
	TTACAAACCC	AGTTCTCTAA	AAGAATGTGA	CAGTGAAGAA	GACAGCAGCA	AAAAGTCAGT	4380
20	CTTCCACCTC	CACATCCGGT	GCCAAAAAAA	GGGCTGCCCC	AAAAGGAACT	AAAAGGGATC	4440
	CAGCTTTGAA	TTCTGGTGTG	TCTCAAAAGC	CTGATCCTGC	CAAAACCAAG	AATCGCCGCA	4500
	AAAGGAAGCC	ATCCACTTCT	GATGATTCTG	ACTCTAATTT	TGAGAAAATT	GTTTCGAAAG	4560
	CAGTCAACA	CAAGAAATCC	AAGGGGAGAG	GTGATGACTT	CCATATGGAC	TTTGACTCAG	4620
	CTGTGGCTCC	TCGGGCAGAA	TCTGTACGGG	CAAAGAAACC	TATAAAGTAC	CTGGAAGAGT	4680
25	CAGATGAAGA	TGATCTGTTT	TAAAAATGTA	GGCGATTATT	TTAAGTAATT	ATCTTACCAA	4740
	GCCCAAGACT	GGTTTTAAAG	TTACCTGAAG	CTCTTAACCT	CCTCCCCTCT	GAATTTAGTT	4800
	TGGGGAAGGT	GTCTTTAGTA	CAAGACATCA	AAGTGAAGTA	AAGCCCAAGT	GTTCTTTAGC	4860
	TTTTTATAAT	ACTGTCTAAA	TAGTGACCAT	CTCATGGGCA	TTGTTTTCTT	CTCTGCTTTG	4920
	TCTGTGTTTT	GAGTCTGCTT	TCTTTTGTCT	TAAAAACCTG	ATTTTTAAGT	TCTTCTGAAC	4980
30	TGTAGAAATA	GCTATCTGAT	CACCTCAGCG	TAAAGCAGTG	TGTTTATTAA	CCATCCACTA	5040
	AGCTAAAACT	AGAGCAGTTT	GATTTAAAG	TGCTACTCTT	CCTCCTTTTC	TACTTTCAGT	5100
	AGATATGAGA	TAGAGCATAA	TTATCTGTTT	TATCTTAGTT	TTATACATAA	TTTACCATCA	5160
	GATAGAACTT	GCTATCTCTA	GTACAGATAC	TCTACTACAC	TCAGCCTCTT	ATGTGCCAAG	5220
	TTTTTCTTTA	AGCAATGAGA	AATTGCTCAT	GTTCTTCATC	TTCTCAAATC	ATCAGAGGCC	5280
35	AAAGAAAAAC	ACTTTGGCTG	TGTCTATAAC	TTGACACAGT	CAATAGAATG	AAGAAAAATTA	5340
	GAGTAGTTAT	GCTATCTGAT	CAGCTCTTGA	CCTGTCCCCT	CTGGCTGCCT	CTGAGTCTGA	5400
	ATCTCCCAAA	GAGAGAAACC	AATTTCTAAG	AGGACTGGAT	TGCAGAAGAC	TCGGGGACAA	5460
	CATTTGATCC	AAGATCTTAA	ATGTTATATT	GATAACCATG	CTCAGCAATG	AGCTATTAGA	5520
	TTCAATTTGG	GAAATCTCCA	TAATTTCAAT	TTGTAAACTT	TGTTAAGACC	TGTTCTACAT	5580
40	GTTATATGTG	TGTGACTTGA	GTAATGTTAT	CAACGTTTTT	GTAATATTTT	ACTATGTTTT	5640
	TCTATTAGCT	AAATTCCAAC	AATTTTGTAC	TTTAATAAAA	TGTTCTAAAC	ATTGC	

Seq ID NO: 178 Protein sequence:
Protein Accession #: NP_001058.1

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	MWVYDEDVGI	NYREVTFVPG	LYKIFDEILV	NAADNKQRDP	KMSCIRVTID	PENNLISIWV	120
	NGKGIPVVEH	KVEKMYVPAL	IFGQLLTSSN	YDDDEKKVTG	GRNGYGAQLC	NIFSTKFTVE	180
50	TASREYKKMF	QQTWMDNMGR	AGEMELKPFN	GEDYTCITFQ	PDLKSKFMQS	LKDIDIVALMV	240
	RRAYDIAGST	KDVVKVFLNG	KLPVKGFRSY	VDMYLKDLD	ETGNSLKVIV	EQVNHREWVC	300
	LTMSEKGFQ	ISFVNSIATS	KGGRHVYDVA	DQIVTKLVDV	VKKKNKGVA	VKAHQVKNHM	360
	WIFVNALIEN	PTFDSQTKEN	MTLQPKSFGS	TCQLSEKFIK	AAIGCGIVES	ILNWKFKFAQ	420
55	VQLNKKCSAV	KHNRIKGIPE	LDDANDAGGR	NSTECTLILT	EGDSAKTLAV	SGLGVVGRDK	480
	YGVFPLRGKI	LNVREASHKQ	IMENAEINNI	IKIVGLQYKK	NYEDEDLTKT	LYRGKIMIMT	540
	DQDQDGSHIK	GLLINFIHNN	WPSLLRHRFL	EEFITPIVKV	SKNKQEMAFY	SLPEFEWKS	600
	STPNHKKWKV	KYYKGLGTST	SKEAKEYFAD	MKRHRIFQFY	SGPEDDAAIS	LAFSKKQIDD	660
	RKEWLTNFMF	DRRQRKLLGL	PEDYLYGQTT	TYLTYNDFIN	KELILFSNSD	NERSIPSMVD	720
60	GLKPGQRKVL	GTCFKRNDKR	EVKVAQLAGS	VAEMSSYHNG	EMSLMMTIIN	LAQNPFVGSNN	780
	LNLLQPIGQF	GTRLHGGKDS	ASPRYIFTML	SSLARLLFPP	KDHTLTKFLY	DDNQREVEPW	840
	YIPIIPMLVI	NGAEGIGTGW	SKIPNFDVNR	EIVNNIRRLM	DGEELPMLP	SYKNFKGTIE	900
	ELAPNQYVTS	GEVALNSTT	IEISELPVRT	WTQTYKEQVL	EPMLNGTEKT	PPLITDYREY	960
	HTDITVKFVV	KMTEKLEAE	ERVGLHKVFK	LQSLTLCNSM	VLPDHYGCLK	KYDVTLDILR	1020
65	DPFELRLKYY	GLRKEWLLGM	LGAESAKLNN	QARFILEKID	GKIIIEKNPK	KELIKVLIQR	1080
	GYSDPVPKAW	KEAQQKVPDE	EENESDNEK	ETEKSDSVTD	SGPTFNYLLD	MPLWYLTKEK	1140
	KDELCLRLNE	KEQELDTLKR	KSPDLWKED	LATFIEELEA	VEAKEKQDEQ	VGLPGKGGKA	1200
	KGKKTQMAEV	LSPRGRQRTI	PRITIEKMAE	AEKKNKKKIK	NENTEGSPQE	DGVELEGLKQ	1260
	RLEKKQKREP	GTKTKKQTLI	AFKPIKKGKK	RNPWPDSESD	RSSDESDFDV	PPRETEPRRA	1320
70	ATKTKFTMDL	DSDEDFSDFD	EKTDDDFVFP	SDASPPKTKT	SPKLSNKKEL	PQKSVVSDLE	1380
	ADDVKGSVPL	SSSPATHFPF	DEBITNPVP	KKNVTVKKTA	AKSQSSTSTT	GAKKRAAPKG	1440
	TKRDPALNSG	VSKQPDPAKT	KNRKRKPKST	SDDSDSNFEK	IVSKAVTSKK	SKGESDDPHM	1500
	DFDSAVAPRA	KSVRAKKPIK	YLEESDEDDL	F			

75 Seq ID NO: 179 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

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	CGCGAGGGGG	CCGACAGACC	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
85	TTTGTGTAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420

	AACACATTCA	TTCCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTIT	AAAGCAAGCA	AGATAACTTT	TCAGTGGGGA	540
	AAATGCAATA	TGTCTCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
5	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATAGTCTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
10	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTCTTTTGTG	AAGTTCCTAC	AATGCAACAA	960
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
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	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGAGT	TTTGTACCAG	1200
15	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTG	TCATAAATTT	GCTACCCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACGT	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTATCA	1500
20	AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCCATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTCT	AAATGATGGC	TCTAAACTGT	TTCTTAGATC	TCCACATATG	1800
25	AACCTTGTCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CATCTCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTATCAGG	TTTCAAGAA	TCATAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
30	GTGTGGTTTC	TGAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTCTC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTTCTG	CAGGCCCACT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCCCT	TTCTCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTGCGAGAC	AACCAACCCG	2400
	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
35	ACCCCTTTGT	TCCTTGACAA	CAGATCTCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TCGGCCTTGC	ATGCTACGCC	TGTATTTCCC	AGTGTGATG	TGTCATTGTA	ATCCATCCTG	2580
	TCTTCTCTATG	ATGGTGACCC	TTTGCTTCCA	TTTTCCTCTG	CTTCTTCAG	TAGTGAATTG	2640
	TTTTCGCCATC	TGCTGCAATC	TTCTCAAAAT	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
40	GATAAGGTGC	CCTTGATGTC	TTCTCTGCCA	GTGGCTGGGG	GTGATTTGCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATCTGTA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	CTTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
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Protein Accession #: Eos sequence

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Seq ID NO: 181 DNA sequence
Nucleic Acid Accession #: Eos sequence

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 Protein Accession #: Eos sequence

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Seq ID NO: 183 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4494

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Seq ID NO: 184 Protein sequence:
Protein Accession #: EOS sequence

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Seq ID NO: 185 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

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	TTATAGAGGT	TAGGAATTTCC	AAACTACAGA	AAATGTTTGT	TTTTAGTGTC	AAATTTTATG	4860
	CTGTATTGTT	AGCAATATATC	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCCTGA	4920
85	AATAAAACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
	GAAATAATCT	GTTACTTATT	GTAATACTG	CCCTAGTGTC	TCCATGGACC	AAATTTATAT	5040
	TTATAATTTAT	AGTTTATTAT	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATTG	5100
	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTCTT	GACATTGTAT	5160

TGTGTACCT AAGTCATTAA CTTTGTTCAT GCATGTAATT TTAACITTTG TGGAAAATAG 5220
 AAATACCTTC ATTTTGAAAG AAGTTTTTAT GAGAATAACA CCTTACCAA CATTGTTCAT 5280
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5

Seq ID NO: 186 Protein sequence:
 Protein Accession #: EOS sequence

10 1 11 21 31 41 51
 MVFKASKITF HWGKCNMSSD GSEHSLEGQK FPLEMQIYCF DADRFSSFEE AVKGGKGLRA 60
 LSILFEVGT E NLDPKAID GVESVSRFGK QAALDPFILL NLLPNSTDYK YIYNGSLTSP 120
 PCTDTVDWIV FKDTVSISES QLAVFCEVLT MQQSGYVMLM DYLNQNFREQ QYKFSRQVFS 180
 15 SYTGKEEIH AVCSSEPENV QADPENYTS LVTWERPRV YDTMIEKFAV LYQLDGEDQ 240
 TKHEFLTDGY QDLGAILNNL LPNMSYVLQI VAICTNGLYG KYSDQLIVDM PTDNPELDLF 300
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 NDGSKTVLRS PHMLLSGTAE SLNVTVSITEY EEESLLTSFK LDTGAEDSSG SSPATSAIPF 480
 20 ISENISQGYI FSSNPETIT YDVLIPESAR NASEDSTSSG SEESLKDPSM EGNVWFPSST 540
 DITAQPDVGS GRESFLQTN Y TEIRVDESEK TTKSFSAGPV MSQGPSVTDL EMPHYSTPAY 600
 FPEVTPHAP TPSSRQQLDV STVNVSYSQT TQPVYNEASN SSHESTRIGLA EGLESEKKAV 660
 IPLVIVSALT FICLVVLVGI LIYWRKCFQT AHFYLEDSTS PRVISTPPTP IFPISDDVGA 720
 IPIKHFPKHV ADLHASSGFT EEFETLKEFY QEVQSTVDL GITADSSNHP DNKHKNRYIN 780
 IVAYDHSRVK LAQLAEKDGK LTDYINANYV DGYNRPKAYI AAQGPLKSTA EDFWRMIWEH 840
 25 NVEVIVMVTN QVEGRRKCD QYWPADGSEE YGNFLVTQKS VQVLAYYTVR NFLRNTKIK 900
 KGSQKGRPSG RVVTQYHYTQ WPDGMVPEYS LPVLTFVRKA AYAKRHAVGP VVHCSAGVG 960
 RTGTIYIVLD MLQQLQHEGT VNIFGFLKHI RSQRNYLVQT EEQYVFIHDT LVEAILLSKET 1020
 EVLDSHIHAY VNALIIPGA GKTKLEKQFQ LLSQSNQIQS DYSAAKQCN REKNRTSSII 1080
 30 PVERSRVGIS SLSGEGTDYI NASYIMGYQ SNEFIITQHP LLHTIKDFWR MIWDHNAQLV 1140
 VMIPDQGNMA EDEFVYWNPK DEPINCSEFK VTLMAEEHKC LSNEELKLIQ DFLEATQDD 1200
 YVLEVRHFQC PKWPNPDSPI SKTFELISVI KEEAANRDGP MIVHDEHGGV TAGTFCALTT 1260
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 GAALPDGNIA ESLESIV

35

Seq ID NO: 187 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4632

40 1 11 21 31 41 51
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 45 CAGCTCTCTC GTGTTTCCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
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 AATATCCAA CATGTAATAG CCCAAAAACA TCTCCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420
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 50 GTCAGCGGAG GAGTTTCAGA AATGGTGTTT AAAGCAAGCA AGATAAAGTTT TCACTGGGGA 540
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 GATTTCAAAG CGATTATTGA TGGATTCGAA AGTGTAGTC GTTTTGGGAA GCAGGCTGCT 780
 55 TTAGATCCAT TCATACTGTT GAACCTCTCG CCAAACTCAA CTGACAAGTA TTACATTTAC 840
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 60 TTCTCTAGAC AGGTGTTTTT CTCATACACT GGAAGGAAG AGATTCTGA AGCAGTTTGT 1080
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 65 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAAGT AAGAAATAAT CAAGGAGGAG 1440
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	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AAACAGACAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	3000
5	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTTATGTGCA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	GAAATGTGGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	3120
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCTATT	ATACTGTGAG	GAATTTTACT	3180
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	3240
	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
10	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTC	3360
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	AGAAATATT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	3540
	GCCATACTTA	GTAAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCTA	TGTTAATGCA	3600
15	CTCCTCATT	CTGGACCAGC	AGGCAGGACA	AAGCTAGAGA	AACAATTCCA	GGGTCTCACT	3660
	CTGTCAACCA	GGCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCTCTCCCT	3720
	GGCTTAAGTG	ATCCTCCTAC	CTCAGCCTCC	CGAGTGGCTG	GGACTATACT	CCTGAGCCAG	3780
	TCAAATATAT	ACGAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAAAGAT	3840
	CGAACTTCTT	CTATCATCCC	TGTGGAAGA	TCAAGGGTTG	GCATTTCATC	CCTGAGTGGA	3900
20	GAAGGCACAG	ACTACATCAA	TGCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	3960
	ATCATTACCC	AGCACCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
	CATAATGCC	AAGTGTGGT	TATGATTCTT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAAAATAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTTTATG	4140
25	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAAACTTA	TAATTCAGGA	CTTTATCTTA	4200
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAGTGTCC	TAAATGGCCA	4260
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACCTATAA	GTGTTATAAA	AGAAGAAGCT	4320
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	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	GTGGGCACAA	GGCAGGAAGA	GAATCCATCC	4560
	ACCTCTCTGG	ACAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
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	CTAAATATAG	CGAGGAATGT	CAGTCTAGTT	CTGTTATCTG	TGATTTCCTC	ATCACCTGAC	4740
	AGTAACCTTC	ATGACATAGG	ATTCTGCCGC	CAAAATTATA	TCATTAAACAA	TGTGTGCTTC	4800
35	TTTGAAGAC	TGTAATTTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	4860
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40	TAAACACTC	TTCATATGTA	TATTCACAT	TTTCAACTG	CAGTATTAC	CTAAAGTAGA	5100
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	ATAATTGTAG	ATTTTATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTCTG	TGTAATTGTT	5220
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	AAAAAATAAA	AAAAAATAAA	A				

Seq ID NO: 188 Protein sequence:
Protein Accession #: EOS sequence

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	QSPINIDEDL	TQVNVNLKLL	KFGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
55	FKASKITFW	GKCNMSSDGS	EHSLEGQKFP	LEMQUIYCPDA	DRFSSFEEAV	KGKGLRLALS	180
	ILPEVGTEN	LDPKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFG	DTVSISSESL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHFAV	CSSEPEVQQA	DPENYTSLLV	TWERPRVVDY	TMIEKPAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILLNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPPE	420
60	LIGTEEIIKE	EEEGKDIIEG	AIYNPGRDSA	TNQIRKKEPO	ISTTTHYNRI	GTYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPHT	VEGTSASLND	540
	GSKTVLRSFH	MNLSGTAESL	NTVSIETEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSAQPVMS	QGPSVTDLEM	PHYSTFAYFP	720
65	TEVTPHAFPT	SSRQQLDVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAVIP	780
	LVIVSALTFI	CLVVLVGLIL	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCVTDLGI	TADSSNHPDN	HKKNRYINIV	900
	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPLKSTAE	FWRMIWEHNV	960
	EVIVMITNLV	EKGRKRCDOY	WPADGSEYEG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
70	SQKGRPSGRV	VTQHYHTQWP	DMGVPEYSLP	VLTFFVRKAA	AKRHAVGPVV	VHCSAGVGRT	1080
	GTIYVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	EAILSKETE	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQGL	TLSPRLCEGR	TISAHCNLPL	PGLTDPPTSA	1200
	SRVAGTILLS	QSNIQQSDYS	AALKQCNREK	NRTSSIIPEV	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYYSQNE	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMAGE	FVYWFNKDEP	1320
75	INCESFKVTL	MAEHEKCLSN	EEKLIQDFI	LEATQDDYVL	EVRFQCPKW	PNPDSPISKT	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TPCALITLMH	QLEKENSVDV	YQVARMINLM	1440
	RPGVFADIEQ	YQFLYKILS	LVGTRQENP	STSLDSNGAA	LPDGNIAESL	ESLV	

Seq ID NO: 189 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304..831

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	CGTGTAACA	CACCTACTTAT	CATTGATGCA	TATATAAAAC	CATTTTATTT	TCGCTATTAT	180

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 GTGCCCTCCT GCGGGCGCTC GGTGGAGGGT CTCAGCCGCC GCCTCAAAAG AGCTGTGTCT 420
 5 GAACATCAGC TCCTCCATGA CAAGGGGAAG TCCATCCAAG ATTTACGGCG ACGATTCTTC 480
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 10 AAGACACCTG GGAAGAAAAA GAAAGGCAAG CCCGGGAAAC GCAAGGAGCA GGAAGAGAAA 720
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 ATCTTCATAA TTGCTGGAG AAGTGTATTT CTTCCTCTTA CTCTCACACC TGGGCAAACT 1200
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Seq ID NO: 190 Protein sequence:
 Protein Accession #: NP_002811

1 11 21 31 41 51
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 35 HHLIAEIHIA EIRATSEVSP NSKPSFNTKN HPVRFSGSDE GRYLTQETNK VETYEQPLK 120
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Seq ID NO: 191 DNA sequence
 Nucleic Acid Accession #: XM_059328
 Coding sequence: 52..1023

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 CTATATTAA AAAATAACGT GTGTCTTTC

Seq ID NO: 192 Protein sequence:
 Protein Accession #: XP_059328

1 11 21 31 41 51
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 75 GLHANLSEGR PVGPARRGAS SLLGPEGFFL GKMGFREAVA AGDVDLPQVR EELEAQLSCF 120
 RELLGRAPTH ADGHQHVHVL PGVCQVFAEA LQAVGVRFTR LPLERGVGGC TWLEAPARAF 180
 ACAVERDARA AVGPFSRHGL RWTDAFVGLS TCGRHMSAHR VSGALARVLE GTLAGHTLTA 240
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 SKRPGEVPC EPTLEPFLEP SLL

Seq ID NO: 193 DNA sequence
 Nucleic Acid Accession #: NM_005688.1
 Coding sequence: 126..4439

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	GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	COGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTGTGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
5	TCCTCTTGA	TGCTCTCAT	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
	ACCCAGTGGG	CAATGCTGGG	CTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	ACCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TAGAGAGACT	TGCAGAAGAC	GTGGCAAGAA	GAGCTGAATG	600
10	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCTGTCT	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCTCT	CTCCTGACGG	AAATCGTGCG	GTCTTGGTCG	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGCGGGG	GGCCATCCTA	ACCATGGCAT	900
15	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGCTCCAA	CGATGGGCGA	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTGTGG	ATCAGCTGTT	TTTATCCCTC	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CGGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
20	AGAGTGTTC	AAAATCCCG	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTATAT	GACCTTGGGC	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATTC	CCTTAAGTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
25	AAGCCTCAGT	GGCTGTGTAC	AGATTAAAGA	GTTTGTCTT	AATGGAAGAG	GTTCACATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCCTC	CCACTCTGTT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGCGGTGTCT	GGCAGAGCAG	AAAGGCCACC	TCCTCCTGGA	CAGTGACGAG	CGGCCCACTC	1800
30	CCGAAGAGGA	AGAAGCCAG	CACATCCACC	TGGGCCCACT	CGCCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	TTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACTCTC	GCTTATGTGG	CCAGCAGGCG	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CTGAGGGCCT	GACCTGGCCA	TTCTTCCCAG	CAGCGACCTG	ACGGAGATTG	2160
35	GAGAGCGAGG	AGCCAACTCT	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTT	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACTGGTTTG	ACTGTGATGA	AGTGTCTTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
40	CCATTTTAA	TAACCTGTTG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCAAGTG	TTTCAAGAG	AAGTCACAAG	ACAAGGGTCC	TAAACACGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAGTGCC	CTGGTCAGTA	TATGTTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
45	TCCTGGTTAT	TATGGCCTTG	TATGCTCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACTGGT	2760
	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAAACACC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	CGCAGTCATG	GTGATCCTGA	AAGCCATTCT	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
50	CTATGAAGTT	TTTTGACACG	ACGCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGCGG	CTGCCGTTCC	AGGCCGAGAT	GTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCTCT	GTGGCAGTGG	3180
	GGCCCTCTGT	CATCCTCTTT	TCAGTCTCTC	ACATTTGTCT	CAGGTCCTCT	ATTCCGGAGC	3240
	TGAAGCGTCT	GGACAATATC	AGCAGTCCAC	CTTCTCTCTC	CCACATCACG	TCCAGCATA	3300
55	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
	AGCTGTCTGA	TGACAACCAA	GCTCCTTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCACGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAACGGGGCT	GTCCAGATTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCACTT	3600
60	CGGTGGAGAG	GATCAATATG	TACATTAAGA	CTCTGTCTCT	GGAAAGCACC	GCCAGAATTA	3660
	AGAACAAGGC	TCCCTCCCCT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCAG	3720
	AGATGAGGTA	CCGAGAAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAA	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAAGTCTCG	CTGGGGATGG	3840
	CCCTCTTCCG	TCGTGGTGGG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGGCCAG	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
65	TGTTCAAGTG	CACGTCTAGA	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTGA	AGTGATGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
70	CCATGGACAC	AGAGACAGAC	TTATTGATT	AAGAGACCAT	CCGAGAAGCA	TTTGCAGACT	4260
	GTACCATGTCT	GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGGCCA	GGGACAGTGT	TGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAACGACA	4380
	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCTGCTGC	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGAT	TCTTTTCTTT	AGAGCATTGC	CATTCCCTGC	CTGGGGCGGG	4500
75	CCCTCATGT	CGTCTCTCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	GTTCCGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTTTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAATAAT	AGCACTGTGC	TAAATAACAGT	GCATATTCTT	TTCTATCATT	TTGTACAGT	4860
80	TTGCTGTACT	AGAGATCTCG	TTTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCATTCTT	4920
	CTCTAGCTGG	TGGTTTCACG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCTCTGCCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	AGCATGTCAG	AGCGCCGTGA	GTCTCAGGGT	CTCCTGCCTT	5100
	CTGTCTCTGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTT	5160
85	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTCTTTTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCACTGCC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340

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 GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCACT AGTTGAATGG TCACGCTTGC 5700
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Seq ID NO: 194 Protein sequence:
 Protein Accession #: NP_005679.1

1 11 21 31 41 51
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 VAHKKGELSM EDVWLSKHE SSDVNCRLLE RLWQEEELNEV GPDAASLRV VWIFCRTRI 180
 LSIIVCLMITQ LAGPSGPAFM VKHLLLEYTQA TESNLQYSLL LVGLLLTEI VRSWSLALTW 240
 ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
 PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRRCVAA TDERVQKME 360
 VLTYYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV 420
 HMTLGFDLTA AQAPTUVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMBEVBHMIK 480
 NKPASPHIKI EMKNATLAWD SSHSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA 540
 VLAEQKGHLL LDSDERPSPE EEEGKHILG HLRQLRTLHS IDLEIQEGL VGICGSVSG 600
 KTSLSAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD BERYNSVLNS 660
 CCLRPDLAIL PSSDLTEIGE RANLSSGQR QRLSLARALY SDRSIYILD PLSALDAHVG 720
 NHIFNSAIRK HSKKTIVLTF THQLQYLVD DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
 FNNLLLGTEP PVEINSKKEK SGSQKKSQDK GPKTGSVKKE KAVKPEGQL VQLEEKQGS 840
 VPWSYGVYI QAAGGPLAFL VIMALFMINV GSTAFSTWWL SYWIKQSGN TTVTRGNETS 900
 VSDSMKDNPH MQYVASYIAL SMVMLILKA IRGVVFKGT LRASSRLHDE LFRRLRSPM 960
 KFPDTPPTGR ILNRFSKMD EVDVRLPFA EMFIQNVILV FFCVGMIAV PFWFLVAVGP 1020
 LVILFSLVHI VSRRLWEL RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL 1080
 LDDNQAPFPL FTECARWELV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWQPB GEVTFENAEM 1200
 RYRENLPVLV KKVSTPIFK EKIGIVGRTE SGKSSSLGMA FRLVELSGGC IKIDGVRISD 1260
 IGLADLRSL SIPOPEVLF SGTVRSLNDP FNQYTEDQIW DALERTHMEK CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT 1380
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Seq ID NO: 195 DNA sequence
 Nucleic Acid Accession #: NM_006470
 Coding sequence: 228..1922

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 TGGGCCAAGG GACAGAAGAA AGACAGCCTA GGAGCAGAGC CTCCAGATG GCTGAGTTGG 240
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 CAGACTCTGG GTCACCCAGC CCAGATTCTG GGTGAGCCAG CCCAGTGGAA GAAGAGGACG 360
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 ATAACTCTC GGGCATCCGC AAGTTATCA CGGAATCCAC TGTACACTTA ATCCAGTTGC 1200
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Seq ID NO: 196 Protein sequence:
 Protein Accession #: NP_006461

1 11 21 31 41 51
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 LDLERLKLN ENAISRLQAN QKSVLVSVSE VKAVAEMQFG ELLAAVRKAQ ANVMLFLEEK 240
 EQAALSQANG IKAHLEYRSA EMEKSKQELE RMAAISNTVQ FLSEYCKPKN TEDITFPSVY 300
 VGLKDKLSGI RKVITESTVH LIQLLENYKK KLQEFSEKEE YDIRTQVSAY VQRKYNTSKP 360
 EPSTREQFLQ YAYDITFDPD TAHKYLRLOE ENRKVTNTTP WEHPYPDLPS RFLHWRQVLS 420
 QQSLYLHRY YFEVEIFGAD YVGLTCKGID RKGEERNSCI SGNNFSWSLQ WNGKEPTAWY 480
 SDMETPLKAG PPRRLGVYID PPGGILSPYG VEYDTMTLVH KPACKFSEPV YAAFWLSKKE 540
 NAIRIVDLGE EPEKPAPSLG VTAP

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 Nucleic Acid Accession #: NM_004316
 Coding sequence: 433-1149

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 TTGCTCCAC TCTAAGAAGT CTCCCGGGA TTTGTATAT ATTTTAAAC TTCGTCAGG 300
 GCTCCCGCTT CATATTTCTT TTTCTTTCCC TCTCTGTTCC TGCACCCAAG TTCTCTCTGT 360
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Seq ID NO: 198 Protein sequence:
 Protein Accession #: NP_004307

1 11 21 31 41 51
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 AVARRNERER NRVKLVNLGF ATLREHVPNG AANKKMSKVE TLRSAVEYIR ALQQLLDEHD 180
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Seq ID NO: 199 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1-1005

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 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
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 TTTAAATAGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTCCA GAATGGCATC 360
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 ATGCCATGTA GCTGGTGGGT GGGCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT 1020
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATT AAGGAGGTTG 1080
 ATGCTGATGG GACCATAAAA TATTTTAC ACGAGCCTGA GCGGTTATTC TTGACACTCT 1140
 TAACAGAATT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAATGCA CTGAAAGGGT 1200
 AGTTCAAGTC TAAATCGCA TAACCCCGTT ATTTGTTATT TTTTATTTGC ATTGATTTGC 1260
 CATAAGTCTT CCCTGTCTTG CATCTTCCAA AGCTATTTCG AAATAAACAC GAAATTTTAC 1320
 AGTTTGCC

Seq ID NO: 200 Protein sequence:
 Protein Accession #: NP_008946

1 11 21 31 41 51
 MTENS DKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
 AFYFWKGS DS HIYNVHYTMS INGLQDGS M EIDAGNNLET FKMGS GAE EA IAVNDFQNGI 120
 TGI RPA GGEK CYIKAQVKAR IPEVGAVTKQ SISKLEBKI MPVKYEENSL IWVAVDPQVK 180
 DNSFLSSKVL ELCDGLPIFW LKPTYPKBIQ RERREVRKI VPTTTKRPHS GPRSNPGAGR 240
 LNNETRPSVQ EDSQAFNP DN PYHQEGESM TFDPRLDHEG ICCIECRRSY THCQKICEPL 300
 GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: 201 DNA sequence
 Nucleic Acid Accession #: NM_000728.2
 Coding sequence: 112..495

1 11 21 31 41 51
 GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCACAGC AGGTGTGGTG TTCATCCCGG 60
 GTCGACCGGC CGCTCGCGCT GCCCTGAAAC TCTAGTCGCC AGAGAGGCGG CATGGGTTTC 120
 CGGAAGTTCT CCCCCTTCTT GGCTCTCAGT ATCTTGGTCC TGTACCAGGC GGGCAGCCTC 180
 CAGGCGCGGC CATTCAGGTC TGCCCTGGAG AGCAGCCAGC ACCCGGCCAC ACTCAGTAAA 240
 GAGGACGCGC GCCTCCTGCT GGCTGCACTG GTGCAGGACT ATGTGCAGAT GAAGGCCAGT 300
 GAGCTGAAGC AGGAGCAGGA GACACAGGGC TCCAGCTCCG CTGCCAGAA GAGAGCCTGC 360
 AACACTGCCA CTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG 420
 GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGCAG GCGCCGCAGG 480
 GACCTTCAAG CTGAGCAGA TGAATGACTC CAGGAAGAAG GTGTGTCTTA AATCCAATGA 540
 CATATCCTTA TAAGAGATT CACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC 600
 AAGGAGGCAC AAGCCCAAGGA AGTCTGTGTC TACCAGAAGC CAGAATCACA GAACAGTCTC 660
 TGGAGAAGA GACAGCCCTGC TGACACCTAG AGTTTGGACT TCCAGCTTCC AGAACTGTGA 720
 GAGAATAATT TCTGTGTTT TAAGCCACAA AGTTTGTGGT AATTGTGTTAT GACAGCCCTA 780
 GGAACATAAT ACAATACATT TTCAATTATT TGGGTAAAT GCCTTGGAGT GGGATTGCTG 840
 GGTATTGTTG AAAGTGTGTA TTAACTCTG TAAGAACTG CCAAATATT TTCTGAAGTG 900
 ACTGTACCAC TTGCCTTCTT TGCCAGCCAC ATATGAGAGC TCTAGTATT CCACAAATAG 960
 GTATGTAGCA GTATCTCATT GCTGPTTTAA TTTGTATTTC CCCAATGACT AATGACGTTG 1020
 AGCATCTATT TTACCATATG TTTATCACCT TTATTGAAGG GTCTGTGTTAA ATCTTCTGCT 1080
 AAATTTTGTG TGCTTGTCTT GCTTTATTAG TGTGTAGTTT TTAGAGCTCT TTATATGTTG 1140
 TGGATGCAAG ATTGTTTTCA GATATATAGT TTGGAACCTT CCTTCCCTG AATCTGCGGA 1200
 TTGCTTTTTT ATTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA 1260
 TCCAAATCAT CTTTTTTTTT CTTTATGTA TTGTGCTTTT AGTTCATGTC TAAGAACTCT 1320
 TTGCCTAACT AAGGTCCCAA GGTCACAATA ACCTTATTCT ATACTTTCTT GTAAAAAGTTT 1380
 TATAGTTTTA TATTTTATAT GTAGATTAGT GATCTATTTT GAGTTAATTT TTGTATAAGG 1440
 TGAGAGGTGT AGGTGAAAT TCATACCTGT GAATATAGAT ACCCAATTGT TTCAGTGCCA 1500
 TTTGTTAAAA AGACTGTTAT TTACCATTT AATTGCCCTT GCACCTTTGT CAAAAAGCAA 1560
 CTGATCATAT TTGTGTGGGT ATATTCTGCG GTTCTCAATT CTGTCTCATT GATTGATTG 1620
 ACCATTCTTT TGCCAATGTC ATACTGCCCT GATTAGTGTA GTGTTAAAGT GAATCTCAAA 1680
 CTAATAATATT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT 1800
 TTCTGATGAG ATTTTAATG GGTATGTGTT AAATCAGTGG GTTAATTTTG GGAGAATTAG 1860
 CATATTAATA ATATTAATG GTTCAATTCA TGAACACAAT ACATGTTTTC ACTTATTAG 1920
 GTTTTCTCTG TTTTTTTTTT TTTAACAGTG TTCTCAGTTT TCAACAGAAA TATTCTACAC 1980
 ATATCTTGTT AGATTTTAA CTATTTTATT TTTTGTGCT AATGTAAATG GTACTTAAAC 2040
 ATTTTGTGTT TTAATTGTTT ATTGCTAGTA GATAGAAATA CAATATTTAA AATATTAGGA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 202 Protein sequence:
 Protein Accession #: NP_000719.1

1 11 21 31 41 51
 MGFRKFSFPL ALSILVLYQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM 60
 KASELKQEQE TQSSSSAAQK RACNTATCVT HRLAGLLSRS GGMVKS NFVP TNVGSKAFGR 120
 RRRDLQA

Seq ID NO: 203 DNA sequence
 Nucleic Acid Accession #: NM_001741
 Coding sequence: 71..496

1 11 21 31 41 51
 CTCTGGCTGG ACGCCGCGCC GCGCGCTGCC ACCGCTCTG ATCCAAGCCA CCTCCCGCCA 60
 GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCTG GCTCTCAGCA TCTTGGTCTC 120
 GTTGCAAGCA GGCAGCCTCC ATGCAGCACC ATTCAGTCT GCCCTGGAGA GCAGCCAGC 180
 AGACCCGCCC ACGCTCAGTG AGGACGAAGC GCGCCTCCTG CTGGCTGCAC TGGTGCAGGA 240
 CTATGTGCAG ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT 300

GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCATGCTGG GCACATACAC 360
 GCAGGACTTC AACAAAGTTTC ACACGTTCCC CCAAAGTGA ATTGGGGTTG GAGCACCTGG 420
 AAAGAAAAGG GATATGTCCA GCGACTTGGG GAGAGACCAT CGCCCTCATG TTAGCATGCC 480
 CCAGAAATGC AACTAAATCT CTCCCTTTCC TTCCTAATTT CCCTTCTTGC ATCCTTCTTA 540
 TAACTTGATG CATGTGGTTT GGTTCCTCTC TGGTGGCTCT TTGGGCTGGT ATTGGTGGCT 600
 TTCTTGTGG CAGAGGATGT CTCAAATTC AGATGGGAGG AAAGAGAGCA GGACTCACAG 660
 GTTGAAGAG AATCAGCTGG GAAAATACCA GAAATGAGG GCCGCTTTGA GTCCCCCAGA 720
 GATGTCATCA GAGCTCCTCT GTCTGCTTC TGAATGTGCT GATCATTGTA GGAATAAAAT 780
 TATTTTCCC C

Seq ID NO: 204 Protein sequence:
 Protein Accession #: NP_001732

1 11 21 31 41 51
 | | | | |
 MGQKFSFPL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVQ 60
 MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKFTFTFPQTA IGVGAPGKKR 120
 DMSSDLERDH RPHVSM PQNA N

Seq ID NO: 205 DNA sequence
 Nucleic Acid Accession #: NM_005361
 Coding sequence: 1-945

1 11 21 31 41 51
 | | | | |
 ATGCTCTTGG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGCCTTGA GGCCCGAGGA 60
 GAGGCGCTGG GCCTGGTGGG TGCAGAGGCT CCTGCTACTG AGGAGCAGCA GACCGCTTCT 120
 TCCTTCTCTA CTCTAGTGA AGTTACCTTG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT 180
 CCTCCCCACA GTCTCAGGG AGCCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG 240
 AGACAATCCG ATGAGGGCTC CAGCAACCAA GAAGAGGAGG GGCCAAGAAT GTTCCCGAC 300
 CTGGAGTCCG AGTTCCAAAG AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG 360
 CTCTCAAGT ATCGAGCCAG GGAGCCGGTC ACAAAGGCAG AATGCTGGA GAGTGTCTCT 420
 AGAAATTGCC AGGACTTCTT TCCCGTGATC TTCAGCAAAG CCTCCGAGTA CTTCAGCTG 480
 GTCTTTGGCA TCGAGGTGGT GGAAAGTGTC CCCATCAGCC ACTTGTACAT CCTTGTCAAC 540
 TGCTGGGCC TCTCTACGA TGGCTGTCTG GGCAGCAATC AGGTCTATGCC CAAGACAGGC 600
 CTCTCTGATA TCGTCTGTC CATAATCGCA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA 660
 ATCTGGGAGG AGCTGAGTAT GTTGGAGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCGCA 720
 CATCCAGGA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCCGAG 780
 GTGCCCGGCA GTGATCTGTC ATGCTACGAG TTCCTGTGGG GTCCAAGGC CCTCATTGAA 840
 ACCAGCTATG TGAAGTCTCT GCACCATACA CTAAAGATCG GTGGAGAACC TCACATTTC 900
 TACCCACCCC TGCATGAACG GGCTTTGAGA GAGGGAGAAG AGTGA

Seq ID NO: 206 Protein sequence:
 Protein Accession #: NP_005352

1 11 21 31 41 51
 | | | | |
 MPLEQRSQHC KPEEGLEARG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS 60
 PPHSPQGASS PSTTINYTLW RQSDGSSNQ EEEGRPMFPD LESEFQAIS RKMVELVHFL 120
 LLKYRAREPV TKAEMLESLV RNCQDFFPVI FSKASEYLQL VFGIEVVEVV PISHLYILVT 180
 CLGLSYDGLL GDNQVMPKTG LLIIVLAIIA IEGDCAPEEK IWEELSMLEV FEGREDSVFA 240
 HPRKLLMQDL VQENYLEYRQ VPGSDPACYE FLWGPRLIE TSYVKVLHHT LKIGGEPHIS 300
 YPPLHERALR EGEE

Seq ID NO: 207 DNA sequence
 Nucleic Acid Accession #: NM_021115
 Coding sequence: 743-2893

1 11 21 31 41 51
 | | | | |
 AAAGGAAGGG AGGGAGGGAG AAAGGAGAAG TTGGTTTAGA GGCCAGCCGG ACGAGCTTTG 60
 GGACACGCCC TTAGGAGGGC CACCCTCAGA GTCTGACAGC AGGTGAAGGT CCTAAATCTC 120
 CCCAACTAA CTGGTGTCTT TTCTCCTCTT CCAAGATGCT CTTCCCGAGG GAGATGCTAG 180
 CCCTTTGGGT CCTTACCTCC TGCCCTCAGG AGCCCGGAG AGAGGCAGTC CTGGCAAAGA 240
 GCACCTGAA GAGAGAGTGG TAACAGCGCC CCCCAATTCC TCACAGTCGG CGGAAGTGCT 300
 GGGCGAGCTG GTGCTGGATG GGACCGCACC CTCTGCACAT CACGACATCC CAGCCCTGTC 360
 ACCGCTGCTT CCAGAGGAGG CCGGCCCAA GCACGCCCTTG CCCCCAAGA AGAAACTGCC 420
 TTCGCTCAAG CAGGTGAAC TCGCCAGGAA GCAGCTGAGG CCCAAGGCCA CCTCCGAGC 480
 CACTGTCCAA AGGGCAGGGT CCCAGCCAGC GTCCAGGGC CTAGATCTCC TCTCTCTCTC 540
 CACGGAGAAG CTGGGCCAC CGGGGGACCC GGACCCCATC GTGGCCTCCG AGGAGGCATC 600
 AGAAGTGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCCTG CCTACAACAC CCGCACCCCT 660
 GCAAATCTCC CCCTTCACTT CGCAGCCCTA TGTGGCCAC AACTTCCCC AGAGGCCAGA 720
 ACCCGGGGAG ACCCTGCTCA ACATGGCCCA GGAGGCCCCC CAGGAGGACA CCAGCCCAT 780
 GGCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAGG AGAGCCAGGA 840
 GACCACTACC TCCACCATTA TCACCAACAC GGTTCATCACC ACCGAGCAGG CACCAGCTCT 900
 GTGCACTGTG AGCTTCTCCA ATCCTGAGGG GTACATTGAC TCCAGCGACT ACCCACTGCT 960
 GCCCTCAAC AACTTCTCG AGTGACATA CAACGTGACA GTCTACACTG GCTATGGGGT 1020
 GGAGCTCCAG GTGAAGAGTG TGAACCTGTC CGATGGGGAA CTGCTCTCCA TCCGCGGGGT 1080
 GGACGGCCCT ACCCTGACCG TCGTGGCCAA CCAGACACTC CTGGTGGAGG GGCAGGTAAT 1140
 CCGAAGCCCC ACCAACACCA TCTCGTCTA CTTCCGAGC TTCCAGGACG ACGGCCTTGG 1200
 GACCTTCCAG CTTCACTACC AGGCCCTTCAT GCTGAGCTGC AACTTCCCC GCCGCGCTGA 1260
 CTCTGGGGAT GTCACTGCTA TGGACCTGCA CTCAGGTGGG GTGGCCCACT TTCACTGCCA 1320
 CCTGGGCTAT GAGCTCCAGG GCGCTAAGAT GCTGACATGC ATCAATGCCT CCAAGCCGCA 1380
 CTGGAGCAGC CAGGAGCCCA TCTGCTCAGC TCCTTGTGGA GGGCAGTGC ACAATGCCAC 1440
 CATGGGCCGC GTCTCTCCC CAAGTTACCC TGAACACCA AATGGGAGC AATTCTGCAT 1500
 CTGGACGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GGCTGTTGCT 1560

5
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15
20
25

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GCATGACAAAG GACAGGATGA CGGTTCCAGC CGGGCAGACC AACAAAGTCAG CTCCTCTCTTA 1620
CGACTCCCTT CAAACCGAGA GTGTCCCTTT TGAGGGCCTG CTGAGCGAAG GCAACACCAT 1680
CCGCATCGAG TTCACGTCCG ACCAGGCCCG GCGGGCCTCC ACCTTCAACA TCCGATTGTA 1740
AGCGTTTGAG AAAGGCCACT GCTATGAGCC CTACATCCAG AATGGGAAGT TCACTACATC 1800
CGACCCGACC TATAACATTG GCACTATAGT GGAGTTCACC TGCGACCCCG GCCACTCCCT 1860
GGAGCAGGGC CCGGCCATCA TCGAATGCAT CAATGTGCGG GACCCATACT GGAATGACAC 1920
AGAGCCCTG TGACAGAGCCA TGTGTGGTGG GGAGCTCTCT GCTGTGGCTG GGGTGGTATT 1980
GTCCCCAAAC TGGCCCGAGC CTACGTGGA AGGTGAAGAT TGTATCTGGA AGATCCACGT 2040
GGGAGAAGAG AAACGGATCT TCTTAGATAT CCAGTTCCTG AATCTGAGCA ACAGTGACAT 2100
CTTGACCATC TACGATGGCG ACGAGGTCAT GCCCCACATC TTGGGGCAGT ACCTTGGGAA 2160
CAGTGGCCCC CAGAAACTGT ACTCCTCCAC GCCAGACTTA ACCATCCAGT TCCATTGGGA 2220
CCCTGCTGGC CTCATCTTTG GAAAGGCCCA GGGATTATC ATGAACTACA TAGAGGTATC 2280
AAGGAATGAC TCCTGCTCGG ATTTACCCGA GATCCAGAAT GGCTGGAATA CCCTTCTCA 2340
CACGGAGTTG GTGCGGGGAG CCAGAATCAC CTACCAAGT GACCCCGGCT ATGACATCGT 2400
GGGGAGTGAC ACCCTCACCT GCCAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTTTG 2460
TGAGAAAATT ATGTACTGCA CCGACCCCGG AGAGGTGGAT CACTCGACCC GCTTAATTTC 2520
GGATCCTGTG CTGCTGGTGG GGACCAACAT CCAATACACC TGCAACCCCG GTTTTGTGCT 2580
TGAAGGGAGT TCTCTTCTGA CTGTCTACAG CCGTGAACA GGGACTCCCA TCTGGACGTC 2640
TCGCCTGCC CACTGGCTTT CAGAAGCGGC AGCAGAGACG TCGCTGGAAG GGGGGAACAT 2700
GGCCTGGCT ATCTTCATCC CGGTCTCAT CATCTCCTTA CTGCTGGGAG GAGCCTACAT 2760
TTACATCACA AGATGTGCT ACTATTCCAA CCTCCGCTG CCTCTGATGT ACTCCACCC 2820
CTACAGCCAG ATCAGCTGG AAACCGAGT TGACAACCCC ATTTACGAGA CAGGGGGAAC 2880
CCAAAAGGTT TAGGGTTTCA TTTAAAAGA GGTACCCTTT AAAAAGGGGC TTGTGAATC 2940
AACCCTAATT TCCCCGAGAC ATTTATCCAA AGGCCTGGG GGCCTTGATT TAAACCCCA 3000
AAAGGCGGCT GTTTTGTGGT TAAACTTTT AACAAAGGT TACGGGTTT TTCCCGGAT 3060
TTTATAAATT TTTAAAGTG

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Seq ID NO: 208 Protein sequence:
Protein Accession #: NP_066938

30
35
40
45

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1 11 21 31 41 51
| | | | |
MAQEAPQEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN 60
PEGYIDSSDY PLLPLNNFLE CTYNVTVYTG YGVELQVKS V NLSGDELISI RGVGDGPTLV 120
LANQTLLVEG QVIRSPNTI SVYFRFTQDD GLGTFQLHYQ AFMLSCNFPR RPDSGDVTVM 180
DLHSGGVAHF HCHLGYELQG AKMLTCLINAS KPHWSSQEPI CSAPCGGAVH NATIGRVLSP 240
SYPTNTGSG FCIWTIEAPE GQKLHLHFER LLLHDKDRMT VHSQGTNKA LLYDSLQTES 300
VPFEGLLSEG NTRIEFTSD QARAASTFNI RFEAFKQHC YEPYIQNGNF TTSPTYNIG 360
TIVEFTCDPG HSLSEQPAII ECINVRDPYV NDTEPLCRM CCGELSAVAG VVLSNPWPEP 420
YVEGEDCIWK IHVGEERKIF LDIQFLNLSN SDILTIYDGD EVMPHILQY LGNSGPKLY 480
SSTPDLTIQF HSDPAGLIFG KGGGFIIMYI EVSRNDSGSD LPEIQNGWKT TSHTELVRGA 540
RITYQCDPGY DIVGSDTLTC QWDLWSWSDP PFCEKIMYCT DPGEVDHSTR LISDPVLLVG 600
TTIQTCTNPG FVLEGGSLLT CYSRETGTPI WTSRLPHCVS EAAAETSLEG GNMALAIPIP 660
VLIISLLGG AYIYITRCRY YSNLRPLMY SHPYSQITVE TEFDNPIYET GGTQKV

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Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89-631

50
55
60
65

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1 11 21 31 41 51
| | | | |
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GGCAGAGGCT CCGAGGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTCT 120
CAGCGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCCT GATGGCCAG GGGCAATGC 180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCAGGGCG CAGGGGCAGC 240
AAGGCGCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCG CATGGCGGCG CGGCTTCAGG 300
GCTGAATGGA TGTGTCAGAT GCGGGGCCAG GGGGCCGAG AGCCGCTGC TTGAGTTCTA 360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
GGATGCCCCA CCCTTTCGCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGTG TGTCGGGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACGCCCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTTCCT TGTGATGTG GATCAGCGAG TGCTTCTGTC CCGTGTTTT 600
GGCTCAGCCT CCCTCAGGGC AGAGCGGCTA AGCCAGCCT GGCGCCCTT CCTAGGTCAT 660
GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGCCAG TTCATTGTGG GGCCTGATT 720
GTTTGTGCTG GGAGGAGGAC GGCTTACATG TTTGTTCTG TAGAAAATAA AACTGAGCTA

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Seq ID NO: 210 Protein sequence:
Protein Accession #: NP_001318.1

70
75

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1 11 21 31 41 51
| | | | |
MQAEGRTGG STGDADPGG PGIPDGPNGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEALARRSLA QDAPPLPVPG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQQLSLLM WITQCFLPVF LAQPPSGQRR

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Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52-459

80
85

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1 11 21 31 41 51
| | | | |
CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
GAAGGCCAGG GCACAGGGGG TTGACGGGCG GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCCCGGGGGT 240
CCGCATGGCG GTGCCCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGC CAGGAGGCCG 300

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GACAGCGGCC TGCCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
 ATCAGCTCCT GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC 420
 GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCCTTC 480
 TAGGTCATGC TCCTCCCTC AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTTGTGGG 540
 GCTGATGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAAATAAG 600
 CTGAGCTA

Seq ID NO: 212 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
 PRGFPHGGAAS AQDGRCPGCA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 FLPVFLAQAP SGQRR

Seq ID NO: 213 DNA sequence
 Nucleic Acid Accession #: NM_000555
 Coding sequence: 416..1498

1 11 21 31 41 51
 CTTATTTTTT ATGAATGTGC GATAGCTGCA CCAGCTTGGT GGGGAAAGGG TTTGATGAAT 60
 AGCACAAAGA CACTGGCTGT TCCTGGAGG CTGTCCCTTT AAAGGAGAAT CTTAGTTTAT 120
 TCTGGGGGGA GGGGATGCAC ACATTAGAGT AGGAAAGAGG GCTTGAATA AAATGAAAC 180
 ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCTAAGC TGGAGATGCT 240
 AACCTTGGGT AGCTCCTTCT GTTCTCTTCA AGGGGAATTT TGTCAAGCTA TGGATTCATT 300
 TACAACGTGT AGTCATGTGG GCATGTGTGA GGAAACAGAT GCCAGTTTAT ATGTATTAG 360
 CCGGAAGTTC CAATTTGATA GGAGCCACTG TCAGTCTCTG AGGTTCACCC AAAATATGGA 420
 ACTTGATTTT GGACACTTTG ACGAAAGAGA TAAGACATCC AGGAACATGC GAGGCTCCCG 480
 GATGAATGGG TTGCCCTAGCC CCACTCACAG CGCCCACTGT AGCTTCTACC GAACAGAAC 540
 CTTGCAGGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
 CCCTACTTTC AAGGGGATGG TGTACGCTGT GTCCCTGAC CGTTCCTGCA GCTTTGACGC 660
 TTTGCTGGCT GACCTGACGC GATCTCTGTC TGACAAACATC AACCTGCCTC AGGGAGTGCG 720
 TTACATTTAC ACCATTGATG GATCCAGGAA GATCGGAAGC ATGGATGAAC TGGAGGAAGG 780
 GGAAGAGTAT GTCTGTCTCT CAGACAACTT CTTTAAAGAG GTGGAGTACA CCAAGAAATGT 840
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 GACAGCCCACT TCTTTTGAGC AAGTCTCTAC TGATATCACA GAAGCCATCA AACTGGAGAC 1080
 CGGGGTTGTG AAAAATCTCT ACACCTGGA TGGAAACAG GTAACCTGTG TCCATGATTT 1140
 CTTTGGTGAT GATGATGTGT TTATTGCCTG TGGTCTGAA AAATTTGCTC ATGCTCAGGA 1200
 TGATTTTCT CTGGATGAAA ATGAATGCCG AGTCATGAAG GGAACCCATC CAGCCACAGC 1260
 TGGCCCAAGG GCATCCCAAC CACCTCAGAA GACTTCAGCC AAGAGCCCTG GTCCTATGCG 1320
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 CAAGTCTAAG CAGTCTCCCA TCTCTACGCC CACCAGTCTC GGCAGCCTCC GGAAGCACA 1440
 GGACCTGTAT CTGCCCTGTG CTTGGATGTA CTCGGACTCG CTTGGTGATT CCATGTAAAG 1500
 GAGGGGAGAG TGCTCAGAGT CCAGAGTACA AATCCAAGCC TATCATGTGA GTAGGGTACT 1560
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 TATTTTGAAA AACACATTGT AATATGTTGG GTTTATTTTC CTGTGATTTT TCCTCTGGGC 1680
 CACTGATCCA CAGTTACCAA TTATGAGAGA TAGATTGATA ACCATCCTTT GGGGCAGCAT 1740
 TCCAGGGATG CAAATGTGTC TAGTCCATGA CCTTCAATG GAAAGCTTAG GGGCCTGGG 1800
 TAAATTTGCC CCGTTTAAAT TTGCCCAAAC AGTTTTCCTT TTGTAGAGGG GTGTTTAAAT 1860
 ATACAGCAAT TAAAGATTTT GTGTGGGGAA AAAAAAACT CATTGGCAGA TCCAAGAAATG 1920
 ACAACACAAA GTGCCCTTT TCTCTGGATC TCAAGAAATG TGGAGGACCC TGAAGGACA 1980
 GCAAGGCAGC TCCCCCTGCT CACTCTTAC TCTGATTGA GGCCCGGTTT TGTGTGCCAG 2040
 CACCAATTTCT GGCTGTCAAT GGGGAGAAAT AAACCAACAA CTTATAATTG TGACACCAGA 2100
 TGCTTAGGAT CCTGGTGCTG GGTTAGCTAA GAGAAATAGAC AGAATTGGAA AATACTGCAG 2160
 ACATTTCCGA AGAGTTTATA AAGCACAGTG AATTCTGGT CAATCTCTCC ACTGAGGCAA 2220
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 TCTAGAAGGC TGTCTAACAT ACCACATGAT TACATGAAC GTATGGTATC CATCTATCTC 2340
 TGTTCTATTG AATGGCTTGT TAACAGCCAA CACTGAAAC ACTGTGAGAA TTTGTTTCA 2400
 GGTCCTGACAC CTTTCACTCT CTTTATATAG CAAGAAATCA ATATCCTTTT TATAAAAAAT 2460
 CATGTCTGTA TTTCAAGAGC AAACCTCTCA GGCTCCTTTT TTATAAACTG GTGATTTTTC 2520
 TTTTGTCTAA AAAACACATG AAGAAAATTT ACCAGAAAAA AAAAAAAAG CCGAAGAAAT 2580
 ATGTTATTTA GAAATATGTC TGTCACTGCC AAACAGTAAC CTCAGGAGA AAACAAGATG 2640
 AATAGCAGAG GCCAATTCAT TAGAATCAGT TTTTGTATAG CTTTTTAACT GTTATGCTTG 2700
 CATTAATAAT TTCAATGTGG ACCAGACATT CTAATTATAT TTTAAATGAA ATGTTACAGC 2760
 ATATTTTAAG CAACTCTTTT TATCTATAAT CCTAATATT CATACTGAAG ACACAGAAAT 2820
 CTTTCACTTG TCTTTAATAT TAGAAAGGAT TTCTCTTAC TAAGGACTGA TCATTGAAA 2880
 TAGTTTTTTC TCTTTTGAAG TACAGTTTGA TAACACTGCT TTTTTCCTCC TGTAAACATA 2940
 GCCCATAAAT GCAAAAACAA CTAATTTTAA TTGAAGGTCT TGCTTGCCAN TCCTGTGTTG 3000
 GCTTTNACCA AATATAAAAA TTCCCTTATT CCTTGGTAAT GGTGCAAAAT TTTGAAAAGG 3060
 CACAGCATCC AAACCATGCT GCTGTTTGGC TACTGAATGG CTGTGAGTTG TTTCTCCACT 3120
 CTAAATGGAA TAGCTTGCT GTGTGTGTGT GTGGTGGTGG TGGGAGGGGG TGGTGCAATG 3180
 GTGTGTGTGT GTGTGCATCT GCAGCTGCTT CAAAATTAAG AAATACTACA AGACACCCCT 3240
 GTAATGGATT GTGGGCAACT GCTGATGTGC ACTGTGTAGG GGGGAACCCA 3300
 GTGGTGGTGG GGTATCTCAA ATGCCCTAG ACAAGCTTCA GATGTCTGTA GCTACCAAAA 3360
 ACATTTTCGG TTCAAGAAAA GTGAGATGAT GGTAGTACTG GTTTCCTGGT AAATGAAAA 3420
 ACCCAAAATG ATGAGGACTC CTTTTCCTTT TTTTGTAAAC CCATTCAAAA 3480
 CCATTAATAA GCCCAATTTA CTAANCCCTT ATTTCTTTCT AGAAGCTCAG GGTTCNCTTA 3540
 GTGCCCTCCA NAACATTTTG TAGTTAATTT GGAAGAAAGT ATACTTGGAT TAGGGGGTGT 3600
 GGGCATAAAG AATGGTGGGA GGCCTGATT TAAATTCAG GCCAGAACCC CCAATGACTC 3660
 CACCCATAGT NTCACTTTAG GTCTCATTTA GTCCATCACC TTTATTTTAA GTTGAGGAAG 3720
 TGGAGGCTGG TAAGAGCAGC GACCAGAGGA AGAATCCAGA TTTCTTATG CTTGGGCCTC 3780
 ACCTAGCTC TINTGATATT TCGTATATGT ACTACTAGAA AATACCAAT 3840
 GGATATATTT TCTTTAGGAT AACCTTTGAA CCAACAATNT TCAATAACAA TAGTACATCT 3900

272

CAGACCCCTT TCATCTCCTG TGCTGTAAAC ACCCTCTCTC CCCCACCCCC TCCGCAATTC 9180
 AATGAGGGCT TTCTTGGGTC AGAGGACTTC AAGGTGTCT AGAGAAGTTT GCCATGTGTG 9240
 TAAGGTGCTG TGAACCTGTGA GTGCTGAAGA TTCGAGCAT TCAATACCAG GCAGCCAAAG 9300
 AGCTGCTCTT GCAATTATT TGGCTCTCAA GCTCTGTTCT TCATCGCATT CTCATTTCTG 9360
 TGTACATTTG CAAGATGTGT GTAATGTCAT TTTCCAAAA TAAATTTGA TTTCAAT

Seq ID NO: 214 Protein sequence:
 Protein Accession #: NP_000546

1 11 21 31 41 51
 MELDFGHFDE RDKTSRNMRG SRMNGLPSP T HSAHCSFYRT RTLQALSNEK KAKKVRFYRN 60
 GDRYFKGIVY AVSSDRFRSF DALLADLTRS LSDNINLPQG VRYIYTTIDGS RKIGSMDELE 120
 EGESYVCSSD NFFKKEVEYTK NVNPNWSVNV KTSANMKAPQ SLASSNSAQA RENKDFVRPK 180
 LVTIIRSGVK PRKAVRVLN KKTAFSFEQV LTDITEAIKL ETGVVKKLYT LDGKQVTCLEH 240
 DFFGDDVFI ACQPEKFRYA QDDFSLDENE CRVMKGNPSA TAGPKASPTP QKTSKSPGP 300
 MRRSKSPADS AMGTSSSQLS TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DSDSLGDSM

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_130467
 Coding sequence: 312..644

1 11 21 31 41 51
 GGCACGAGGC AGAGCTCTGC AAGGAGAGGT TGTGTCTTCG TTCCTTCCGC CATCTTCGTT 60
 CTTTCCAACA TCTTCGTCTT TTCTCACTGA CCGAGACTCA GCCGGTAGGT CTGCAGAGTG 120
 GTCTTCCTGG TAATTAGTGT GTGAGTGAAT GTGTGGAGGA GCCAGCGGGC TTAGGACAGG 180
 TCTCTGGCA CAGTCCGTGG CTTTGAGGGA AAAGGGCCTC GCGGTGGTCC TCCGCTTCC 240
 CCCAGGTCGT GATGCAGGCG CCATGGGCGG GTAATCGTGG CTGGGCTGGA ACGAGGGAGG 300
 AAGTGAGAGA TATGAGTGAG CATGTAACAA GATCCCAATC CTCAGAAAGA GGAAATGACC 360
 AAGAGTCTTC CCAGCCAGT GGACCTGTGA TTGTCCAGCA GCCCACTGAG GAAAAACGTC 420
 AAGAAGAGGA ACCACCAACT GATAATCAGG GTATTGCACC TAGTGGGGAG ATCAAAAATG 480
 AAGGAGCACC TGCTGTTCAA GGGACTGATG TGAAGCTTT TCAACAGGAA CTGGCTCTGC 540
 TTAAGATAGA GGATGCACCT GGAGATGGTC CTGATGTCAG GGAGGGGACT CTGCCACTT 600
 TTGATCCAC TAAAGTGCTG GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA 660
 ATGAAGACTG AAACCAAGAA TATTGTTCTT ATGCTGGAAA TTTGACTGCT AACATTCTCT 720
 TAATAAAGTT TTACAGTTT CTGCAAAAAA AAAAAAAAAA AAA

Seq ID NO: 216 Protein sequence:
 Protein Accession #: NP_569734

1 11 21 31 41 51
 MSEHVTRSQS SERGNDQESS QPVGPFVIVQQ PTEEKQEEE PPTDNQGIAP SGEIKNEGAP 60
 AVQGTDEVEF QQELALLKIE DAPGDPDVR EGTLPFTDPT KVLEAGEGQL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: NM_001476.1
 Coding sequence: 82..435

1 11 21 31 41 51
 GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT TTCCTCTAC 60
 TGAGATTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCCTAGA 120
 CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCTTA TGCGGCCCGA GCAGTTCAGT 180
 GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACACG CAAGTCAACG TCAGGATCCT 240
 GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
 GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGAT 360
 GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAAG 420
 CAATCACAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCCTA TGTGGAAAT 480
 TTGTTCAATTA AAATTCTCCC AATAAAGCTT TACAGCCTTC TGCAAAA

Seq ID NO: 218 Protein sequence:
 Protein Accession #: NP_001467.1

1 11 21 31 41 51
 MSWRGRSTY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATOR QDPAAAQEGE 60
 DEGASAGQGP KPEADSQEQG HPQTGCECED GPDGQEVDP NPEEVKTPBE GEKQSQC

Seq ID NO: 219 DNA sequence
 Nucleic Acid Accession #: NM_001476
 Coding sequence: 90-3671

1 11 21 31 41 51
 ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCGG GGCAGCGACC CTGCAGCGG 60
 AGACAGAGAC TGAGCGGCCC GGCACCGCCA TGCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
 GCTTCTCGCT CTCTCTGCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAACT GGTAATGGAT 240
 TCCGCTCGCT CAAGTGAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG 300
 GCTTTTACC GCACAGAGAA AGGGACCGCT GTTGGCCCTG CAATTGTAAC TCCAAAGGTT 360

	CTCTTAGTGC	TCGATGTGAC	AACTCTGGAC	GGTGCAGCTG	TAAACCAGGT	GTGACAGGAG	420
	CCGATGCGGA	CCGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAAG	480
	ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540
5	ACGCGGGCCG	CTGTGTCTGC	AAGCCAGCTG	TTACTGGAGA	ACGCTGTGAT	AGGTGTGAT	600
	CAGGTTACTA	TAATCTGGAT	GGGGGAACC	CTGAGGGCTG	TACCCAGTGT	TTCTGTCTATG	660
	GGCATTACAG	CAGCTGCCGC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
	TTCATCAAGA	TGTTGATGGC	TGGAAGGCTG	TCCAACGAAA	TGGGTCTCCT	GCAAAGCTCC	780
	AATGGTCACA	GCGCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840
10	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCTC	900
	TTGACTACCG	TGTGGACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
	GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
	TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140
15	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAAATGTGAC	CCTGATTCCA	GCCCCCCTG	1200
	TCTCTGGAGC	CCCAGCACCC	TGGGTTGAAC	AGTGTATATG	TCCTGTTGGG	TACAAAGGGC	1260
	AATTCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTG	AGCGAGACTG	GGGCCCTTTG	1320
	GCACTGTAT	TCCTTGTAA	TGTCAAGGGG	GAGGGGCTG	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTACAG	GGATGAGAA	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
20	ACGATCCGCA	CGACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAAGGGG	TTGAGCTGCT	1500
	CAGTGATGCC	GGAGATCGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTCACCGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTGTGTGAA	CATGGCCCG	1620
	TGAGGCCTTG	TCAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
	GTGACCGGCT	GACAGGCTAG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTGCG	1740
25	ACCAGTGCAA	AGCAGGCTAC	TTCCGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTC	1800
	GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTGCAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTC	AGCTGTCCAG	1920
	CTTGCTATAA	TCAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
	AGGCCCTGAT	TTCAAAGGCT	CAGGTTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
30	GCAGGATGCA	CAGAGCTGAG	CAGGCCCTTC	AGGACATCTC	GAGAGATGCC	CAGATTTTCA	2100
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAGGT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	AGTTCCGGCT	CTGGGAAGTC	2220
	AGTACCAGAA	CCGAGTTCGG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCTCGG	2280
	CAGAAAGTGA	AGCTTCTCTG	GGAAACACTA	ACATTCCTGC	CTCAGACCC	TACGTGGGGC	2340
35	CAAAAGGCTT	TAAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CAGTTTGAGT	2400
	CAGCCAGTAA	CATGGAGCAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACTGGTGCG	CAAGGCCCTG	CATGAAGGAG	TCGGAAGCGG	AAGCGGTAGC	CCGACGGGTG	2520
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTTG	AGAAAAACCA	GTCCCTGGCC	CAGCAGTTGA	2580
40	CAAGGGAGGC	CACCAAGGCG	GAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCG	2640
	TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCTTTTCAG	GTGGAAGAAG	2700
	CAAAGAGGAT	CAAAACAAA	GCGGATTCAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAG	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAATGGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
45	AGACAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTTGAGAGCA	2940
	TCCTTAAAA	CTTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
50	CCGGGAGGC	CCTGGAAATG	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTTG	3180
	AAGCCAAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
	TGAGATGAG	GGAAAGTGGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAGAACG	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCCTGCAT	CTGATGGACC	3420
55	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAAGCT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCAGCTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAACTTGGA	GAACATTAGG	GACAACTGCG	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTCTC	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
60	GGCTCGGGAG	CCATGTCTATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTTGTCTTAT	3840
	TGACCATATC	CTCTGCTTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCTC	CATAATAGTG	GTAAGTGGAG	TCCTGGAATT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATTCTTTGA	GTAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCCAGGC	4080
	ATGAAATTC	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
65	ACTATTGCTC	CATATGTGCT	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCC	CCTACTTACA	4200
	ACCCAGGGTG	TGAACATGAT	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCCC	ATTCAGAGCT	ATGGTGCTTG	CTGGTGCCCTG	CCACCTTCAA	4320
	GTCTTGAGCC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
	ATTTTTATTA	AAGCATTTCC	TACCAGCAAA	GCAAAATGTTG	GGAAAGTATT	TACTTTTTCG	4440
70	GTTTCAAAGT	GATAGAAAAG	TGTGGCTTGG	GCATTGAAA	AGGTAAAATT	CTCTAGATTT	4500
	ATTAGTCCTA	ATTCAATCCT	ACTTTTCGAA	CACCAAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTTACT	4620
	CACACTTCAG	CTGGGTCACA	TCCATCCCTC	CATTATCCTT	TCCATCCATC	TTTCCATCCA	4680
	TTACCTCCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
75	GTGGACAGT	GGTGACATGT	TCTTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTTTA	AAAAATAAAT	TTAACTTAC	AACTTTGTT	TGTCACAAGT	GGTGTTTATT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTC	CTCAACAGAA	CATATGTGTC	AAGACCCCTC	4920
	CATGGGGGCA	CTTGATTTTC	TGCAAGGCTG	ACAGAGCTCT	GGGTGTGCA	CATTCTTTG	4980
	CAITCCAGCT	GTCACTCTGT	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
80	TAACACCACT	GGGAATTGCT	GGAGGAACCA	GAGGCACTTC	CACCTTGCTG	GGGAAGACTA	5100
	TGGTGCTGCC	TTGCTTCTGT	ATTTCTTGG	ATTTCTCTGA	AAGTGTTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 220 Protein sequence:
Protein Accession #:NP_005553

1 11 21 31 41 51
| | | | |

MPALWLGCCCL CFSLLLPAAAR ATSRREVCDC NGKSRCQCFD RELHRQTGNG FRCLNCNDNT 60
 DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCCKPGVTG ARCDRCCLPGF 120
 HMLTDAGCTQ DQRLLDKSKD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGGN 180
 5 PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVGWKA VQRNGSPAKL QWSQRHQDVF 240
 SSAQRLLDPVY FVAPAKPLGN QQVSYGQSL SFDYRVDRGGR HPSAHDVILE GAGLRITAPL 300
 MPLGKTLPCG LTKTYTFRNL EHPNNWSPQ LSYFEYRRL RNLTLALRIRA TYGEYSTGYI 360
 DNVTLSARP VSGAPAPWE QICPVGKYG QFCQDCASGY KRDSARLPGF GTCIPCNQCG 420
 10 GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRCK PCPCCHNGPSC SVMPEETREVV 480
 CNNPCPGVTG ARCELADGTY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK 540
 CIHNTAGIYC DQCKAGYFYG PLAPNPADKC RACNCPMGS EPVGCERSDGT CVCKPGFGGP 600
 NCEHGAFCSP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEOAL 660
 QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLLDLKM TVERVRALGS QYQNRVRDTH 720
 RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 15 ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL EKTKSLLAQOL TREATQAEIE 840
 ADRSYQHSLL LLDVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNL 900
 NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRQAQALSM GNATFYEVES ILKNLREFDL 960
 QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALBISSE 1020
 IEQIGISLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEPDTN MDAVQMVITE 1080
 20 AQKVDTRAKN AGVTIQDTLN TLDGLLHLM DQLSVDEEGL VLLEQKLSRA KTQINSQLRP 1140
 MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ

Seq ID NO: 221 DNA sequence
 Nucleic Acid Accession #: NM_016529
 Coding sequence: 13-1854

1 11 21 31 41 51
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 GTCAAGAAAA GAATGTCTGT AATTGTTCGA ACTCCTTCAG GACGACTTCG GCTTTACTGT 60
 30 AAAGGGGCTG ATAATGTGAT TTTTGAGAGA CTTTCAAAAG ACTCAAAATA TATGGAGGAA 120
 ACATTATGCC ATCTGGGAATA CTTTGCCACG GAAGGCTTCG GGACTCTCTG TGTGGCTTAT 180
 GCTGATCTCT CTGAGAAATGA GTATGAGGAG TGGCTGAAG TCTATCAGGA AGCCAGCACC 240
 ATATTGAAGG ACAGAGCTCA ACGGTGGAAG GAGTGTACG AGATCATTGA GAAGAATTG 300
 CTGCTACTTG GAGCCACAGC CATAGAAGAT CGCCTTCAAG CAGGAGTTCC AGAAACCATC 360
 35 GCAACACTGT TGAAGGCAGA AATTAAATA TGGGTGTTGA CAGGAGACAA ACAAGAACT 420
 GCGATTAATA TAGGGTATTC CTGCCGATTG GTATCGCAGA ATATGGCCCT TATCCTATTG 480
 AAGGAGGACT CTTTGGATGC CACAAGGGCA GCCATTACTC AGCACTGCAC TGACCTTGGG 540
 AATTGTCTGG GCAAGGAAAA TGACGTGGCC CTCATCATCG ATGGCCACAC CCTGAAGTAC 600
 GCGCTCTCCT TCGAAGTCCG GAGGAGTTTC CTGGATTGG CACTCTCGTG CAAAGCGGTC 660
 40 ATATGCTGCA GAGTGTCTCC TCTGCAGAAG TCTGAGATAG TGGATGTGGT GAAGAAGCGG 720
 GTGAAGGCCA TCACCCCTCG CATCGGAGAC GCGCCCAACG ATGTCGGGAT GATCCAGACA 780
 GCCCACGTGG GTGTGGGAAT CAGTGGGAAT GAAGGCATGC AGGCCACCAA CAACTCGGAT 840
 TACGCCATCG CACAGTTTTC CTACTTAGAG AAGCTTCTGT TGGTTCATGG AGCCTGGAGC 900
 TACAACCGGG TGACCAAGTG CATCTTGATC TGCTTCTATA AGAACGTGGT CCTGTATATT 960
 45 ATTGAGCTTT GGTTCGCTT TGTAAATGGA TTTTCTGGGC AGATTTTATT TGAACGTTGG 1020
 TGCACTCGCC TGATCAATGT GATTTTCACC GCTTTGCCGC CCTTCACTCT GGGAACTTT 1080
 GAGAGGTCTT GCATCAGGA GAGCATGCTC AGGTTTCCCC AGCTCTACAA AATCACCAG 1140
 AATGGCGAAG GCTTCAACAC AAAGGTTTTC TGGGGTCACT GCATCAACGC CTTGGTCCAC 1200
 TCCCTCATCC TCTTCTGGTT TCCCATGAAA GCTCTGGAGC ATGATCTGT GTTTGACAGT 1260
 50 GGTCACTGTA CCGACTATT ATTTGTTGGA AATATGTGTT ACACATATGT TGTGTGTTACT 1320
 GTTTGTCTGA AAGCTGGTTT GGAGACCACA GCTTGGACTA AATTCAGTCA TCTGGCTGTC 1380
 TGGGGAAGCA TGCTGACCTG GCTGGTGTGT TTTGGCATCT ACTCGACCAT CTGGCCACAC 1440
 ATTTCCATTG CCACTCAGGA GAGAGGACAG GCAACTATGG TCCTGAGCTC CGCACACTTC 1500
 TGGTTGGGAT TATTTCTGGT TCCTACTGCC TGTTTGATTG AAGATGTGGC ATGGAGAGCA 1560
 55 GCCAAGCACA CCTGCAAAAA GACATTGCTG GAGGAGGTGC AGGAGCTGGA AACCAAGTCT 1620
 CGAGTCTGG GAAAGCGGT GCTGCGGGAT AGCAATGGAA AGAGGCTGAA CGAGCGCGAC 1680
 CGCTGATCA AGAGGCTGGG CCGGAAGACG CCCCCGACGC TGTTCGGGG CAGCTCCCTG 1740
 CAGCAGGGCG TCCCGCATGG GTATGCTTTT TCTCAAGAA AACACGGAGC TGTAGTCAG 1800
 GAAGAAGTCA TCCGTGCTTA TGACACCACC AAAAAGAAAT CCAGGAAGAA ATAAGACATG 1860
 60 AATTTTCTCT ACTGATCTTA GGAAAGAGAT TCAGTTTGT GCACCCAGTG TTAACACATC 1920
 TTTGTGAGAG AAGACTGGCG TCCAAGGCCA AAACACCAGG AAACACATTT CTGTGGCCTT 1980
 AGTTAAGCAG TTTGTTAGTT ACATATTCCC TCGCAAACTT GGAGTGCAGA CCACAGGGGA 2040
 AGCTATCTTT GCCCTCCCAA CTCGTCTGCA GTGCTTAGCC TAACTTTGT TTAGTCTGTT 2100
 ATGAAGCATT CAACTGTGCT CTGTGAGGTC TCAAATTAAT AACATTATGT TTCACCAATA 2160
 65 AGAAAAA AAAAAA

Seq ID NO: 222 Protein sequence:
 Protein Accession #: NP_057613

1 11 21 31 41 51
 | | | | |
 MSVIVRTPSG RLRLYCKGAD NVIFERLSKD SKYMEETLCH LEYPATEGLR TLCVAYADLS 60
 70 ENYEWEWLKV YQEASTILKD RAQRLEECYE IIEKNLLLLG ATAIEDRLQA GVPETIATLL 120
 KAEIKIWLVT GDKQETAINI GYSCRLVSQN MALILLKEDS LDATRAAITQ HCTDLGNLLG 180
 75 KENDVALIID GHTLKYALSF EVRRSFLDLA LSCKAVICCR VSPLOKSEIV DVVKRVRKAI 240
 TLAIGDGAND VGMQTAHVIG VGISGNEGMQ ATNNSDYAIA QFSYLEKLLL VHGAWSYNRV 300
 TKCILYCFYK NVVLYIIEIW FAFVNGFSQO ILFERWCIGL YNVIFTALPP FTLGIFERSC 360
 TQESMLRFPQ LYKITONGEG FNTKVFWGHG INALVHSLIL FWFPMKALEH DTVFDSGHAT 420
 DYLFVGNIVY TYVVVTVCLK AGLETTAWTK FSHLAVWGSN LTWLVFVFGIY STIWPITPIA 480
 80 PDMRGQATMV LSSAHFWLGL FLVPTACLE DVAWRAAKHT CKKTLLEEVQ ELETKSRVLG 540
 KAVLRDSNGK RLNERDRLIK RLGRKTPTPL FRGSSLQQGV PHGYAFSQEE HGAVSQEEVI 600
 RAYDTTKKKS RKK

Seq ID NO: 223 DNA sequence
 Nucleic Acid Accession #: BC017001
 Coding sequence: 1-394

1 11 21 31 41 51

AACCGTGGGC AGGGCCCGCG CGGGTCGGGG GCGCCCGGAG GGGCCCGGGC CGAGCGGGCG 60
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 CGTGCTCATC CGGCCGCTGC CGTCCGTGTT GGACCCCGCC AAGGTGCAGA GCCTCGTGGA 180
 5 CACGATCCGG GAGGACCCAG ACAGCGTGCC CCCCATCGAT GTCCTCTGGA TCAAAGGGGC 240
 CCAGGGAGGT GACTACTTCT ACTCCTTTGG GGGCTGCCAC CGCTACGCGG CCTACCAGCA 300
 ACTGCAGGGA GAGACCATCC CCGCCAAGCT TGTCCAGTCC ACTCTCTCAG ACCTAAGGGT 360
 GTACCTGGGA GCATCCACAC CAGACTTGCA GTAGCAGCCT CCTTGGCACC TGCTGCCACC 420
 10 TTCAAGAGCC CAGAAGACAC ACCTGGCCTC CAGCAGGCTG GGCATGACAG AAGGGATAGC 480
 AGGGGTGCAT TCTCTTTGCA CCTGGCGAGA GGGTCTGACT CTGGGCACCC CTCTCACCGG 540
 CTACAAGGCC TTGGACTCAG TGACAGTGT GGGAGCCCCA GTTCCACCT CTGTGACAAT 600
 AGGATCATGG CCTTACCCTT GAAGCATTAC CGAGAAGGAG AACAGAGATG GGCCTGAAGA 660
 GCCACGTGCT GCCGGCTCCA AATTCCCAAG GACAAGGATC CCTCTGCATT TTTGTCTATG 720
 15 TAACCTCTTA TATGGACTAC ATTCACTGTC AAGGAAAGGA AAACCTTGAT TGCAGTGGTT 780
 TAAACAAACA GAAGATTGTT TTTCCACATA GCATGGATTG TGGAGATGGG TGGCTAATGG 840
 TATTGGTTCA ACAACTCCAC GGAGGTAGGG GTCACGTCTT GGATCCTTTT GCCTTAATCT 900
 CAGTGCTCGT TACTTCATGG TCCCAAGATG GCTGCTGTAT CCCCAGAAAT CATGCTCGG 960
 TTCAAGGAAG GAGGGGTGGA GGAAGAGGAA GGGCCAAACT AGCTGGACCC GTCACCTTCT 1020
 20 ATCAGAAATG AAAACCTCGT CAGAAGTCTG TTTCTGCTC TCTCCCTCTG CATATCTTCA 1080
 CTTAGATGCC CTTGGCCGCA GCCAGCTACC ATTGCACCTC TAGCTGCAAA CAAAGCTAAG 1140
 ACAGCAGGGA ACAGAATTGT CATGGCTGAA TAGACCAATC GTGTTCCATC TACTGAGACT 1200
 GGCACACTGC CTCCTGCAAT AAAACTGGGA TCCCATTACC AAGAGAGAAA TGCAGAATTG 1260
 TGTACCAATT AGCTTTTGGT GTGTAAACAA CCATCCCCAA ACTTGGCAGC TAGAAACAAA 1320
 25 CCCTGTATTT TCCCAACAAT CTATGGGTG GCAATTTGGG CTGGGCTCAA CAGGGCAGTT 1380
 CTGCTGCTCA CACCTGGGAT CCCTCATGGA GCTAAGGTCA GCTGTTACCT CAGCTGGGCC 1440
 TGGATGGTCT AGGTATAGCT TACTCACTTG CCTGGCAGGT GACAGGCTGT TGGCTGGAAT 1500
 TGCTTGGTTC TCCTCCATGT GGCCTCTCCA GCAGGCTAGC TCAGGCTTAT TCACATGATG 1560
 GCCTCAGGAT TCCAAAGAGA GTGAGAGTAG AAGCTGAAG ACTTCTTGAG TTCTTGGCCT 1620
 30 GGAACCTGGA CTTGCTGCTG GTCACCTCTG CTAAGTCTTT TTGGTCAGAG CAAATCACA 1680
 GGCTTTACCC AGATTCAAGG GATGAGAAAC AGACTACATG TCTTGATGAG GGAACCACA 1740
 AAGAGCTTGT GGCCATTTT CACCTATCAC AAATAATTTT GGATGGGTAT TTATTTGGAT 1800
 AAAGGTATTT CCTCTTCCC CTTTCTCTC TGTCTCATGG GGCCTCACTC TGCCAAAGTTG 1860
 GAAGGCACTA AGACATTGTC CTGGCCCTCA GGGTCTAGGG GAAGAGGTGT TGGGGCAGGA 1920
 35 AGTGAGTCTC TCCATGGGCT GGACCCACTG TAGTAGGAGT GCCTCCTTGT CTGCACTGCT 1980
 GGTATGGGGT TAGGCCAGGT AGGACATTCC AGAGGGGCTT CTGAAACCA AGAGTCCCTG 2040
 GGGAAAGGGA ACAGAGTAAG GCAGGCCCTG TTCTCACTGC CCTCTAAGGG AACTTGGTCA 2100
 CTCGGCACTT TTAAGCCCTCA GTTCTCCAG TTCAATAATA AGGACAAGAG CTTTTCCTCAT 2160
 GCATTTCTCT TCCCAGGGA AGTTGACTGA GGTGACCAGT AATAGAAATG AAAAGGAGA 2220
 40 GTGTCTTCAG TGCAATGTGG CATCTGGAT TGGGTCTTGG AACAAAACA GGACATTAGT 2280
 GGGAAAATTG GAAATCTGAA AAAAGTCTGA ATTTTAGTTA ATATACCAAT TTCAGTCTCT 2340
 TGGTTTGGAC AGATCTGACA TGGTGATGTA AGATGTTGAC CTTGGGTTAG GCTGGGTGAA 2400
 GGGTATACAG GAACCTCTTG TACTATCTCT GCAACTTCTC TGTAATCTA GTATCATTCC 2460
 AAAATAAAG TTTATTTAAT TTAATAAATA AAAAAAATA AA

Seq ID NO: 224 Protein sequence:
 Protein Accession #: AAH17001.1

1 11 21 31 41 51
 TLGRAGAGRG APEGPGPSGG AQGGSIHSGR IAAVHNVPLS VLIRPLPSVL DPAKVQSLVD 60
 TIREDPDSVP PIDVLWIKGA QGGDYFYSFG GCHRYAAYQQ LQRETIPAKL VQSTLSDLRV 120
 YLGASTPDLQ

Seq ID NO: 225 DNA sequence
 Nucleic Acid Accession #: NM_021048
 Coding sequence: 1..1110

1 11 21 31 41 51
 ATGCCTCGAG CTCCAAAGCG TCAGCGCTGC ATGCCTGAAG AAGATCTTCA ATCCCAAAGT 60
 GAGACACAGG GCCTCGAGGG TGACAGGCT CCCCTGGCTG TGGAGGAGGA TGCTTCATCA 120
 65 TCCACTTCCA CCAGCTCCTC TTTTCCATCC TCTTTTCCCT CCTCCTCTC TTCTCCTCC 180
 TCCTCTGCT ATCCTCTAAT ACCAAGCACC CCAGAGGAGG TTTCTGCTGA TGATGAGACA 240
 CCAAATCCTC CCCAGAGTGC TCAGATAGCC TGCTCCTCCC CCTCGGTCTG TGCTTCCCTT 300
 CCATTAGATC AATCTGATGA GGGCTCCAGC AGCCAAAAGG AGGAGAGTCC AAGCACCCTA 360
 CAGGTCTCTG CAGACAGTGA GTCTTTACCC AGAAGTGAGA TAGATGAAAA GGTGACTGAT 420
 70 TTGGTGCACT TTCTGCTCTT CAAGTATCAA ATGAAGGAGC CGATCACAAA GGCAGAAATA 480
 CTGGAGAGTG TCATAAAAAA TTATGAAGAC CACTTCCCTT TGTGTTTAG TGAAGCCTCC 540
 GAGTGATGCT TGCTGGTCTT TGGCATTGAT GTAAGGAAG TGGATCCAC TGGCCACTCC 600
 TTTGTCCTTG TCACCTCCCT GGGCCTCACC TATGATGGGA TGCTGAGTGA TGTCCAGAGC 660
 ATGCCCAAGA CTGGCATTCT CATACTATC CTAAGCATAA TCTTCATAGA GGGCTACTGC 720
 75 ACCCTGAGG AGGTCTCTG GGAAGCACTG AATATGATGG GGCTGTATGA TGGGATGGAG 780
 CACCTCATTT ATGGGGAGCC CAGGAAGCTG CTCACCCAAG ATTGGGTGCA GGAAGACTAC 840
 CTGGAGTACC GGCAGGTGCC TGGCAGTGT CCTGCACGGT ATGAGTTTCT GTGGGTCCA 900
 AGGGCTCATG CTGAAATTAG GAAGATGAGT CTCCTGAAAT TTTTGGCCAA GGTAAATGGG 960
 80 AGTGATCCAA GATCCTTCCC ACTGTGGTAT GAGGAGGCTT TGAAAGATGA GGAAGAGAGA 1020
 GCCCAGGACA GAATTGCCAC CACAGATGAT ACTACTGCCA TGGCCAGTGC AAGTCTAGC 1080
 GCTACAGGTA GCTTCTCCTA CCTGAATAA

Seq ID NO: 226 Protein sequence:
 Protein Accession #: NP_066386

1 11 21 31 41 51
 MPRAKPRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSPFS SFPSSSSSSS 60

SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDGESS SQKEESPSTL 120
 QVLPDSSESLP RSEIDKVD TD LVQFLLFKYQ MKEPITKAEI LESVIKNYED HFPLLPSEAS 180
 ECLMLVFGID VKEVDPTGHS FVLVTSGLTL YDGM LSDVQS MPKTGILILI LSIIFIEGYC 240
 TPBEVIWEAL NMMGLYDGM EHLIYGEPRKL LTQDWDVQENY LEYRQVPGSD PARYEFLWGP 300
 RAHAIEIRKMS LLKPLAKVNG SDPRSFPPLWY EEALKDEBER AQDRIATD TD TTAMASASSS 360
 ATGSFSYPE

Seq ID NO: 227 DNA sequence
 Nucleic Acid Accession #: NM_005025.1
 Coding sequence: 82-1314

1 11 21 31 41 51
 | | | | |
 GCGGAGCACA GTCCGCCGAG CACAAGCTCC AGCATCCCGT CAGGGGTGTC AGGTGTGTGG 60
 GAGGCTTGAA ACTGTACAA TATGGCTTTC CTGGACTCT TCTCTTGCT GGTCTGCAA 120
 AGTATGGCTA CAGGGGCCAC TTCCCTGAG GAAGCCATG CTGACTGTGTC AGTGAATATG 180
 TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAAATATTC TCTTCTCTCC ATTGAGTATT 240
 GCTCTTGCAA TGGGAATGAT GGAACCTGGG GCCCAAGGAT CTACCCAGAA AGAAATCCGC 300
 CACTCAATGG GATATGACAG CCTAAAAAAT GGTGAAGAAT TTTCTTTCTT GAAGGAGTTT 360
 TCAAACATGG TAACTGCTAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCCTTGTTT 420
 GTGCAAAATG GATTTTCATG CAATGAGGAG TTTTTCGAAA TGATGAAAAA ATATTTTAAT 480
 GCAGCAGTAA ATCATGTGGA CTTCAGTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG 540
 TGGGTGGAGA ATAACACAAA CAATCTGGTG AAAGATTGG TATCCCAAG GGATTTTGAT 600
 GCTGCCACTT ATCTGCCCTT CATTAATGCT GTCTATTTC AAGGGAACTG GAAGTCGCGA 660
 TTTAGGCTG AAAATACTAG AACCTTTTCT TTTACTAAAG ATGATGAAAG TGAAGTCCAA 720
 ATTCCAATGA TGTATCAGCA AGGAGAATTT TATTATGGGG AATTTAGTGA TGGCTCCAAT 780
 GAAGCTGGTG GTATCTACCA AGTCTTAGAA ATACCATATG AAGGAGATGA AATAAGCATG 840
 ATGCTGGTGC TGTCCAGACA GGAAGTTCCT CTGTCTACTC TGGAGCCATT AGTCAAAGCA 900
 CAGCTGGTTG AAGAATGGGC AAACCTCTGT AAGAAGCAAA AAGTAGAAGT ATACCTGCCC 960
 AGGTTACAG TGAACAGGA AATTGATTGA AAAGATGTTT TGAAGGCTCT TGAATAAAT 1020
 GAAATTTTCA TCAAAGATGC AAATTTGACA GGCCTCTCTG ATAATAAGGA GATTTTCTT 1080
 TCCAAGCAAA TTCACAAGTC TTCTCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT 1140
 GTCTCAGGAA TGATTGCAAT TAGTAGGATG GCTGTGCTGT ATCTCTCAAGT TATTGTGAC 1200
 CATCCATTTT TCTTTCTTAT CAGAAACAGG AGAAGTGGTA CAATCTATT CATGGGACGA 1260
 GTCATGCATC TGAACAACAT GAACACAAGT GGACATGATT TCGAAGAACT TTAAGTTACT 1320
 TTATTGGAAT AACAAGGAAA ACAGTAACTA AGCACATTAT GTTTGCAACT GGTATATATT 1380
 TAGGATTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTCC AGATAAAAAC 1440
 AATATATGTA AATTATAAGT AACTTGTCAG GGAATGTTAT CAGTATTAAAG CTAATGGTCC 1500
 TGTATATGTA TTGTGTTTGT GTGCTGTTGT TTAATAATAA AGTACCTATT GAACATGTG

Seq ID NO: 228 Protein sequence:
 Protein Accession #: NP_005016.1

1 11 21 31 41 51
 | | | | |
 MAFLGLPSLL VLQSMATGAT FPPEAIADLS VNMYNRLRAT GEDENILFSP LSIALAMGMM 60
 ELGAQGSTQK EIRHSMGYDS LKNGEEFSFL KEFSNMVTAK ESQYVMKIAN SLFVQNGFHV 120
 NEEFLQMKMK YFNAAVNHVD FSQNVAVANY INKVVNNNTN NLVKDLVSPR DFDAATYLAL 180
 INAVYFKGNW KSQFRPENTR TFSFTKDDDES EVQIPMMYQQ GEFYYGEFSD GSNEAGGIYQ 240
 VLEIPYEGDE ISMMLVLSRQ EVPLATLEPL VKAQLVEEWA NSVKKQKVEV YLPRFTVEQE 300
 IDLKDVLKAL GITEIFIKDA NLTLGLSDNKE IFLSKAIHKS FLEVNEEGSE AAASVGMIAI 360
 SRMAVLYPQV IVDHPFFFLI RNRTGTILF MGRVMHPETM NTSGHDFEEL

Seq ID NO: 229 DNA sequence
 Nucleic Acid Accession #: NM_003695
 Coding sequence: 12-398

1 11 21 31 41 51
 | | | | |
 CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGACAGC CCTGGCTGTG GCTACAGGGC 60
 CAGCCCTTAC CTGCGCTGC CACGTGTGCA CCAGCTCCAG CACTGCAAG CATTCGTGTG 120
 TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
 ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCCTG CAGGCCCAGG 240
 TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
 ACAACGCTGC ACCCACCCGC ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
 TGAGCCTCCT GGCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
 TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG 480
 GGGTGCCAGG AGCCCCAGGC TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
 CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
 ACAGAGGATG CAGCCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
 GATTTCACAC TCTTCTGTGT TTGTTGCCGT TTATTTGTGA CTCAATCTC TACATGGAGA 720
 TAAATGATTT AAACC

Seq ID NO: 230 Protein sequence:
 Protein Accession #: NP_003686

1 11 21 31 41 51
 | | | | |
 MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTTNT VEPLRGNLVK 60
 KCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSLL 120
 AVILAPSL

Seq ID NO: 231 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 126-752

1	11	21	31	41	51	
CCGGGCGAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTTGAGGC	60
AGGGGCGCAG	GAATTCGTAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
AGAAAGTAGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
TCTCTCTTGA	TGCCTCCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
GAAGATACCA	TCATGCTTGG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
ACCCAGTGGG	CAATGCTGGG	CTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
AAGTTGGGCG	AGACGCTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAAAT	720
TTCAAGATGG	CTGTATCTTG	CGGTCAAGAT	GAGAGAGTCA	AGCTGGGCAG	AATCTCTCGC	780
CAAGAGTTCA	GGCTTCTTTT	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
TTCACTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACGTGAGG	AAAAGGGGGC	TTTGGCCCTG	900
TGACTCAGTT	CCAGATTTTG	GATTGCATAC	TGGAAAAGAA	GCCATCTTTC	TTGCTAGTAA	960
ACCAAGCAAC	CGCGTGTATA	CAGTGGTGAC	CCAAGCAATG	GATATAAACC	TAAAAATCTG	1020
AGGGAGGGGA	GAGGTGGAAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGATCAGG	1080
TTATTTCTGT	GGACTTGGCA	AAAATCTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
TCTGGTATTA	ATTAACTCTC	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
GGAAATCAGC	GTAGTACCTT	CCAGACCGTG	GTGTCTGGCC	TCCATTTTTC	TCTGTCAATC	1260
AGCTCTGACT	TACAGCTGCA	GTCACTTTTG	CTATAAGGCA	CCTGGGTAGA	AGGGTGGATG	1320
GGCTTCACAT	CAATTTTCTT	CTTCTTTTAG	GGTGGGGGAT	TGGTTTGGCT	TTCTTTTGTT	1380
GTGGTTTTTT	GTTTTATTTT	TGTCAAGATT	GATTTTTTGA	TGCAAGGACT	TGAAAAGACC	1440
CAGAAGGATG	CCACCAAGTT	TTCTTTGAGG	CCTAGGATTT	TTTATTCTGT	CCCCAGCAGA	1500
GGTAATTCCT	CACAACCTTAG	TGCACCAGTA	GCACCAGCCA	TTTGGAGCAG	AGTACCTCTT	1560
TGGGGAGGCT	TTGTTTGTGT	TTTGTTTTTA	ATTCTCTTTC	CTTAGCAGCA	AGGTCTTTTT	1620
TCCTAGAGAA	TCTACTCCGT	TGCAGAACTA	TTGCAACCTC	AGGAGCCCTC	ACTGATTGAG	1680
TGCTGTGAGC	CTGATATACT	ACTTTGGACT	CTGGAAACAG	ATATGGGTTT	TATTCTCTAT	1740
TTCTACTGTG	TGTCGTTAAA	CAACCGTCGG	AGACCAGATG	ACCTGTTAGA	TGGCTAGTCC	1800
TGTATAACTC	GACTCTGTAT	GTTTCAATGT	ATGTTACTGC	AATGCTTCAC	CTGCTGTACA	1860
GTGTTTGTGA	GATGCTCTTT	GAAGATGGTA	CTTTTATATT	T		

Seq ID NO: 232 Protein sequence:
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLECQDAL	ETAARAEGLS	60
LDASMSHQLR	ILDEEHPKKG	YHGLSALKP	IRTSKHQHP	VDNAGLFSCM	TFSWLSLLAR	120
VAHKKGELSM	EDVWSLSKHE	SSDVNCRRLB	RLWQEBLNEV	GPDAASLRV	WVIFCRTRLI	180
LSIVCLMITQ	LAGFSGPNFQ	DGCILRSE				

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
TTTAAATGGT	GCTCATATAT	ACTGTATTTT	TGTTGTTTAA	GTTTACTTAA	TTGAGAGTGT	60
CACACATGA	ATCACATAAT	CATGATTTT	TTTTTTTACT	TTTACTCCCC	AAATTATICA	120
TGTTTCTTAG	ATCGTAGTCA	TTGAGAAGTC	CCAATAACTC	TAAACTTTTG	AGTTATAACG	180
TAGTAAACTT	CTCTTTCATC	TTTGTGTTAG	CTCTGTAGTC	TAACTCTGGA	TTTAAATTTT	240
TTTGTTTCCA	AAGTCACAA	TGAATTATTC	TTAGATACCT	TAAAGCACTG	AATTCAGTTC	300
TGTTTGACTG	AAAGCAAAAC	AACGTGACAG	TTTATTTTCA	AACACTAACT	TCTTGATATT	360
TTGTATAGGT	ATATCTTTTT	ATTAAATATT	TATTTTGACT	AAGCTTTCAT	AAAATATTTC	420
AAGCTATTTT	AATCATCAAG	TATGGAAGAA	AAATTACTAT	TGCATTTTCC	TATATATGCA	480
TATATTATGG	ATTAACCCAGA	ATTGTATCAT	TTTTGGCCTA	ATGCTCGGAT	ATAAAAGATA	540
ATTAGCCTAC	TATAGTATTA	ATAAATTTTT	CAGTTGGTTT	GGGCAAAATT	AAACCTGAAA	600
AAATAGTTAA	AAAGTAGTTA	CAAATTAAC	TTACTAATTT	ATACCTGATT	TTTTTCTTGT	660
AATTAAGTAA	CATTTTAAAG	GAGCTTTTAA	ATACCTTAAA	AAGTTGGTTC	TAATTTAAAA	720
TATGAAAGCT	CTGGCTATCA	TCTTGGGATA	GTAATTTCTA	ATTATATAGT	ATTTCAAAAC	780
TATATATTTT	TTAGTTCCTT	TGAGATAACT	AATTTCTAAT	TATATATGTT	TCAAAAACCA	840
TATCCTGTAT	TTTTTTTAA	AATTGTTTTA	TAAATAGGTC	ATAAGATACA	AGGTCTGCAT	900
TAGAAGACCC	ACTCTTACTA	GGTCCCTTAA	GGATCTGCCA	TAGATTTTTT	TTTTTTTTTT	960
TTTTTTTCTG	GTAGTTTAAA	GCAAGCACTG	ATACCAAGTG	GAGTTGGTCT	TGATCTAGGA	1020
GATTCTGTGA	AGCATCCAAA	AACAATGCCT	AATTTCAAGT	CTTAGGTTAT	GGCTTGTGAC	1080
TCCAGATAAA	AGATGGAGAA	TACCTCATGT	ACTGTGACTT	GAAAATGAAT	TCTTAAAATT	1140
CTTAGGCTCT	CTCCATGTAT	TTTCTTAA	GAAAAGTTTC	TGAGTGTGAT	CTCTCTTTTG	1200
CCATAGTATC	AAGTGGAGGG	TAGTTTCAAG	AAGTTAATAG	GAAATCTTTT	GTGACAGCAG	1260
ACTATAATAG	AAGTTTGAGT	AATATTTTAA	TAAATTTATA	TAATTCAAAT	GATAAAAATG	1320
TATCAATGTT	ATCCAATGAT	TTTTATTAAA	AAATTACCTT	ATTATTAGAA	CTGTGCCTAT	1380
TACATAAAAA	GTGCTCATGT	ATTGGAATTT	TAAATAATTT	ATTTAAATCA	AGACCACCAT	1440
AAGTCATTA	TAAATTAATA	ATTGTTTAAA	ATCAGTGGTT	TTCACCCCTC	ACTTCATATT	1500
AGAACTCATC	GAGGACTTTT	AATATGGAAT	CCACCTCATA	ACAATTAAGT	CTAAATTTCT	1560
GGAAGATGGA	GCCATGCTTG	TTTTTCCAAA	AGCTCTTTGA	GTGATTCTAA	TTTGTAGTCA	1620
GAGTTGAAGA	CACTGCTCTC	AAATAGTGC	AGGAAAATGC	TTTTATTCTC	CCCATGTTAA	1680
CTTTTAAAC	TAGTAATGTA	CCCAGTTAAG	TTTTGATGGT	TAAATTTCCA	CTAAAGAAC	1740
TATCTTCTTA	ATAACTAGCA	TTTATTACAT	GAAATTTAAG	AGTTTAAAGT	CCATCAAACT	1800
AGCCCTTGTG	TAAAGATTAT	ATTCTTCTC	TATAACTTCA	AAATAGATAT	TTCATTCAAA	1860
CTGTTCAAGT	GAGAAAACAT	AATGGATTTT	TTTTTTTTTC	CTCTGGAGCT	CCCTGTTTCA	1920
TGAGATGGAG	GAGGTGGGCA	CATTTAAGGT	CAGTTCACTA	ACCTATGGTT	CAGAGTTCTG	1980
ATCATATGGA	AGTTTGGAAA	AGAGAGCTTA	TCACAGGTTT	GTATGCTGGT	GAATGGATAG	2040
TTTTAATCTC	CAGTCTCTCA	AAAGAGAATC	AGCTCTCCAG	CAGTTCTAGA	AAAGCTTTGA	2100
CAATCCCCAA	GGGGCAGTGT	TACCTTACTC	CTTCACTGCT	TCTTAGAAGG	TAGAATTAAG	2160
TTTCTGGAAT	TGCACCTACA	TGTTTCTTAA	TTAACATTCA	GAAATGGGAA	TATTAATTTT	2220

TCCAGTGTAGT AGTTTTCTGA AATTGGTAAC TTGAGAGTA AAATAACGTA TTTTGCTTTT 2280
 CAATTTTGTG TTTGTTTACT TTTATGTAAT AATTGTATAT GTGAATTACA CAGTTCTAAT 2340
 AAAACCTCAT GCCTTTTCAT TACATCTAAT TTGAACCTCTC AACTTCAGTG CCAGAAGTGC 2400
 TTTAAAGATG CTTTAAATGAA AAGTATTAAG AAAATATATA GATTGTATG TCAGTTTATA 2460
 CTTTCAGAAAT CCATATATTT GTCATATTTA TTTTITTAGA AACCTCCTAA TTGGATAACT 2520
 AGATGGTATT TAAATGAAT GCCCAAAAT ATCTGTACC TTGTCCAAA AGTTTATCTG 2580
 TTGAAGCCG CCAGCCATTC ATGTAGAGAG TTTATAAGAA AATAATTTAA AATTGTATGC 2640
 ATTTTATATT ACTATGGTAT CTGTGTACCA TATTTCTAAG TATTCATTAT TAAATTGGTA 2700
 CTTCTTAAAA CCATAACCTG GCTTGCTTTT TAGTGTATA CACAAAATCC AACATTGTAT 2760
 ATAGAGATTG TCTTTTATG AAGAAGAGCT GACGTAATTT ATTACCAGTG CATCTGCACA 2820
 AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAACCA 2880
 CCACATTAAA CAACCCAGCGC AACACTCAGA CTGGGCACTT TCCTACGAAT CCATCCTATA 2940
 TGTGCCTGGT ATCGCCTCTG GCATAACTTA CACGAATCGT CCTCCCTACT TGTCTACGCT 3000
 CCTTCATCAA GCACTTGCCA ACACATTAC CTCTAACTTG TACAACCTTA CCAACTCACC 3060
 ACAACATCTG CAACTCTACC CTATCAACTG CCAACCTAAA GACCCCAAC ACAACACAAC 3120
 CCCCAACAC AAAACCACTA AATCATAACC ACCACACACG CCACACACCA CACACCCACC 3180
 CACACAACCA ACACACACG ACCAAACACC CCACCACAAA CAAGCTAACA ACCACAACA 3240
 GACACACAT CACATACACT CACTACCCCC CCATACCTCC ACCCACA

Seq ID NO: 234 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 27-281

1 11 21 31 41 51
 AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT 60
 GTCTACCGCG TAGCAGTTAC ATCAGACTGA GACACTTCCT GTTTACAGGA GACTATAAAA 120
 TTCTGCCCC GTGCTCATTT GGGGCTGACG CCATTTTAGG CCTCAGCCCA TCTGCACCCA 180
 GGGCGTCACT GAAACAGTGT GTTGCTCCAC ACCGCCTTGT TTTGCTTGT GCGCGCTCT 240
 CAGGGTTCGG ACCAATCCAA GAGCCTTGCA GAAAGCATT ACGTGCTTT CTCTTTGGCA 300
 GAGTTTTTCT TTGCTCTGAT CTTGGAGACA TCCCTCTGCC TAGTGGAAAC ATAAGGAATA 360
 CAGAAAGAAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCATGCACT CAAGAGAAAG 420
 ATGTTGCAGG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCCAGC 480
 TTTTCTTCTC CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAACA GGAAATGTTT 540
 ATAAAACTG TTCAGCGGTT CGCCAACAAG AAGTGGTAAA GTAGCAAAAA TGGGGATGGA 600
 GATGCCAGGA GGAAGATGCG CAGGGGTAAA GTGGGAAAT GGAACCTGA AGCCAGGAGG 660
 TCAAGCCAAG CCAACAGGTG TCTGTTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA 720
 CTCAAACCGG GGAAGCCGCT CTCTAGAACC CATGCTGGTC ATCCATATCC CCAAGGCCCT 780
 GGTCAAGACA CAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAGGA 840
 AGACAGCCTG TGACGTTTCA AAAGCAAAAG TCCCTACCA GCCAGTGAAG CTACCTGATT 900
 TCTCAGTATC TTACGCCAGG TGACAGCATC TACCTCAAA ACTTAAAAAA AAAAGGGAAA 960
 CATAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAA TAAGAAAAAA 1020
 GGAAAGGTCT CCTGTGACTG TTTTATTTTT AGGGAACAG AGAGGAAGAA GAATGATTTT 1080
 TCTTTTATG ACTCTATATC CACTCTGAG GTTTGATTAA AGAAATGACC TTGAACCACA 1140
 GCAAAGAAAA ATAAAGACA ATTTCCAGTA AGTATGCCAG TTGGAATTAA TGATTTACTT 1200
 TTTATTTTAA AACTGAATTC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA 1260
 TTTGACCTTG AAATAATCTT TACATTGTAA ATTCTTAATG ATCAAAACAA GGTCTCAGT 1320
 GATTAACA TATTAGTAAT TAATTATTA AGGAGAATAA TTGCAATAC AACATTCTTA 1380
 AAATCTCAAG GCTTTTAAAG CATTGTGACA AATGACTGGA CATTTTTTAA ATTTGAAAAA 1440
 AAAAAAAGC CTTGAGCTCG ATTCTCATTT TCATTGTGAG TGCAACAACA AAAAGGTAT 1500
 GCACCTCTCT TCTCATTTTC CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA 1560
 TCCCATCAA GCCAAAGAAA GAAAGAAAAA TTGTTCTGTA CAGATATATG ACATTAATAA 1620
 ATAAATCCC

Seq ID NO: 235 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MHPLKTQREA VCLPRSSYIR LRHFLFTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCVA 60
 PHRLVLLVGA LSGFRPIQEP CRKH

Seq ID NO: 236 DNA sequence
 Nucleic Acid Accession #: NM_002075
 Coding sequence: 406..1428

1 11 21 31 41 51
 CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCCA 60
 ACAGGATCAG ACCCAGAGGC AGCTGGTTGG GGTGTGCGA GAAGAAGGAT TATCCAGATC 120
 AGTCCTTTCT AATCTCAGCT CCTGCCTGTA CCTCCCATTA CTCACCAAAC CCTCTTCCCC 180
 ACCACCTTGA GCTGAGGAGC ACAGTTTGAG GCCCCCCCAA CCCCCCGCGG GTCGGGGCCA 240
 GGGCAGGCGA GGCAGCTTCC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG 300
 CGTCGCAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAACCC CGGCCGAGGT 360
 CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTCGACCTGT CAGCCATGGG GGAGATGGAG 420
 CAACTGCGTC AGGAAGCGGA GCAGCTCAAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT 480
 GCTGACGTTA CTCTGGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGACG AGTCCAGATG 540
 CGGACGCGGC GGACGTTAAG GGGACCTTG GCCAAGATTT ACGCCATGCA CTGGGCCACT 600
 GATTCTAAGC TGCTGGTAAG TGCCTCGCAA GATGGGAAGC TGATCGTGTG GGACAGCTAC 660
 ACCACCAACA AGGTGCAGCG CATCCACTG CGCTCCTCCT GGGTCATGAC CTGTGCCTAT 720
 GCCCCATCAG GGAACCTTGT GGCATGTGGG GGGCTGGACA ACATGTGTTT CATCTACAAC 780
 CTCAAATCCC GTGAGGGCAA TGTCAAGTCT AGCCGGGAGC TTTCTGCTCA CACAGGTTAT 840
 CTCTCCTGCT GCCGCTTCTT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACCACG 900
 TGTGCCTTGT GGGACATTGA GACTGGGCAG CAGAAGACTG TATTTGTGGG ACACACGGGT 960
 GACTGCATGA GCTGGCTGTG GTCTCCTGAC TTCAATCTCT TCATTTGCGG GGCCTGTGAT 1020
 GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGCGCAC 1080

5
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GAGTCGGACA TCAACGCCAT CTGTTTCTTC CCAATGGAG AGGCCATCTG CACGGGCTCG 1140
GATGACGCTT CCTGCCGCTT GTTTGACCTG CGGGCAGACC AGGAGCTGAT CTGCTTCTCC 1200
CACGAGAGCA TCATCTGGGG CATCACGTCC GTGGCCTTCT CCCTCASTGG CCGCTACTA 1260
TTGCTGGCT ACAGCACTT CAACTGCAAT GTCTGGGACT CCATGAAGTC TGAGCGTGTG 1320
GGCATCCTCT CTGGCCACGA TAACAGGGTG AGCTGCCTGG GAGTCACAGC TGACGGGATG 1380
GCTGTGGCCA CAGGTTCTCT GGACAGCTTC CTCAAATCT GGAACCTGAGG AGGCTGGAGA 1440
AAGGGAAGTG GAAGGCAGTG AACACACTCA GCAGCCCCCT GCCCGACCCC ATCTCATTCA 1500
GGTGTCTCTT TCTATATTCC GGGTGCCATT CCCACTAAGC TTTCTCCTTT GAGGGCAGTG 1560
GGGAGCATGG GACTGTGCTT TTGGGAGGCA GCATCAGGGA CACAGGGGCA AAGAACTGCC 1620
CCATCTCTCT CCATGGCCTT CCTTCCCCAC AGTCCTCACA GCCTCTCCCT TAATGAGCAA 1680
GGACAACCTG CCCCTCCCCA GCCCTTTGCA GGCCAGCAGC ACTTGAGTCT GAGGCCCCAG 1740
GCCCTAGGAT TCCTCCCCCA GAGCCACTAC CTTTGTCCAG GCCTGGGTGG TATAGGGCGT 1800
TTGGCCCTGT GACTATGCTT CTGGCACCAC TAGGGTCTCT GCCCTCTTCT TATTTCATGT 1860
TTCTCCTTTT TCTACCTTTT TTTCTCTCCT AAGACACCTG CAATAAAGTG TAGCACCTTG 1920
GT

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Seq ID NO: 237 Protein sequence:
Protein Accession #: NP_002066

20
25

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1      11      21      31      41      51
|      |      |      |      |      |
MGEMEQLRQE AEQLKKQIAD ARKACADVTI AELVSGLEV V GRVQMRTRRT LRGLHLAKIYA 60
MHWATDSKLL VSASQDGKLI VWDSYTTNKV HAIPLRSSWV MTCAYAPSGN FVACGGLDNM 120
CSIYNLKSRE GNVKVSRELS AHTGYLSCCR FLDDNNIVTS SGDITCALWD IETGQKTFP 180
VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFTGHESDIN AICFPNGEA 240
ICTGSDDASC RLFDLRADQE LICFSHESII CGITSVAFSL SGRLLFAGYD DFNCNVWDSM 300
KSERVGLISG HDNRVSLGLV TADGMAVATG SWDSFLKIWN

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30
Nucleic Acid Accession #: CAT cluster

35
40
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50

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1      11      21      31      41      51
|      |      |      |      |      |
TCCCAATGTG TNGAACCTAC CATAAATTCT TTTCTTACNG GACAACTCTA TNCTAANCAA 60
TACCAATTGC TTTTAAGGCA GATAATCCTC CAAGTTTCTT AATGATATCT GAAACTATTA 120
ACTGATTCTG TGAATTATGA AATCTGAAAA GGAATTGGAA GTTGCTAAAA ATCTATCATT 180
TGCAATTGACC AGTGTGAGC ACAGTGGAAAT GAGAATGCGT GCCCTGACAC CAAAGAAAAA 240
TAAGTGACTG GAAAGCTGAA GAATCACCGG CTTCACTGAC ATGGAACCCA GTGATTGTAT 300
TTTGTACGAG TATCGGGTGA CTTTGAGGTG GTCAAGAAAC CACACTTTAA GAACAATGTC 360
CAAAAAGGGG AAAAAAAGA GCAACCAAAAG AAAAAAATC CATAAAATG CACAGAAGAA 420
AAGAAAGAAA AATAAATAT ACAAATATGGA CGATGGAGAA AAACAGTTAC ATTTCTTTAT 480
GGATCAAGAA GTTTGTGTAC ACATAATCTC ATTTTGAGAT ATATACTAT TTTTGTCTTT 540
CAGAAGTGAA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCAGAT 600
TAGAAAAATT TTTCTGTAAA AGTCAGATAG TAAATATTTT AGGTTTTCGA GTGTCTTTTG 660
CAACTACTCA ACTTTCCTAC TGTCAGACAA GAGTAGCTGT GGTACTGTGC AAATAAATTG 720
CTTGTGTTC AATAAGCTT CATTTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780
ACTGTTGTTT GCCAAGTCTT AATATAGTTG CTTAGCAAGT ATTGTGAGCT ATTTGAGGAA 840
GACATGAAAG TTCAATGGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAATT 900
TAGGCTAAGT TATAATACAC TGTTTAAACA ATTGTAAAT GTAAGAGAAA TTTACAAATA 960
AAAAATCCAA ATAAAA

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Seq ID NO: 239 DNA sequence
Nucleic Acid Accession #: NM_001786.1
Coding sequence: 130-1023

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1      11      21      31      41      51
|      |      |      |      |      |
GGGGGGGGGG GGCACTTGGC TTCAAAGCTG GCTCTTGGAA ATTGAGCGGA GAGCGACGCG 60
GTTGTTGTAG CTGCCGCTGC GGCGCGCGG GAATAATAAG CCGGGATCTA CCATACCCAT 120
TGACTAACTA TGAAGATTA TACCAAATA GAGAAAAATG GAGAAGGTAC CTATGGAGTT 180
GTGTATAAGG GTAGACACAA AACTACAGGT CAAGTGGTAG CCATGAAAAA AATCAGACTA 240
GAAAGTGAAG AGGAAGGGGT TCCTAGTACT GCAATTCGGG AAATTTCTCT ATTAAGGAA 300
CTTCGTATC CAAATATAGT CAGTCTTCAG GATGTGCTTA TGCAGGATTC CAGGTATAT 360
CTCATCTTTG AGTTTCTTTC CATGGATCTG AAGAAATACT TGGATTCTAT CCTCCTGGT 420
CAGTACATGG ATTCTTCACT TGTTAAGAGT TATTTATACC AAATCTACA GGGGATTGTG 480
TTTTGTCACT CTAGAAGAGT TCTTCACAGA GACTTAAAC CTCAAATCT CTTGATTGAT 540
GACAAAGGAA CAATTAACCT GGCTGATTTT GGCTTGCCA GAGCTTTTGG AATACCTATC 600
AGAGTATATA CACATGAGGT AGTAACACTC TGGTACAGAT CTCCAGAAGT ATTGCTGGGG 660
TCAGCTCGTT ACTCAACTCC AGTTGACATT TGGAGTATAG GCACCATATT TGCTGAACCTA 720
GCAACTAAGA AACCACCTTT CCATGGGGAT TCAGAAATG ATCAACTCT CAGGATTTTC 780
AGAGCTTTGG GCACTCCCAA TAATGAAGTG TGGCCAGAAG TGGAACTCTT ACAGGACTAT 840
AAGAATACAT TTCCCAATG GAAACCAGGA AGCCTAGCAT CCCATGTCAA AAACCTGGAT 900
GAAAATGGCT TGGAATTGCT CTCGAAAATG TTAATCTATG ATCCAGCCAA ACGAATTTCT 960
GGCAAAATGG CACTGAATCA TCCATATTTT AATGATTGGA ACAATCAGAT TAAGAAAGATG 1020
TAGCTTTCTG ACAAAAGTT TCCATATGTT ATGTCAACAG ATAGTTGTGT TTTTATGTG 1080
AACTCTTGTC TATTTTGTG TATATATAT TTCTTTGTTA TCAAACCTCA GCTGTACTTC 1140
GTCCTCTAAT TTCAAAAATA TAACTTAAAA ATGTAATAT TCTATATGAA TTTAAATATA 1200
ATTCTGTAAA TGTGAAAAAA AAAAAAATA AAAAA

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Seq ID NO: 240 Protein sequence:
Protein Accession #: NP_001777.1

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1      11      21      31      41      51
|      |      |      |      |      |
MEDYTKIEKI GEGTYGVVYK GRHKTTQGVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKSYLY QILQGIVFCH 120

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SRRVLHRDLK PQNLLIDDKG TIKLADFLGA RAFGIPIRVY THEVVTWLWYR SPEVLLGSAR 180
 YSTPVDIWSI GTIFAEALATK KPLFHGDSEI DQLFRIFRAL GTPNNEVWPE VESLQDYKNT 240
 FPKWKPGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGKM ALNHPYFNDL DNQIKKM

Seq ID NO: 241 DNA sequence

Nucleic Acid Accession #: NM_033379.1

Coding sequence: 132-854

1 11 21 31 41 51
 CGCCCGCGCG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTGGCAGAG CGCGCGGCCA 60
 GCTTTGCAGA GAGCGCCCTC CAGGGACTAT GCGTGCAGG ACACGGGATC TACCCATACC 120
 ATTGAATAAC TATGGAAGAT TATACCAAAA TAGAGAAAA TGGAGAAGGT ACCTATGGAG 180
 TTTGTATATA GGGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC 240
 TAGAAAGTGA AGAGGAAGGG GTTCTAGTA CTGCAATTCG GGAATTTCT CTATTAAAGG 300
 AACTTCGTCA TCCAAATATA GTCACTCTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT 360
 ATCTCATCTT TGAGTTTCTT TCCATGGATC TGAAGAAATA CTGGATTCT ATCCCTCCTG 420
 GTCAGTACAT GGATTCCTCA CTGTGTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG 480
 TATTGCTGGG GTCAGCTCGT TACTCAACT CAGTTGACAT TTGGAGTATA GGCACCATAT 540
 TTGCTGAAGT AGCAACTAAG AAACCACTTT TCCATGGGGA TTCAGAAAT GATCAACTCT 600
 TCAGGATTTT CAGAGCTTTG GGCACCTCCA ATAATGAAGT GTGGCCAGAA GTGGAATCTT 660
 TACAGGACTA TAAGAAATACA TTTCCCAAAT GGAAACCAGG AAGCCTAGCA TCCCATGTCA 720
 AAAAATTGGA TGAATATGGC TTGGATTGCT TCTCGAAAAT GTTAATCTAT GATCCAGCCA 780
 AACGAATTTT TGCCAAATAT GCACTGAATC ATCCATATTT TAATGATTG GACAATCAGA 840
 TTAAGAAGAT GTAGCTTTCT GACAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900
 TTTTATTGTT TAACCTCTGT CTATTTTGT CTATATATA TTTCTTTGTT ATCAAACCTC 960
 AGCTGTACTT CGTCTCTTAA TTTCAAAAAT ATAACCTAAA AATGTAAATA TTCTATATGA 1020
 ATTTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAA

Seq ID NO: 242 Protein sequence:

Protein Accession #: NP_203698.1

1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPQYIM DSSLVKVVTL WYRSPVLLG 120
 SARYSTPVDI WSIGTIPAEI ATKPLPHGD SEIDQLFRIF RALGTFNNEV WPEVESLQDY 180
 KNTFPKWKPG SLASHVKNLD ENGLDLLSKM LIYDPAKRIS GKMLNHPYP NDLDNQIKKM

Seq ID NO: 243 DNA sequence

Nucleic Acid Accession #: AF101051.1

Coding sequence: 221-856

1 11 21 31 41 51
 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGGCC CGGGCGCGCG ACCCCAACCC 60
 CGACCCAGAG CTTCTCCAGC GCGCGCGCAG CGAGCAGGGC TCCCGGCCCT AACTTCTCTC 120
 GCGGGGCCCA GCCACCTTCG GAGATCCGGG TTGCCACCT GCAAACTCTC CGCCTTCTGC 180
 ACCTGCCACC CTTGAGCTAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAAC CGGGGCTGCA 240
 GCTGTGCGGC TTCACTCTCG CTTCTCTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300
 GCCCCAGTGG AGGATTACTT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCTT GCGTGTGCGA GAGCACCAGG CAGATCCAGT GCAAAGTCTT 420
 TGACTCTCTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG 480
 CATCTCTCTG GAGTGTATAG CAATCTTTGT GGCACCGGTT GGCATGAAGT GTATGAAGTG 540
 CTTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600
 TCTTGCAGGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660
 ATTTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTGTGTCAGG CTCTCTTCC 720
 TGGCTGGGCT GCTGCTTCTC TCTGCCCTCT GGGAGGTGCC CTACTTTGCT GTTCTCTGCC 780
 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCCAGCGG 840
 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAATCA TGTGAAACA AACCGAAAA 900
 GGACATTGAG ATACTATTAG TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAAACAACA CAACAACAACA AAAAACCCAT GTGTTAAAT ACTCAGTGCT 1020
 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCATC GAGTAATCAT ACTCAATGG GGAAGGGGT GCTCCTTAAA 1140
 TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAT GTATTTAATT 1260
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTT GTCCCTATAT ACATATGTAA 1320
 CAGTCAATA TCATTTACTC TTCTTCATTA GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCTTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT 1440
 TTATTTTTTA CCATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTGTG 1500
 TTTCAATGGT CTCTATCTCC TGAATCTAAC ACATTTCTATA GCCTACATT TAGTTTCTAA 1560
 AGCCAAGAAG AATTTATATC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAAA 1620
 GTGATAAATT GCTGTTGACC TTCCACACA ATCCCTGTAC TCTGACCAT AGCACTCTTG 1680
 TTTGCTTTGA AAATATTGTT CCAATTGAGT AGCTGCATGC TGTTCCTCCA GGTGTTGTAA 1740
 CACAACCTTA TTGATTGAAT TTTTAAGCTA CTATTTCATA GTTTTATATC CCCCTAACT 1800
 ACCTTTGTGT TCCCATCTC TTAATGTAT TGTTTTCCCA AGTGTAATTA TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAAGCA AGTCACTTAA TCTTCTTACC 1980
 TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG 2040
 AATATTAATT AGTTTATATT ACTCTCATT TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
 TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AAAAAACCT ACACACGTAC 2160
 CTTCAATGTA TTCACTGCTT TCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
 ACACATACCT TCATGTGGTT CAGTGCCCTC CTCTCTCTAC CAGTCTATT CCACTGAACA 2280
 AAACCTAGCG ACATACCTTC ATGTGGCTCA GTGCCCTTCT CTCTCTACCA GTCTATTTC 2340
 ATCTTTTCTG CTGTGCTGTA CATGTTTGTG CTCTGTTCCA TTTTAAACAC TGCTCTTACC 2400
 TTTCCAGTCT GTACAGAAATG CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGTGTTG 2460

5 GCACCTGGTGT CTGGAGACCT GGATTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
 AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCAGAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 GTGGTTTTGT AATTGAAAAA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAACTGCATA 2700
 CGTTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
 GCGTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAAACGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATGTAA TGGGAAGAAA TAAAGCCTA CGTGTGGTA AATCCAACAG CAAGGGAGAT 2940
 TTTTGAATCA TAATACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTTGC 3000
 10 TGTTAGCTGG CAGCTGAGCG TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
 CTACACAAGG AAAGTCAGCC ACCGTGTCTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTAAA ATTTAAATGG CTTTGGCCAC 3180
 ATACATAGAT CTTTATGATG TGAGTGTGA ATTCCATGTG GATATCAGTT ACCAAACATT 3240
 15 ACAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTTGTATA AAGCATTACT CTTTTTCAAT AAATTGTTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAA AAA

20 Seq ID NO: 244 Protein sequence:
 Protein Accession #: AAD16433.1

25 1 11 21 31 41 51
 | | | | | |
 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGE WMSCVSQSTG 60
 QIQCKVFDLS LNLSSITLQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120
 IGGATFLLAG LAIIVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGA 180
 LLCCSCPRTK TSYTPRPYP KPAPSSGKDY V

30 Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: CAT cluster

35 1 11 21 31 41 51
 | | | | | |
 TTTTTTTTTT TTTTTTTTTT TTTTCAAGG AGAGCACAAG GAACCTTATT AATGACTTTC 60
 TTAATGGTTA AATGCTGTTT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
 AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAAATCC TTCTTTTGTG TTCACTTAGT 180
 TTTTCTTCTT GAGATTGTAG TTCTTCATCG TTAACAATGA GGATATTAAAT ATGTTTCACA 240
 40 CAGTTGTGTAT GAAGAATGCA TATATTAGAA TGCCTGTAGT CTCAGTACT CAGGAGGCTA 300
 AGGTGGGGAG GTCGCTCAAG CCCAGGAATT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
 TTAATAGCCA CTGCACCTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTCGGAGG 420
 GTCCTACGCC CACGGAGTCT CGTGATTGC TAGCACAGCA GTCTGAGATC AAACCTGCA

45 Seq ID NO: 246 DNA sequence
 Nucleic Acid Accession #: XM_058553.2
 Coding sequence: 897-1400

50 1 11 21 31 41 51
 | | | | | |
 AATTTTCAGA AGTTTCGTAT GGGGATGGTT TTATATAAAT TCAGGTTTTT CCCACAATAA 60
 TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTCTT AATAGAAAAG GATTCAAACCT 120
 GTGAAACCAT TTCTCTTTTA ATGTTTCACA TTCCTGTTAC AGATTGTGTC TCTTGTGACT 180
 CTGTTATCCA TAATATGGAG AGTTCCTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
 55 ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAAGTATT GCCACTTAG CACTGAAGAT 300
 TGGGATGAGA GGAGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCCT 360
 GATCATGTTT AAGAAAATGG ATGAAAATGG TGAAGTAGTG TTTCCAAGCA TATTGGAAGG 420
 GTTGAGTGTG TACTGTCTGT CAAAGACTTC CAGCATTTC AGGTCCTAGA GAGGAACAAG 480
 ACTGGTAACC TGCTATCTG TATTTTAAAG AACCAGGAG GAAAGCTTTA TAATAGAACA 540
 60 TTATTTCTGT GTTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
 TTGTCCAGGC CAAGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAG TGATCTGCCT 660
 GCCTTTGCCT CCGTGTAGT TGGGACTACA GGCATGAGCC CCCATGCCCT GCTAAGTTTG 720
 TTTTGTGTTT TTTTGTGTTG TTTGTTTTTG GGGGGGTTG TTTTGTGTTT TGTAGAGACG 780
 TAGTCTTGCT TTGTTGCCAG GCTAGTCTCA AACTCCTGGC TTCAAGTGAT CCTCCTGCCT 840
 CAGCCTCCCA GAGTGCTAGG ATTACAGCAC TTGGATTGAG CTCTCTCATT TCCAACATGG 900
 65 AAGAACTTA CACCGACTCC CTGGACCCTG AGAAGCTATT GCAATGCCCC TATGACAAAA 960
 ACCATCAAA CAGGGCTTGC AGGTTTCCTT ATCATCTTAT CAAGTGCAGA AAGATCATC 1020
 CTGATGTTGC AAGCAAAATG GCTACTTGTC CCTTCAATGC TCGCCACCAG GTTCCTCGAG 1080
 CTGAAATTAG TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAAGATGTTG 1140
 70 TCAACCAAA CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTGG CAGTGCCCTC 1200
 CTGCGATGA AGACTGGGAT AAAGATTGTT GGGAGCAGAC CAGCACCCCA TTTGTCTGGG 1260
 GCACAACCTA CTAATCTGAC AACCAACAGC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
 ATAACCTGGC TTCAGGCATG CGAGTTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
 ACAATGGAAA TGCACAGTAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
 75 GTTGCTTCTT TCTTCTACAG TGGGTTCTCA TTTTCTCTCT AATCTAATTA TAGAATGGTA 1500
 AACTCCCTGT GACTTTCCAA ACTGACAAGC ACACCTTTTT CTCCCCCTT TGAATCCTCA 1560
 TTTAATGCAA GAACCTCAT ACTCAGAAGC TTCCAAATAA ACCTTTGATA CAGATTG

80 Seq ID NO: 247 Protein sequence:
 Protein Accession #: XP_058553.1

85 1 11 21 31 41 51
 | | | | | |
 MEETYDLSLD PEKLLQCPYD KNHQIRACRF PYHLIKCRKN HPDVASKLAT CFPNARHQVP 60
 RAEISHHIS CDDRSCIEQD VVNQTRSLRQ ETLAESTWQC PPCEDEDWDK LWEQTSTPFV 120
 WGTTHYSNN SPASNIVTEH KNNLASGMRV PKSLPYVLPW KNNGNAQ

Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

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1	11	21	31	41	51	
TTAAGGAAAT	CCGGGCTGCT	CTTCCCCATC	TGGAAGTGGC	TTTCCCCACA	TCGGCTCGTA	60
AACGTATTAT	GAACATACG	ATGTTAATTC	GGAGCTGCAT	TTCCCAAGCTG	GGCACTCTCG	120
CGCGCTGGTC	CCCGGGGCTT	CGCCCCCAC	CCCCTGCCCT	TCCCTCCCGC	GTCTTGCCCC	180
CATCTCCAC	CCCCCGCGCT	GGCCACCCCG	CCTCCTTGGC	AGCCTCTGGC	GGCAGCGCGC	240
TCCACTCGCC	TCCCGTGCTC	CTCTCGCCCA	TGGAATTAAT	TCTGGCTCCA	CTTGTTGCTC	300
GGCCCAAGTT	GGGAGAGGA	CGAGGGTGG	CGCAGCGGG	TTCTGAGTGG	AATTACCCAG	360
GAGGAGCTGA	GCACAGCACC	AACAGAGAG	GGGTGAGGG	GTGCGGACT	CGAGCGAGCA	420
GGAAGGAGGC	AGCGCTGGC	ACCAGGGCTT	TGACTCAACA	GAATTGAGAC	ACGTTTGTA	480
TCGCTGGCGT	GCCCGCGCA	CAGGATCCCA	GCGAAATCA	GATTTCTGG	TGAGTTGCG	540
TGGTGGATT	AATTTGGA	AAGAACTGC	CTATATCTTG	CCATCAAAA	ACTCACGGAG	600
GAGAAGCGCA	GTCATCAAC	AGTAACTTA	AGAGACCCCC	GATGCTCCCC	TGGTTTAACT	660
TGTATGCTTG	AAAATTATCT	GAGAGGGAAT	AAACATCTTT	TCCTTCTTCC	CTCTCCAGAA	720
GTCCATTGGA	ATATTAGCC	CAGGAGTTGC	TTTGGGATG	GCTGGAAGTG	CAATGTCTTC	780
CAAGTTCTTC	CTAGTGGCTT	TGGCCATATT	TTTCTCTTTC	GCCCAAGTTG	TAATTGAAGC	840
CAATTCCTGG	TGGTCGCTAG	GTATGAATAA	CCCTGTTTCA	ATGTCAGAAG	TATATATTAT	900
AGGAGCACAG	CCCTCTGCGA	GCCAACTGGC	AGGACTTTCT	CAAGGACAGA	AGAAACTGTG	960
CCACTTGTAT	CAGGACCACA	TGCAGTACAT	CGGAGAAGGC	GCGAAGACAG	GCATCAAGA	1020
ATGCCAGTAT	CAATTCGAC	ATCGACGGTG	GAACCTGCAG	ACTGTGGATA	ACACCTCTGT	1080
TTTGGCAGG	GTGATGAGA	TAGGACGGCC	CGAGACGGCC	TTACATACG	CCGTGAGCGC	1140
AGCAGGGGTG	GTGAACGCCA	TGAGCGGGC	GTGCGCGGAG	GGCAGCTGT	CCACCTGCGG	1200
CTGACGCGCG	GCCGCGCGCC	CCAAGGACCT	GCCGCGGGAC	TGGCTCTGGG	CGCGTCTGGG	1260
CGACAACATC	GACTATGGCT	ACCCTTTTGC	CAAGGAGTTC	GTGGACGCCC	GCGAGCGGGA	1320
GCGCATCCAC	GCCAAGGGCT	CCTACGAGAG	TGCTCGCATC	CTCATGAACC	TGCACAAACA	1380
CGAGGCGGGC	CGCAGGACGG	TGTACAACCT	GGCTGATGTG	GCTTCAAGT	GCCATGGGGT	1440
GTCCGGCTCA	TGTAGCCTGA	AGACATGCTG	GCTGCAGCTG	GCAGACTTCC	GCAAGGTGGG	1500
TGATGCCCTG	AAGGAGAAGT	ACGACAGCGC	GGCGGCCATG	CGGCTCAACA	GCCGGGGCAA	1560
GTTGTGACAG	GTCACAGCC	GCTTCAACTC	GCCCACCACA	CAAGACCTGG	TCTACATCGA	1620
CCCCAGCCCT	GATCTACTGG	TGGCCTATGA	GAGCACCAGC	TGCTGGGCGA	CGCAGGGCGG	1680
CCTGTGCAAC	AAGACGTGG	AGGGCATGGA	TGGCTGCGAG	CTCATGTGCT	GCGGCCGTGG	1740
GTACGACACG	TTCAGACCG	TGCAGACGGA	GCGCTGCCAC	TGCAAGTTC	ACTGGTGCTG	1800
CTACGTCAAG	TGCAAGAGAT	GCACGGAGAT	CGTGACCCAG	TTTGTGTGCA	AGTAGTGGGT	1860
GCCACCCAGC	ACTCAGCCCC	GCTCCAGGA	CCGCTTATT	TATAGAAAGT	ACAGTGATTC	1920
TGGTTTTTGG	TTTTTAGAAA	TATTTTTTAT	TTTTCCCCAA	GAATTGCAAC	CGGAACCAAT	1980
TTTTTCTCTG	TTACCATCTA	AGAACTCTGT	GGTTTATTAT	TAATATTATA	ATTATTATT	2040
GGCAATAATG	GGGTGGGAA	CCACGAAAAA	TATTTATTTT	GTGGATCTTT	GAAAAGGTAA	2100
TACAAGACTT	CTTTTGGATA	GTATAGAATG	AAGGGGAAAA	TAACACATAC	CCTAAGTTAG	2160
CTGTGTGGGA	CTGTGTACAC	ATCCAGAAAG	TAAAGAAATA	CATTTTCTTT	TTCTCAATA	2220
TGCCATCATA	TGGATGGGT	AGGTTCCAGT	TGAAAGAGGG	TGGTAGAAAT	CTATTACAA	2280
TTCACTTCT	ATGACAAAAA	TGAGTTGTAA	ATTCTCTGGT	GCAAGATAAA	AGGTCTTGGG	2340
AAAAACAAAC	AAAAACAAAC	AAACCTCCCT	TCCCAGCAG	GGCTGCTAGC	TGCTTTCTG	2400
CATTTTCAAA	ATGATAATTT	ACAATGGAAG	GACAAGAATG	TCATATTCTC	AAGGAAAAAA	2460
GGTATATCAC	ATGTCTCAAT	CTCCTCAAA	ATTCCATTGG	CAGACAGACC	GTCAATTTCT	2520
AATAGCTCAT	GAAATTTGGG	CAGCAGGGAG	GAAAGTCCCC	AGAAATTAAA	AAATTTAAAA	2580
CTCTTATGTC	AAGATGTTGA	TTTGAAGCTG	TTATAAGAAT	TGGATTCCA	GATTTGTAAA	2640
AAGACCCCCA	ATGATTCTTG	ACACTAGATT	TTTTGTTTGG	GGAGGTTGGC	TGAACATAAA	2700
ATGAAATATC	CTGATTCTTC	TTAGGGATAC	TTGGTTAGTA	AATTATAATA	GTAGAAATAA	2760
TACATGAATC	CCATTACAG	GTTTCTCAGC	CCAAGCAACA	AGGTAATTGC	GTGCCATTCA	2820
GCACTGCACC	AGACGAGACA	ACCTATTGTA	GGAACACAG	TGAAATCCAC	CTTCTCTTTC	2880
ACACTGAGCC	CTCTCTGATT	CCTCCGTGTT	GTGATGTGAT	GCTGGCCAGC	TTTCCAAACG	2940
GCAGCTCCAC	TGGTCCCTT	TTGGTTGTAG	GACAGGAAAT	GAAACATTAG	GAGCTCTGCT	3000
TGGAAACAG	TTCATACTT	AGGGATTTT	GTTTCTCTAA	ACTTTTATTT	TGAGGAGCAG	3060
TAGTTTTCTA	TGTTTTAATG	ACAGAACTTG	GCTAATGGAA	TTACAGAGG	TGTTGCAGCG	3120
TATCACTGTT	ATGATCTGT	GTTTAGATTA	TCCACTCATG	CTTCTCTTAT	TGACTGCGAG	3180
GTGTACCTTA	AACTGTTTCC	CAGTGACTT	GAACAGTTGC	ATTTATAAGG	GGGAAATGT	3240
GGTTTAAATG	TGCCGTGATAT	CTCAAAGTCT	TTTGTACATA	ACATATATAT	ATATATACAT	3300
ATATATAAAT	ATAAATATAA	ATATATCTCA	TTGCAGCCAG	TGATTTAGAT	TTACAGCTTA	3360
CTCTGGGGTT	ATCTCTCTGT	CTAGAGCATT	GTTGTCTTTC	ACTGCAGTCC	AGTTGGGATT	3420
ATTCCAAAAG	TTTTTTGAGT	CTTGAGCTTG	GGCTGTGGCC	CCGCTGTGAT	CATACCTTGA	3480
GCACGACGAA	GCAACCTCGT	TTCTGAGGAA	GAAGCTTGAG	TTCTGACTCA	CTGAAATGCG	3540
TGTTGGGTTG	AAGATATCTT	TTTTTCTTTT	CTGCCTCACC	CCTTTGTCTC	CAACCTCCAT	3600
TTCTGTTTCA	TTGTGGGAGA	GGGCATTACT	TGTTGCTTAT	AGACATGGAC	GTTAAGAGAT	3660
ATTCAAACT	CAGAAGCATC	AGCAATGTTT	CTCTTTTCTT	AGTTCACTCT	GCAGAAATGGA	3720
AACCCATGCC	TATTAGAAAT	GACAGTACTT	ATTAATTGAG	TCCCTAAGGA	ATATTACAGC	3780
CACATACATG	ATAGCTTTTT	TTTTTTTTTT	TTTTTTTTTA	TAAGGACACC	TCTTTCCAAA	3840
CAGGCCATCA	AATATGTTCT	TATCTCAGAC	TTACGTTGTT	TTAAAAGTTT	GGAAAGATAC	3900
ACATCTTTTC	ATACCCCCC	TTAGGAGGTT	GGGCTTTCAT	ATCACCTCAG	CCAAGTGTGG	3960
CTCTTAATTT	ATTGCTATAA	GATATCCACA	TCAGCCAACT	GTGGCTCTTT	AATTTATTGC	4020
ATAATGATAT	TCACATCCCC	TCAGTTGCAG	TGAATTGTGA	GCAAAAGATC	TTGAAAGCAA	4080
AAAGCACTAA	TAGTTTAAAA	ATGTCACTTT	TTTGGTTTTT	ATTATACAAA	AACCATGAAG	4140
TACTTTTTTT	ATTGCTTAAA	TCAGATTGTT	CCTTTTGTAG	GACTCATGTT	TATGAAGAGA	4200
GTTGAGTTTA	ACAATCTTAG	CTTTTAAAAG	AAACTATTTA	ATGTAAATA	TTCTACATGT	4260
CATTCAGATA	TTATGTATAT	CTTCTAGCCT	TTATCTGTGA	CTTTTAAATGT	ACATATTTCT	4320
GTCTTGGCTG	ATTGTATAT	TTCACTGGTT	TAAAAACAA	ACATCGAAAG	GCTTATTTCA	4380
AATGGAAGAT	AGAATATAAA	ATAAACGTTT	ACTTGTAAAA	AAAAAAA		

Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

85
1 11 21 31 41 51
| | | | | |

MAGSAMSSKF FLVALAIFFS FAQVVEANS WWSLGMNPV QMSEVYIGA QPLCSQLAGL 60
 SQGQKLCCLL YQDHMQYIGE GAKTGIKECQ YQFRHRRWNC STVDNTSVFG RVMQIGSRET 120
 AFTYAVSAAG VVNAMSACR EGELSTCGCS RAARPKDLPR DNLWGGCGDN IDYGYRFAKE 180
 FVDARERERI HAKGSYESAR ILMHLHNEA GRRTVYNLAD VACKCHGVSG SCSLKTCWLQ 240
 LADFRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRFNSPT TDQLVYIDPS PDYCVRNEST 300
 GSLGTQGRCL NKTSEGMDGC ELMCCGRGYD QFKTVQTERC HCKFWWCYV KCKKCTEIVD 360
 QFVCK

Seq ID NO: 250 DNA sequence
 Nucleic Acid Accession #: NM_014058
 Coding sequence: 56..1324

1 11 21 31 41 51
 | | | | |
 15 TGACTTGGAT GTAGACCTCG ACCTTCACAG GACTCTTCAT TGCTGGTTGG CAATGATGTA 60
 TCGGCCAGAT GTGGTGAAGG CTAGGAAAAG AGTTTGTGTG GAACCCCTGG TTATCGGCCT 120
 CGTCATCTTC ATATCCCTGA TTGTCTTGGC AGTGTGCATT GGACTCAGTG TTCATTATGT 180
 GAGATATAAT CAAAGAAGA CCTACAATTA CTATAGCACA TTGTCATTTA CAACGTGACAA 240
 20 ACTATATGCT GAGTTTGGCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT 300
 TGAATCAATG GTGAAAATAG CATTTTATAA ATCTCCATTA AGGGAAGAAT TTGTCAAGTC 360
 TCAGGTTATC AAGTTCAGTC AACAGAAGCA TGGAGTGTG GCTCATATGC TGTGATTG 420
 TAGATTTTAC TCTACTGAGG ATCCTGAAAC TGTAGATAAA ATTGTTCAAC TTGTTTACA 480
 TGAAAAGCTG CAAGATCTCTG TAGGACCCCT TAAAGTAGAT CCTCACTCAG TTAATAATTA 540
 AAAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTGCGGAA CACGAAGAAG 600
 25 TAAAACTCTA GGTGAGAGTC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG 660
 GCCCTGGCAG CAGATGCTGC TAGGGGATGG GAGTCATCGC TGTGGAGCAA CCTTAATTA 720
 TGCCACATGG CTTGTGAGTG CTGTCTACTG TTTTACAACA TATAAGAACC CTGCCAGATG 780
 GACTGCTTCC TTTGGAGTAA CAATAAAACC TTGAAAATG AAAACGGGTC TCCGGAGAAT 840
 AATTGTCATG GTGAAAATAG AACACCCCAT ACATGACTAT GATATTCTC TTGCAGAGCT 900
 30 TTCTAGCCCT GTTCCCTACA CAAATGCAGT ACATAGAGTT TGTCTCCCTG ATGCATCCTA 960
 TGAGTTTCAA CCAGGTGATG TGATGTTTGT GACAGGATTT GGAGCACTGA AAAATGATGG 1020
 TTACAGTCAA AATCATCTTC GACAAGCACA GGTGACTCTC ATAGACGCTA CAACTTGCAA 1080
 TGAACCTCAA GCTTACAATG ACGCCATAAC TCCTAGAATG TTATGTGCTG GCTCCTTAGA 1140
 AGGAAAAACA GATGATGCC AGGGTGACTC TGGAGGACCA CTGGTTAGTT CAGATGCTAG 1200
 35 AGATATCTGG TACCTTCTCG GAATAGTAGG CTGGGGAGAT GAATGTGCGA AACCAACAA 1260
 GCCTGGTGT TATACTAGAG TTACGGCCTT GCGGGACTGG ATTACTTCAA AAACCTGGTAT 1320
 CTAAGAGAGA AAAGCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTTT GGTGTGGAGG 1380
 CCATTTTTAG AGATACAGAA TTGAGAGAGA AGCTAGATT GACTGATCTC 1440
 40 AATAAACTGT TTGCTTGATG CAAAAAATA A

Seq ID NO: 251 Protein sequence:
 Protein Accession #: NP_054777

1 11 21 31 41 51
 | | | | |
 45 MYRPDVVRAR KRVCEPWI GLVIFISLIV LAVCIGLTVH YVRYNQKITY NYSTLSFTT 60
 DKLYAEFGRE ASNNFTEMSQ RLESMVKNFA YKSPLREEFV KSQVIKFSQQ KHGVLAHMLL 120
 50 ICRFHSTEDP ETVDKIVQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR 180
 RSKTLGQSLR IVGTGTEVEG EWPQASLQW DGSHRGATL INATWLVSAA HCFPTYKNPA 240
 RWTASFGVTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSPPVPTN AVHRVCLPDA 300
 SYEFQPDVDM FVTGFGALKN DGYSQNLHRQ AQVTLIDATT CNEPQAYNDA ITPRMLCAGS 360
 LEGKTDACQG DSGGPLVSSD ARDWYLAGI VSWGDECAKP NKPGVYTRVT ALRDWITSKT 420
 55 GI

Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: NM_003504.2
 Coding sequence: 71-1771

1 11 21 31 41 51
 | | | | |
 60 GGCACGAGGC CTCGTGCCGC CGGGCTCTTG GTACCTCAGC GCGAGCGCCA GCGCTCCGGC 60
 CGCCGTGGCT ATGTTCTGTG CCGATTTCOG CAAAGAGTTC TACGAGGTGG TCCAGAGCCA 120
 65 GAGGGTCTCT CTCTCTGTGG CCTCGGACGT GGATGCTCTG TGTGCGTGCA AGATCCTTCA 180
 GGCCTTGTTG CAGTGTGACC ACGTGCAATA TACGCTGTTT CCAGTTTCTG GGTGGCAAGA 240
 ACTTGAAACT GCATTCTTGT AGCATAAAGA ACAGTTTCAT TATTTTATTC TCATAAACTG 300
 TGGAGCTAAT GTAGACCTAT TGGATATTCT TCAACCTGAT GAAGACACTA TATTCTTTGT 360
 70 GTGTGACACC CATAGGCCAG TCAATGTCGT CAATGTATAC AACGATACCC AGATCAAATT 420
 ACTCATTAAA CAAGATGATG ACCTTGAAGT TCCGCGCTAT GAAGACATCT TCAGGGATGA 480
 AGAGGAGGAT GAAGAGCATT CAGGAAATGA CAGTGATGGG TCAGAGCCTT CTGAGAAGCG 540
 CACACGGTTA GAAGAGGACA TAGTGGAGCA AACCATGCGG AGGAGGCAGC GCGGAGAGTG 600
 GGAGGCCCGG AGAAGAGACA TCCTCTTTGA CTACGAGCAG TATGAATATC ATGGGACATC 660
 75 GTCAGCCATG GTGATGTTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT 720
 GTGGTGGGCC ATCGTGTGAC TAACAGACCA GTGGGTGCAA GACAAGATCA CTCAAATGAA 780
 ATACGTGACT GATGTTGGTG TCCTGCAGCG CCACGTTTCC CGCCACAACC ACCGGAACGA 840
 GGATGAGGAG AACACACTCT CCGTGGACTG CACACGGATC TCCTTTGAGT ATGACCTCCG 900
 80 CCGTGTGCTC TACGAGCACC GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACCGC 960
 AGCCAGGTTT AAGCTGTGGT CTGTGCATGG ACAGAAGCGG CTCCAGGAGT TCCTTGCGAG 1020
 CATGGGTCTT CCCCTGAAGC AGGTGAAGCA GAAGTTCCAG GCCATGGACA TCTCCTTGAA 1080
 GGAGAAATTG CGGAAATAGA TTGAAGAGTC TGCAAAATAA TTTGGGATGA AGGACATGCG 1140
 CGTGCAACTT TTCAGCATTC ATTTTGGGTT CAAGCACAAG TTTCTGGCCA GCGACGTGGT 1200
 CTTTGCCACC ATGTCTTTTG TGGAGAGCCC CGAGAAGGAT GGCTCAGGGA CAGATCACTT 1260
 85 CATCCAGGCT CTGACAGGCC TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA 1320
 ACTCGCCAAG AAGCAGCTGC GAGCCACCCA GCAGACCATG GCCAGCTGCC TTGCAACCAA 1380
 CCTCGTCATC TCCAGGGGCG CTTTCTGTGA CTGCTCTCTC ATGGAGGGGA CTCCAGATGT 1440
 CATGCTGTTT TCTAGGCGCG CATCCCTAAG CCTGCTCAGC AAACACCTGC TCAAGTCTCT 1500
 TGTGTGTTTC ACAAAGAACC GCGCTGCAA ACTGCTGCCC CTGGTGATGG CTGCCCCCT 1560

GAGCATGGAG CATGGCACAG TGACCGTGGT GGGCATCCCC CCAGAGACCG ACAGCTCGGA 1620
 CAGGAAGAAC TTTTITGGGA GGGCGTTTGA GAAGGCAGCG GAAAGCACCA GCTCCCGGAT 1680
 GCTGCACAAAC CATTTTGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT 1740
 TCTGGACGCA CTTATTTCCC TCCTGTCTTA GGAATTGAT TCTTCCAGAA TGACCTTCTT 1800
 ATTTATGTAA CTGGCTTTCA TTTAGATTGT AAGTTATGGA CATGATTGTA GATGTAGAAG 1860
 CCATTTTITA TTAATAAAAA TGCTTATTTT AGGCTCCGTC CCCAAAAAAA AAAAAAAAAA 1920
 AAAAAAAAAA AA

Seq ID NO: 253 Protein sequence:
 Protein Accession #: NP_003495.1

1 11 21 31 41 51
 MFVSDFRKEF YEVVQSQRVL LFVASDVAL CACKILQALF QCDHVQYTLV PVSQWQELET 60
 AFLEHKEQFH YFILINCGAN VDLDLDILQPD EDTIFFVCDT HRPVNVVNVY NDTQIKLLIK 120
 QDDDLVFPAY EDIFRDEED EHSNGNSDG SEPSEKTRL EEEIVEQTM RRRQREWEAR 180
 RDILFDYEQ YEYHGTSSAM VMFELAWMLS KDLNDMLWWA IVGLTDQWVQ DKITQMKYVT 240
 DVGVLQRHVS RHNHRNEDEE NTLSDVCTRI SFEYDLRLVL YQHWSLHDSL CNTSYTAARF 300
 KLWSVHGQKR LQEFADMDGL PLKQVKQKFO AMDISLKENL REMIEESANK FGMKDMRVQT 360
 FSIHFGPKHK FLASDVVPAT MSLMESPEKD GSGTDHFIQA LDSLSRSNLD KLYHGLELAK 420
 KQLRATQQT IASCLTNLVI SQGPFLYCSL MEGTDPVMLF SRPASLSLLS KHLKSPFVCS 480
 TKNRCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAFEKAA ESTSSRMLHN 540
 HFDLSVIELK AEDRSKFLDA LISLLS

Seq ID NO: 254 DNA sequence
 Nucleic Acid Accession #: NM_022337
 Coding sequence: 48..683

1 11 21 31 41 51
 GGCTGCGCTT CCCTGGTCAG GCACGGCAGC TCTGGCCGGC CGCCAGGATG CAGGCCCGGC 60
 ACAAGAGCA CCGTACAGG TTGCTGGTGA TTGGCGACCT GGGCGTGGGG AAGACCAGTA 120
 TCAATCAAGC CTACGTGCAC CAGAACTTCT CCTCGCACTA CCGGGCCACA ATCGGCGTGG 180
 ACTTCGCGCT CAAGGTGCTC CACTGGGACC CGGAGACTGT GGTGCGCCTG CAGCTCTGGG 240
 ATATCGCAGG TCAAGAAAGA TTTGGAAACA TGACGAGGGT CTATTACCGA GAAGCTATGG 300
 GTGCAATTTAT TGTCTTCGAT GTCACCAGGC CAGCCACATT TGAAGCAGTG GCAAAGTGGG 360
 AAAATGATTT GGACTCCAGA TTAAGTCTCC CTAATGGCAA ACCGGTTTCA GTGGTTTGT 420
 TGCCCAACAA ATGTGACCA GGAAGGATG TGCTCATGAA CAATGGCCTC AAGATGGACC 480
 AGTTCTGCAA GGAGCAGCGT TTCGTAGGAT GGTTTGAAAC ATCAGCAAAG GAAAATATAA 540
 ACATTGATGA AGCCTCCAGA TGCCTGGTGA AACACATACT TGCAATGAG TGTGACCTAA 600
 TGAGTCTAT TGAGCCGAGC GTCGTGAAGC CCCATCTCAC ATCAACCAAG GTTGCCAGCT 660
 GCTCTGGCTG TGCCAAATCC TAGTAGGCAC CTTTGTCTGGT GTCTGGTAGG AATGACCTCA 720
 TTGTTCCACA AATTGTGCCT CTATTTTAC CATTTTGGGT AAACGTCAGG ATAGATATAC 780
 CACATGTGGC AAGCCAAAGA TCTATGCCTC TGTTTTTTCA ATGAGAGAGA AATAGCAAAT 840
 GTTCTTTCTA TGCTTTCTC ACCATCATCA CAGTGTCTTAC AAACCTTTGA AATATTTAG 900
 TCTGTTACAA ACTCTCTGTA TGTAGCTGAC CAAAATCCTG CAGGGCCACA GTCGGCACTG 960
 TTATTGCTT CTTTAAATCA GCAAAGGCCT CAAGTCTTAA AATAAAGGG GAGAAGAAAC 1020
 AACTAGCTGT CAAGTCAAGG ACTGGCTTTC ACCTTGCCCT GGTGTCTTTT TCCAGATTTC 1080
 AATATATTCT CTGATGGCCT GACAGGCCTA TTAAGTAGAT GTGATATTTT CTTCGAAGAT 1140
 GACCTCCATT CTCGGCAGAC CTAAGAGTGT CCTCTGAGTT AGCTCTTTGG AATCGTGAAC 1200
 ACAGGTGTGC TATATTGTCC TTGTCTTAAC TGTCACTTGC CATGGCCTGA ATGTTGGCTT 1260
 AACTGAATAT TGTATGAAAA GACATGCCTC CATATGTGCC TTTCTGTAG CTCTCTTTGA 1320
 CTAAGCTGT GGGGCTCCTC TATACATGCT ATACATGTAA TATATATTAT ATATATTTTT 1380
 GCAAGTGAAC AATAAACAT TAAAAGATAA AA

Seq ID NO: 255 Protein sequence:
 Protein Accession #: NP_071732

1 11 21 31 41 51
 MQAPHKEHLY KLLVIGDLGV GKTSIIKRYV HQNFSSHYRA TIGVDFALKV LHWDPETVVR 60
 LQLWDIAGQE RFGNMTRVYV REAMGAFIVF DVTRPATFEA VAKWKNDLDS KLSLPNGKPV 120
 SVVLLANKCD QGKDVLMNNG LKMDQFCKEH GFVGWFETSA KENINIDEAS RCLVKHILAN 180
 ECDLMESIEP DVVKPHLTST KVASCSCAK S

Seq ID NO: 256 DNA sequence
 Nucleic Acid Accession #: NM_016321
 Coding sequence: 25..1464

1 11 21 31 41 51
 GGAACGCGCC GTCGCCAGCC CGGCCAGGCA CCCCTGCAGC ATGGCCTGGA ACACCAACCT 60
 CGCTGGCGG CTGCCGCTCA CCTGCCTGCT CCTGCAGGTG ATTATGGTGA TTCTCTTCGG 120
 GGTGTTCTGT CGCTACGACT TCGAGGCCGA CGCCCACTGG TGGTCAGAGA GGACGCACAA 180
 GAACCTTGAGC GACATCTTCA ACGAATTCTA CTATCGTAC CCAAGCTTCC AGGACGTGCA 240
 CGTGATGGTC TTGCTGGGCT TCGGCTTCTT CATGACTTTC CTGCAGCGCT ACGGCTTCAG 300
 CGCCGTGGGC TTCAACTTCC TGTGGGCAGC CTTGCGCATC CAGTGGCGGC TGCTCATGCA 360
 GGGCTGGTTC CACTTCTTAC AAGACCGCTA CATCGTCTGT GGGCTGGAGA ACCTCATCAA 420
 CGCTGACTTC TCGTGGCCT CTGTCTGCGT GGCCTTTGGG GCAGTCTTGG GTAAAGTCAG 480
 CCCCATTCAG CTGCTCATCA TGACTTCTT CCAAGTGACC CTCTTCGCTG TGAATGAGTT 540
 CATCTCTCTT AACCTGCTAA AGGTGAAGGA TGCAGGAGGC TCCATGACCA TCCACACATT 600
 TGGCGCTTAC TTGGGCTCA CAGTGACCCG GATCCTCTAC CGACGCAACC TAGAGCAGAG 660
 CAAGGAGAGA CAGAACTCTG TGTACCAGTC GGACCTCTTT GCCATGATTG GCACCCTCTT 720
 CCGTGGGATG TACTGGCCCA GCTTCAACTC AGCCATATCC TACCATGGGG ACAGCCAGCA 780
 CCGAGCGGCC ATCAACACCT ACTGCTCTT GGCAGCCTGC GTGCTTACCT CGGTGGCAAT 840

ATCCAGTGCC CTGCACAGA AGGGCAAGCT GGACATGGTG CACATCCAGA ATGCCACGCT 900
 CGCAGGAGGG GTGGCCGTGG GTACCGCTGC TGAGATGATG CTCATGCCCTT ACGGTGCCCT 960
 CATCATCGGC TTGCTCTGGC GCATCATCTC CACCGTGGT TTTGTATACC TGACCCCAT 1020
 CCTGGAGTCC CGGCTGCACA TCCAGGACAC ATGTGGCATT AACAACTGCG ATGGCATTCC 1080
 5 TGGCATCATA GCGGCGATCG TGGGTGCTGT GACAGCGGCC TCCGCCAGCC TTGAAGTCTA 1140
 TGGAAAAGAA GGGCTTGTC ATTCTTTGA CTTCAGAGT TTCAACGGGG ACTGGACCGC 1200
 AAGAACACAG GGAAGTTCC AGATTTATGG TCTCTGGTG ACCCTGGCCA TGGCCCTGAT 1260
 GGGTGGCATC ATTGTGGGCG TCATTTTGAG ATTACCATTC TGGGGACAAC CTTCAGATGA 1320
 10 GAACTGCTTT GAGGATGCGG TCTACTGGGA GATGCCTGAA GGAACAGCA CTGTCTACAT 1380
 CCCTGAGGAC CCCACCTTCA AGCCTCAGG ACCCTCAGTA CCCTCAGTAC CCATGGTGTC 1440
 CCCACTACCC ATGGCTTCTT CGGTACCCCTT GGTACCCCTAG GCTCCAGGG CAGGTGAGGA 1500
 GCAGGCTCCA CAGACTSTCC TGGGGCCCG AGGAGCTGGT GCTGACCTAG CTAGGGATGC 1560
 AAGAGTGAGC AAGCAGCACC CCCACCTGCT GGCTTGGCCT CAAGGTGCCT CCACCCCTGC 1620
 CCTCCCTTC ATCCAGGGG GTCTGMCTGA GAATGGAGAA GGAGAAGCTA CAAAGTGGGC 1680
 15 ATCCAAGCCG GGTCTGGCT GCAGAAAGTTC TGCCTCTGCC TGGGGTCTTG GCCACATTGG 1740
 AGAAAAACAG GCTCAAAGTG GGGCTGGGAC CTGGTGGGTG AACCTGAGCT CTCCAGGAG 1800
 ACAACTTAGC TGCCAGTCAC CACCTATGAG GCTCTTCTAC CCGTGCCTG CACCTGGGCC 1860
 AGCATCTCT ATGCTCCCTG GGTCCCCCAG ACCTCTCTGT GTGTGTGTCG TGGCAGCCTC 1920
 20 CAGGAATAAA CATTCTTGTT GTCCTTTGTA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 257 Protein sequence:
 Protein Accession #: NP_057405

1 11 21 31 41 51
 MAWNTNLRWR LPLTCLLLQV IMVLEGFV RVDFEADAHW WSEETHKNLS DMENEFYYRY 60
 PSFQDVHVMV FVGFGLMTF LQRYGFSAVG FNFLAAFGI QWALLMQGWF HFLQDRYIVV 120
 GVENLINADF CVASVCVAFG AVLKGVSPIQ LLIMTFQVLT LFAVNEFILL NLLKVKDAGG 180
 SMTIHTFGAY FGLTVTRILY RRNLBQSKER QNSVYQSDLP AMIGTLFLWM YWPSFNSAIS 240
 30 YHGD SQHRAA INTYCSLAAC VLTSVAISSA LHKKGKLDV HIGNATLAGG VAVGTAEMM 300
 LMPYGALIIG FVCGIISTLG FVYLTPPLES RLHIQDTCGI NNHIGIPGII GGIVGAVTAA 360
 SASLEVYGKE GLVHSFDFQG FNGDWTARTQ GKFDIYGLLV TLAMALMGGI IVGLILRLPF 420
 WQPSDENCFC EDAVIWEMPE GNSTVYIPED PTFKPSGSPV PSVPMVSPLP MASSVPLVP

Seq ID NO: 258 DNA sequence
 Nucleic Acid Accession #: NM_002358.2
 Coding sequence: 75..692

1 11 21 31 41 51
 GGGAAGTGCT GTTGGAGCCG CTGTGGTTGC TGTCGCGGGA GTGGAAGCGC GTGCTTTTGT 60
 TTGTGTCCCT GGCCATGGCG CTGCAGCTCT CCCGGGAGCA GGAATCACC CTGCGCGGGA 120
 GCGCCGAAAT CGTGCCGAG TCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG 180
 45 GCATATATCC ATCTGAAACC TTTACTCGAG TGCAGAAATA CGGACTCACC TTGCTTGTA 240
 CTACTGATCT TGAGCTCATA AAATACCTAA ATAATGTGGT GGAACAACCTG AAAGATTGGT 300
 TATACAAGTG TTCAGTTCAG AAACCTGGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG 360
 TCCTGGAAAG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGCAC 420
 CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA 480
 50 CAGCTACGGT GACATTTCTG CCACCTGGTG AAGTTTCTTG TGCATTGAT CTGCTGATT 540
 ATACAGACAA AGATTGGTTT GTACCTGAAA AATGGGAAGA GTCGGGACCA CAGTTTATTA 600
 CCAATTCTGA GGAAGTCCGC CTTCGTTTCT TACTACTTAC AATCCACAAA GTAAATAGCA 660
 TGGTGGCCTA CAAAATTCCT GTCAATGACT GAGGATGACA TGAGGAAAAA AATGTAATTG 720
 TAATTTTGAA ATGTGGTTT CCTGAAATCA GGTCTCTAT AGTTGATATG TTTTATTTC 780
 55 TTGGTTAATT TTTACATGGA GAAAACCAAA ATGATACTTA CTGAACCTGTG TGTAAATTGT 840
 CCTTTATTTT TTGGTACCT ATTTGACTTA CCATGGAGTT AACATCATGA ATTTATTGCA 900
 CATTGTTCAA AAGGAACCAG GAGGTTTTTT TGTCAACATT GTGATGTATA TTCCTTTGAA 960
 GATAGTAATC GTAGATGGA AAACCTGTGC TATAAAGCTA GATGCTTTCC TAAATCAGAT 1020
 60 GTTTTGGTCA AGTAGTTTGA CTCAGTATAG GTAGGAGAT ATTTAAGTAT AAAATACAAC 1080
 AAAGGAAGTC TAAATATTCA GAATCTTTGT TAAGGTCCTG AAAGTAACCTC ATAATCTATA 1140
 AACATGAAA TATTGCTGTA TAGCTCCTTT TGACCTTCAT TTCATGTATA GTTTTCCCTA 1200
 TTGAATCAGT TTCCAATTAT TTGACTTTAA TTTATGTAACT TGAACCTAT GAAGCAATGG 1260
 ATATTGTAC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTT TTCTATGTGT 1320
 65 TTATAAAATC AAGTTTAAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGTT TTAATAAAAA 1380
 AAAAAAAAAA

Seq ID NO: 259 Protein sequence:
 Protein Accession #: NP_002349.1

1 11 21 31 41 51
 MALQLSREQG ITLRGSARIV AEFFSFGINS ILYQRGIYPS ETPTRVQKYG LTLVTTDLE 60
 LKLYLNNVVE QLKDLNLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDSDAPREKS 120
 75 QKAIQDEIRS VIRQITATVT FLPLLEVSCS FDLIYTDKD LUVPEKWEES GPQFITNSEE 180
 VRLRSFTTTI HKVNSMVAYK IPVND

Seq ID NO: 260 DNA sequence
 Nucleic Acid Accession #: NM_001211
 Coding sequence: 43..3195

1 11 21 31 41 51
 AAAGGCTGCG AGCAGGACGA GGACCTGAGC CAGGAATGCA GGATGGCGGC GGTGAAGAAG 60
 85 GAAGGGGGTG CTCTGAGTGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA 120
 GAAAAATGTAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGG AGCACTGGCA 180
 CAAGAATCTG CCTGTAACAA TACTCTTCAG CAGCAGAAAC GGCATTGTA ATATGAAATT 240

	CGATTTTACA	CTGGAAATGA	CCCTCTGGAT	GTTTGGGATA	GGTATATCAG	CTGGACAGAG	300
	CAGAACTATC	CTCAAGGTGG	GAAAGAGAGT	AATATGTCAA	CGTTATTAGA	AAGAGCTGTA	360
	GAAGCACTAC	AAGGAGAAAA	ACGATATTAT	AGTGATCCTC	GATTTCCTCA	TCTCTGGCTT	420
5	AAATTAGGGC	GTTTATGCAA	TGAGCCTTTG	GATATGTACA	GTTACTTGCA	CAACCAAGGG	480
	ATTGGTGTTC	CACCTGCTCA	GTTCTATATC	TCATGGGCAG	AAGAATATGA	AGCTAGAGAA	540
	AACTTTAGGA	AAGCAGATGC	GATATTTTCA	GAAGGGATTG	AACAGAAAGC	TGAACCACTA	600
	GAAAGACTAC	AGTCCCAGCA	CCGACAATTC	CAAGCTCGAG	TGTCTCGGCA	AACTCTGTTG	660
	GCACCTTGAGA	AAGAAGAAGA	GGAGGAAGTT	TTTGAGTCTT	CTGTACCACA	ACGAAGCACA	720
10	CTAGCTGAAC	TAAAGAGCAA	AGGGAAAAAG	ACAGCAAGAG	CTCCAATCAT	CCGTGTAGGA	780
	GGTGCTCTCA	AGGCTCCAAG	CCAGAACAGA	GGACTCCAAA	ATCCATTTC	TCAACAGATG	840
	CAAAATAATA	TGAGAAATTAC	TGTTTGTGAT	GAAAATGCTG	ATGAGGCTTC	TACAGCAGAG	900
	TTGTCTAAGC	CTACAGTCCA	GCCATGGATA	GCACCCCCCA	TGCCCAGGGC	CAAAGAGAAT	960
	GAGCTGCAAG	CAGGCCCTTG	GAACACAGGC	AGGTCTCTTG	AACACAGGCC	TCGTGGCAAT	1020
	ACAGCTTCAC	TGATGAGTGT	ACCCGCTGTG	CTTCCAGTT	TCACTCCATA	TGTGGAGAG	1080
15	ACTGCACAAC	AGCCAGTTAT	GACACCATGT	AAAATTGAAC	CTAGATATAA	CCACATCCTA	1140
	AGCACCAGAA	AGCCTGGAAG	GGAGGAAGGA	GATCCTCTAC	AAAGGGTTCA	GAGCCATCAG	1200
	CAAGCGTCTG	AGGAGAAGCT	AGAGAAGATG	ATGTATTGTA	AGGAGAAGAT	TTATGCAGGA	1260
	GTAGGGGAAT	TCTCCTTTGA	AGAAATTCGG	GCTGAAGTTT	TCCGGAAGAA	ATTAAAGAG	1320
	CAAAGGGAG	CCGAGCTATT	GACCAGTGCA	GAGAAGAGAG	CAGAAATGCA	GAACAGATT	1380
20	GAAGAGATGG	AGGAAGATCT	AAAAGAAATC	CAAACTACTC	AGCAAGAAAG	AACAGGTGAT	1440
	CAGCAAGAAG	AGACGATGCC	TACAAAGGAG	ACAACTAAAC	TGCAAAATGC	TTCCGAGTCT	1500
	CAGAAAATAC	CAGGAATGAC	TCTATCCAGT	TCTGTTTGTG	AAGTAAACTG	TTGTGCCAGA	1560
	GAAACTTCAC	TTGCGGAGAA	CATTGGCAG	GAACAACCTC	ATTCTAAAGG	TCCAGTGTA	1620
25	CCTTTCTCCA	TTTTTGATGA	GTTTCTTCTT	TCAGAAAAGA	AGAATAAAG	TCTCCTGCA	1680
	GATCCCCCAC	GAGTTTTCAG	TCAACGAAGA	CCCTTGCAG	TTCTCAAAAC	CTCAGAAAGC	1740
	ATCACCTCAA	ATGAAGATGT	GTCTCCAGAT	GTTTGTGATG	AATTACAGG	AATTGAACCC	1800
	TTGAGCGAGG	ATGCCATTAT	CACAGGCTTC	AGAAATGTAA	CAATTGTGTC	TAACCCAGAA	1860
	GACACTTGTG	ACTTTGCTAG	AGCAGCTCGT	TTTGTATCCA	CTCCTTTTCA	TGAGATAATG	1920
30	TCCTTGAAGG	ATCTCCCTTC	TGATCCTGAG	AGACTGTTAC	CGGAAGAAGA	TCTAGATGTA	1980
	AAGACCTCTG	AGGACCAGCA	GACAGCTTGT	GGCACTATGT	ACAGTCAGAC	TCTCAGCATC	2040
	AAGAAGCTGA	GCCCAATTAT	TGAAGACAGT	CGTGAAGCCA	CACACTCCTC	TGGCTTCTCT	2100
	GGTCTTCTG	CTCCGTTTCG	AAGCACCTCC	TCCATCAAA	GTCTTCAAA	TCCTGAGAAA	2160
	CTAGAACTTA	CTAATGAGAC	TTCAGAAAAC	CCTACTCAGT	CACCATGGTG	TTACAGTAT	2220
	CGCAGACAGC	TACTGAGTTC	CCTACCAGAG	TTAAGTGCCT	CTGCAGAGTT	GTGTATAGAA	2280
35	GACAGACCAA	TGCTTAAGTT	GGAAATTGAG	AAGGAAATTG	AATTAGGTAA	TGAGGATTAC	2340
	TGCATTAAAC	GAGAATACCT	AATATGTGAA	GATTACAAGT	TATTCTGGGT	GGCGCCAAGA	2400
	AACTCTGAG	AATTAACAGT	ATAAAGGTA	TCTTCTCAAC	CTGTCCCATG	GGACTTTTAT	2460
	ATCAACCTCA	AGTTAAAGGA	ACGTTTAAAT	GAAGATTTTG	ATCATTTTTC	CAGCTGTTAT	2520
40	CAATATCAAG	ATGGCTGTAT	TGTTTGGCAC	CAATATATAA	ACTGCTTCAC	CCTTCAGGAT	2580
	CTTCTCCAA	ACAGTGAATA	TATTACCCAT	GAAATAACAG	TGTTGATTAT	TTATAACCTT	2640
	TTGACAAATG	TGGAGATGCT	ACACAAAGCA	GAAATAGTCC	ATGGTGACTT	GAGTCCAAGG	2700
	TGTCTGATTC	TCAGAAACAG	AATCCACGAT	CCCTATGATT	GTAACAAGAA	CAATCAAGCT	2760
	TTGAAGATAG	TGGACTTTTC	CTACAGTGTT	GACCTTAGGG	TGCAGCTGGA	TGTTTTCACC	2820
45	CTCAGCGGCT	TTCCGACTGT	ACAGATCCTG	GAAGACAAA	AGATCCTGGC	TAACGTGTTCT	2880
	TCTCCTTACC	AGGTAGACCT	GTTTGGTATA	GCAGATTTAG	CACATTTACT	ATTGTTCAAG	2940
	GAACACCTAC	AGGTCTTCTG	GGATGGGTCC	TTCTGGAAAC	TTAGCCAAA	TATTCTGAG	3000
	CTAAAGATG	GTGAATTGTG	GAATAAATTC	TTTGTGCGGA	TTCTGAATGC	CAATGATGAG	3060
	GCCACAGTGT	CTGTTCTTGG	GGAGCTTGCA	GCAGAAATGA	ATGGGGTTTT	TGCACTACA	3120
	TTCCAAAGTC	ACCTGAACAA	AGCCTTATGG	AAGGTAGGGA	AGTTAACTAG	TCCTGGGGCT	3180
50	TTGCTCTTTC	AGTGAGCTGT	GCAATCAAGT	CTCACAGATT	GCTGCCTCAG	AGCAATGGTT	3240
	GTATTGTGGA	ACACTGAAAC	TGTATGTGCT	GTAATTTAAT	TTAGGACACA	TTTAGATGCA	3300
	CTACCATTGC	TGTTCTACTT	TTTGGTACAG	GTATATTTTG	ACGTCACTGA	TATTTTAT	3360
	ACAGTGATAT	ACTTACTACT	GGCCTTGTCT	AACTTTGTG	AAGAACTATT	TTATCTAAA	3420
55	CAGACTCATT	ACAAATGGTT	ACCTTGTAT	TTAACCATT	TGTCTCTACT	TTTCCCTGTA	3480
	CTTTTCCCAT	TTGTAATTG	TAAATGTTT	TCTTATGATC	ACCATGTATT	TTGTAATAA	3540
	TAAATAGTA	TCTGTTAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA		

Seq ID NO: 261 Protein sequence:

Protein Accession #: NP_001202

	1	11	21	31	41	51	
	MAAVKKEGGA	LSEAMSLEGD	EWELSKENVQ	PLRQGRIMST	LQGALAQESA	CNNTLQQQKR	60
	AFEYEIRFYT	GNDPLDVWDR	YISWTEQNYP	QGGKESNMST	LLERAVALQ	GKRYYS DPR	120
65	FLNLWLKLR	LCNEPLDMYS	YLNQIGIGVS	LAQFYISWAE	EYEARENFRK	ADAIFQEGIQ	180
	QKAEPLELRQ	SQHRQFQARV	SRQTLALEK	EEEEVFESS	VPQRSTLAE	LKSKGKTARA	240
	PIIRVGGALK	APSNRGLQ	PPQQMQNNS	RITVFDENAD	EASTAELSKP	TVQPWIAPPM	300
	PRAKENELQA	GPWNTGRSLE	HRPRGNTASL	IAVPAVLPSF	TPYVEETAQQ	PVMTPCKIEP	360
70	SINHILSTRK	PGKEEGDPLQ	RVQSHQQASE	EKKEKMMYCK	EKIYAGVGEF	SFEIRAIEVF	420
	RKKLKEQREA	ELLTSAEKRA	EMQKQIEEME	KKLKEIQTTQ	QERTGDQQEE	TMPTKETTKL	480
	QIASESQKIP	GMLTSSSVQC	VNCCARETSL	AENIWQEQPH	SKGPSVPFSI	FDEPLLSEKK	540
	NKSPPADPPR	VLAQRRPLAV	LKTSESITSN	EDVSPDVCDE	FTGIEPLSED	AIITGFRNVT	600
	ICPNPEDTCD	PARAARFVST	PFHEIMSLKD	LPSDPERLLP	EEDLDVKTSE	DQQTACGTY	660
75	SQTLSEIKLS	PIEDSREAT	HSSGFSGSSA	SVASTSSIKC	LQIPEKLELT	NETSENPTQS	720
	PWCSQYRRQL	LKSLPELSAS	AELCIEDRPM	PKLEIEKEIE	LGNEDYCIKR	EYLICEDYKL	780
	FWVAPRNSAE	LTVIKVSSQP	VPWDFYINLK	LKERLNEDFD	HFCSCYQYQD	GCIVVHQVIN	840
	CFTLQDLQSH	SEYITHETIV	LIYNNLLTIV	EMLHKAIEIVH	GDLSRCLIL	RNRHIDPYDC	900
	NKNNQALKIV	DFSYSVDLRV	QLDVFTLSGF	RTVQILEGQK	ILANCSSPYQ	VDLFGIADLA	960
80	HLLLFKEHLQ	VFWDGSPWKL	SQNISELKDG	ELWNKFFVRI	LNANDEATVS	VLGELAAEMN	1020
	GVFDTTFQSH	LNKALWKVGK	LTSPGALLFQ				

Seq ID NO: 262 DNA sequence

Nucleic Acid Accession #: NM_003784

Coding sequence: 365..1507

85	1	11	21	31	41	51
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	GTCTACTTAT	CAATAAGCAG	CTGCCTGTGC	AGAGTGCAGG	CTGCACCTTT	GGACAGCCTT	60
	TAAAACTGAA	TTCTCAGAAT	TTTAGAACAA	ATTTTGTGCT	AGAAATGCTG	ACTTTGGTTC	120
5	ATTAGGTAGT	GGTAAACAG	GCTCCCTTCG	AAGCTCTCCT	TCATCACCTT	CCTAAGTGCA	180
	TGTACAGGGA	AGCTCTCCTT	CATCACCTTC	CTAAGTGCAT	GGGGGAAAAT	ACCTAGGGCT	240
	CAACAGTCTT	GAGAAAGTGT	GAAACATTTT	CTTTGTGAGT	GAGAACAGAT	CACCTAGAGA	300
	AAGGAAACCA	GATTCCTATC	ACTGCTTCTG	GGTATCAGAT	GCTAGCGCTG	CACTCCATTT	360
	TGCAATGGCC	TCCCTTGCTG	CAGCAAATGC	AGAGTTTTCG	TTCAACCTGT	TCAGAGAGAT	420
10	GGATGACAAT	CAAGGAAATG	GAAATGTGTT	CTTTCTCTCT	CTGAGCCTCT	TCGCTGCCCT	480
	GGCCCTGGTC	CGCTTGGCGC	CTCAAGATGA	CTCCCTCTCT	CAGATTGATA	AGTTGCTTCA	540
	TGTTAACACT	GCCTCAGGAT	ATGGAAACTC	TTCTAATAGT	CAGTCAGGGC	TCCAGTCTCA	600
	ACTGAAAAGA	GTTTTTCTG	ATATAAATGC	ATCCCAACAG	GATTATGATC	TCAGCATTTG	660
	GAATGGGCTT	TTTGCTGAAA	AAGTGTATGG	CTTTCATAAG	GACTACATTG	AGTGTGCCGA	720
15	AAAAATTATAC	GATGCCAAGG	TGGAGCGAGT	TGACTTTACG	AATCATTTAG	AAGACACTAG	780
	ACGTAAATAT	AATAAGTGGG	TTGAAAATGA	AACACATGGC	AAAATCAAGA	ACGTGATTGG	840
	TGAAGGTGGC	ATAAGCTCAT	CTGCTGTAAT	GGTGTGGTGG	AATGCTGTGT	ACTTCAAAGG	900
	CAAGTGGCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TGCCATTTC	AATCTCCCAA	960
	GTGCTCTGGG	AAGGCAGTCG	CCATGATGCA	TCAGGAACGG	AAGTTCAATT	TGCTGTATT	1020
20	TGAGGACCCA	TCAATGAAGA	TTCTTGAGCT	CAGATACAAT	GGTGGCATAA	ACATGTACGT	1080
	TCTGCTGCCT	GAGAAATGAC	TCTCTGAAAT	TGAAAACAAA	CTGACCTTTC	AGAATCTAAT	1140
	GGAAATGGAC	AATCCAAGGC	GAATGACCTC	TAAGTATGTT	GAGGTATTTT	TTCCCTCAGT	1200
	CAAGATAGAG	AAGAATTATG	AAATGAAACA	ATATTTGAGA	GCCCTAGGGC	TGAAAGATAT	1260
	CTTTGATGAA	TCGAAAGCAG	ATCTCTCTGG	GATTGCTTCG	GGGGGTCTGC	TGTATATATC	1320
25	AAGGATGATG	CACAAATCTT	ACATAGAGGT	CACGTAGGAG	GGCACCAGAG	CTACTGCTGC	1380
	CACAGGAAGT	AATATTGTAG	AAAAGCAACT	CCCTCAGTCC	ACGCTGTTTA	GAGCTGACCA	1440
	CCCATTCCTA	TTTGTTTATCA	GGAAGGATGA	CATCATCTTA	TTCACTGGCA	AAGTTTCTTG	1500
	CCCTTGAAAA	TCCAATTGCT	TTCTGTTATA	GCAGTCCCCA	CAACATCAAA	GRACCACCAC	1560
	AAGTCAATAG	ATYTGRTGTT	AATTGGAAAA	ATGTGGTGT	TCCTTTGAGT	TTATTTCTTC	1620
30	CTAACATTGG	GAGAAATGAC	ACACTGGTGA	CTTGACCTTC	CCTAGACACC	TGGTTGATTG	1680
	TCCTGATCCC	TGCTCTTAGC	ATTCTACCAC	CATGTGCTCT	ACCCATTCTT	AATTTCAATG	1740
	TCTTTCTTCC	CACGCTCATT	TCTATCATTC	TCCCCCATGA	CCCGTCTGGA	AATTATGGAG	1800
	RGTGCTCAAC	TGGTAAGGAG	AACCTAGAAG	TAGCCCTAGG	GATCCTTTTT	GAAACTCTAC	1860
	AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
35	CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TTGTTGACCT	ATGAAGATTT	TAGAGTTTAC	1980
	CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAAAAAATG	TGAAATTGGG	2040
	ATTAGGGACC	TACCAAAATA	TTTCATTAAT	GCITTCATTT	GACAAATTTT	GGCCTTTCTT	2100
	TGATAAGACA	ATATGTACAT	GTTTTTTCAA	ATATTAAGA	TCITTTAACT	GTGGCAGTT	2160
40	GTATCTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTTCC	TCTATTTATC	2220
	AGAATAAAGA	AATACAACAT	ACCTGTAAA				

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

45	1	11	21	31	41	51	
	MASLAAANAE	FCFNLFREMD	DNQNGNVFF	SSLSLPAALA	LVRIGAQDD	LSQIDKLLHV	60
	NTASGYGNSS	NSQSLQSQL	KRVFSDINAS	HKDYDLSIVN	GLFAEKVYGF	HKDYIECAEK	120
50	LYDAKVERVD	FTNHLEDTRR	NINKWVENET	HGKIKNVIGE	GGISSAVMV	LVNAVYFKGK	180
	WQSAFTKSET	INCHFKSPKC	SGKAVAMMHQ	ERKFNLSVIE	DPSMKILELR	YNGGINMYVL	240
	LPENDLSEIE	NKLTQNLME	WTNPRRMTSK	YVEVFPPQFK	IEKNYEMKQY	LRLGLKIDIF	300
	DESKADLSGI	ASGGRLYISR	MMHKSYLEVT	EEGTEATAAT	GSNIVEKQLP	QSTLPRADHP	360
	FLFVIRKDDI	ILFSGKVSCP					

55 Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

60	1	11	21	31	41	51	
	AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
	CTCTGGGTCC	TTAATGGCAG	CAGCCGCGCG	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
	GCTCCTGCTG	TCCGCTGGT	CCCGGGCTGG	GCGAGCCGAC	CCTCCTCTC	TTTGCTATGA	180
65	CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
	GGATGAAAAA	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCACAC	CTGTCACTCC	300
	CCTGGGGAAG	AACTAAATG	TCACAACGGC	CTGGAAAGCA	CAGAACCAG	TACTGAGAGA	360
	GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTCAG	CTGGAGAAAT	ACACACCCAA	420
	GGAACCCCTC	ACCCTGCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
70	TGGATCTTGG	CAGTTCAGTT	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
	AATGTGGACA	ACGGTTTATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
	GGTTGTGGCC	ATGCTCTTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
	CTTCTTGATG	GGCATGGACA	GCACCCTGGA	GCCAAGTGCA	GGAGCACCAC	TCGCCATGTC	720
	CTCAGGCACA	ACCCAATCA	GGGCCACAGC	CACCACCTCT	ATCCTTTGCT	GCCTCCTCAT	780
75	CATCTTCCCC	TGCTTCTATC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTGA	840
	AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
	CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
	TGAGCCCAAT	AGCTCATTTA	CTGCCCTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
	TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACTTAAAG	1080
80	TTCTGGCTGA	CTAAACAAGA	TATATCATTT	TCITTTCTCT	CTTTTGTGTT	GGAAAAATCAA	1140
	GTACTTCTTT	GAATGATGAT	CTCTTCTTGG	CAAAATGATAT	TGTCAGTAAA	ATAATCACGT	1200
	TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGCTCTGAAA	GAGAAATTTT	AAATTATTTA	1260
	ATAAGAAAAA	ATTTATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
85	TTTAAATAAA	GAGTTCATTT	TCCCAAAAAA	AAAAAATAAA	A		

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1

1 11 21 31 41 51
 | | | | | |
 MAAAAATKIL LCLPLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGGVDEKT 60
 FLHYDCGNKT VTPVSPGLGKK LNVTTAWKAQ NPVLREVVDI LTELRLDIQL ENYTPKEPLT 120
 5 LQARMSCEQK AEGHSSGSWQ FSPDGGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVM 180
 SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLLI LCCLLIILFC 240
 FILPGI

Seq ID NO: 266 DNA sequence
 Nucleic Acid Accession #: XM_084853.1
 Coding sequence: 127-444

1 11 21 31 41 51
 | | | | | |
 15 ATTGATGATA TATTTAACGA AATCAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC 60
 GACAAGATCA ACTTACCAGA TTTCTTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT 120
 AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCAAAGGG 180
 AAAAAGGCCA TTCGAAGAGA GGACTTCTCG AGACTGCTCG TTAATAAAGG TGAGCATATG 240
 ACGGAGGAGG AGATGTTGGA TTGCTTTGCT TCACTGTTTG GCCTGAATCC CGAGGGATGG 300
 20 AAATCCGAGC CTGCAACCTG CTCGTCAAA GGTTCAGAAA TTGCTTGA AGAAGAAGCTT 360
 CCAGACGAAA TCACTGCAGA AATATTCGCG ACTGAAATTC TTGGCTTAAC CATTTTCAGAA 420
 GATTCCGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACAA AGGACTTTGG 480
 GTGTGTGTGC ATGCACATGT GTGTGTTTC CATGAGGCAC TGCTTTTAT GCATTTCCCT 540
 25 CCCCCCTCTC ATCTTTAGAA CATTTAGACA TTAAAGCAAG TTTCTGGTGA GCAATG

Seq ID NO: 267 Protein sequence:
 Protein Accession #: XP_084853.1

1 11 21 31 41 51
 | | | | | |
 30 MSGIHKSFV LGYNSKGKK AIRREDLRL LVTKEHMT EEMLDCAFSL FGLNPEGWKS 60
 EPATCSVKGS BICLEELPD EITAEIPATE ILGLTISEDS GQDQG

Seq ID NO: 268 DNA sequence
 Nucleic Acid Accession #: NM_001898
 Coding sequence: 57-482

1 11 21 31 41 51
 | | | | | |
 40 GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCTCTGAG GAGACCATGG 60
 CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCTTGA 120
 GCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180
 AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
 45 ACTACTACAG ACGTCCGCTG CGGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
 ATTACTTCTT CGAGCTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG 360
 ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAAGAA ACAGTTGTGC TCTTTCGAGA 420
 TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
 AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCAC TCCACCCCTC TGTAAGTCTC 540
 50 CCACCCCTGG CTTGGTGCC CCCACCCTGC GGGAGGCCTC CCCATGTGCC TCGGCCAAGA 600
 GACAGACAGA GAAGGCTGCA GGAGTCTTT GTTGTCTCAG AGGGCGCTCT GCCCTCCCTC 660
 CTTCTTCTT GCTTCTAATA GCCCTGTGAC ATGGTACACA CCCCCCACC TCCTGCAATT 720
 AAACAGTAGC ATCGCC

Seq ID NO: 269 Protein sequence:
 Protein Accession #: NP_001889.1

1 11 21 31 41 51
 | | | | | |
 60 MAQYLSLTL LLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK 60
 DDYRRPLRV LRARQQTGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120
 EIYEVWENR RSLVKSRCQE S

Seq ID NO: 270 DNA sequence
 Nucleic Acid Accession #: XM_093210
 Coding sequence: 13-1854

1 11 21 31 41 51
 | | | | | |
 70 ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCACC 60
 AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAG 120
 GGCAGAGGGA ATGGGAGGG GGCATCCTAC CCCATATCTG AGGTGCGACT GCGGGACGTA 180
 GAGCGGACTG GGCTTTCCC GTTGGCGCGT GGCCTCAATC AGGACTTCTT GCCCAGCTGC 240
 75 GCCTTCAAAA CGTTAAGAGC TGAACCTGAA CGTGTGAGAC ATGGTGCAGA TAGGCTGAGA 300
 GCGCGCGGGA GAGATGCCCA TGAACCTAAG TACCCGAGCA CGCCCTCCAC TTCTACCACC 360
 ACGAGTAACA CCGCCCCCAG GGGACCGCTC TCGAGGTCCC CCAAGCCAAG GACGCAAGGA 420
 GGAACGCCCC GCGCGCGG CAGCAGCGGC GGGCACCAGC CCAATGGCCA CGGAACCTCAG 480
 CACTGGCAGT CGGCCCTCT CACACCGCAG GCGTGCAGTG TGGCCGACGG AGCCTCCCGG 540
 GCGGAGGACC CAGCTAGGCC GTCAACCCGG TTGCTCCAC GGAAGGGGCG ACCAGGCAAA 600
 80 CTGCCAAGG CCCGAGCCC AGGTCCCTG GCGGAGGCCT CCGCTGTTCC CGCCAGATC 660
 ATGGCCGCCA CCAGGCTCCC GAGCCATGGC TTCTGTCCG GGAACGGCCC GCGCTCCTGG 720
 CTGTCCAGCT AG

Seq ID NO: 271 Protein sequence:
 Protein Accession #: XP_093210

1 11 21 31 41 51

MLRHGEQKRK	RARKKWDFLP	TCAFKTVRAA	TERVRHGADR	LRGGGRDAHE	LKYPDTPSTS	60
TTTSNTAPTG	PLSRSPKPRP	QGGTPRRRPA	AAGTRANGHG	TQHWQSALLT	PQACSVADGA	120
SRAEDPARPS	PRLLPREGAP	GKLPKAPSPG	SLAEASAGLL	AHVRLQNADA	QRVSISQALP	180
PNSSVGRKEE	RPAGGQORRA	PAPMATELST	GSRPSSHRRR	AVWPTEPPGP	RTQLEPSPRL	240
LPREGAPGKL	PKAPSPGSLA	EASAGPAQIM	AATRLPSRGP	LSGNGPASWL	SS	

Seq ID NO: 272 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..732

1	11	21	31	41	51	
GGATACTGTG	TCACTCAAAG	TAATGGGAGG	GAGAGAGAAC	AGGGAGGGTA	GGGATGCTTT	60
TGAAAAAGCT	TTTTTCCCA	CTTTTAACTT	GCTTTAGCGT	TAAGAGTACT	TACCAGCTAA	120
TAATGTGGAG	GAAATATTTC	TTTCTCATTG	GAGATTACAG	AATATATCTA	TTTATCTTGA	180
ATACCCACTT	GAAGCCTCTG	TAGAAATGTC	TCGTCCTCCG	GTTGTATTTC	TAAACCTAC	240
ATGATTTTGT	CTGTCTTCTG	CAGTGAGAAA	TTACATCCAT	AGCAAAGACA	AAAGTCTTTT	300
TAAATTATTT	TTATTATCTT	TTCATATAGT	TCTTACAATT	TCTAAAAAAT	TAACTACTAT	360
TTAGTATCAC	AATTTATGCG	AGAGGGTTTT	TTGTATTTTT	AAGCATATGT	GGCTTATATA	420
AAAATTGCAG	AAGTCATAGG	ACTGTCATGT	ATTGCAGCTC	TGAGAACCAA	TGCCTGAAAC	480
TTAAGCC						

Seq ID NO: 273 Protein sequence:

Protein Accession #: Eos sequence

1	11	21	31	41	51
MGGRENREGR	DAFEKAFPT	FNLL			

Seq ID NO: 274 DNA sequence

Nucleic Acid Accession #: NM_003976.2

Coding sequence: 299-961

1	11	21	31	41	51	
CTCTGAGCTT	CTCTGAGCCT	TGTTTGCTCA	TCTGGAAAAA	GGGGATTAAA	CCATTTACCT	60
CATGGAGTTG	TGAAAGAATA	GCTGCAAAGC	ACCTAACACA	TAGTAAGGTT	CCCAGTGCAG	120
CTACTTCTGC	TGGGTGAGT	CTAGCTGTGT	AGGCCCTTGG	TTCCTCACCT	GGAGAACTG	180
GGGTGGCAGG	CCGGTCCCCC	ACAAAAGATA	ACTCATCTCT	TAATTTGCAA	GCTGCCTCAA	240
CAGGAGGGTG	GGGGAACAGC	TCAACAATGG	CTGATGGGCG	CTCCTGGTGT	TGATAGAGAT	300
GGAACTTGGA	CTTGGAGGCC	TCTCCACGCT	GTCCCACTGC	CCCTGGCCTA	GGCGGCAGCC	360
TGCCCTGTGG	CCCACTCTGG	CCGCTCTGGC	TCTGCTGAGC	AGCGTCGCAG	AGGCCTCCCT	420
GGGCTCCGG	CCCCGCAGCC	CTGCCCCCG	CGAAGGCCCC	CCGCTGTCC	TGGCGTCCCC	480
CGCCGGCCAC	CTGCCGGGG	GACGCACGGC	CCGCTGGTGC	AGTGAAGAG	CCCGGCGGCC	540
GGCGCGCAG	CCTTCTCGGC	CCGCGCCCC	GCCGCTGCA	CCCCCATCTG	CTCTTCCCCG	600
CGGGGGCCCG	GGGGCGCGGG	CTGGGGGCC	GGGCAAGCCG	GCTCGGGCAG	CGGGGGCGCG	660
GGGCTGCCGC	CTGCCCTCGC	AGCTGGTGCC	GGTGCGCGCG	CTCGGCCTGG	GCCACCGCTC	720
CGACGAGCTG	GTGCGTTTCC	GCTTCTGCAG	CGGCTCCTGC	CGCGCGCGCG	GCTCTCCACA	780
CGACCTCAGC	CTGGCCAGCC	TACTGGGCGC	CGGGGCCCTG	CGACCGCCCC	CGGGCTCCCC	840
GCCCGTCAGC	CAGCCCTGCT	GCCGACCCAC	GCGCTACGAA	GCGGTCTCCT	TCATGGACGT	900
CAACAGCACC	TGGAGAACC	TGGACCGCCT	CTCCGCCACC	GCCTGCGGCT	GCCTGGGCTG	960
AGGGCTCGCT	CCAGGGCTTT	GCAGACTGGA	CCCTTACCGG	TGGCTCTTCC	TGCTGGGAC	1020
CCTCCGCGAG	AGTCCCACTA	GCCAGCGGCC	TCAGCCAGGG	ACGAAGGCCT	CAAAGCTGAG	1080
AGGCCCTTAC	CGGTGGGTGA	TGGATATCAT	CCCCGAACAG	GTGAAGGGAC	AACTGACTAG	1140
CAGCCCCAGA	GCCCTCACCC	TGCGGATCCC	AGCCTAAAAG	ACACCAGAGA	CCTCAGCTAT	1200
GGAGCCCTTC	GGACCCACTT	CTCACAGACT	CTGGCACTGG	CCAGGCCTCG	AACCTGGGAC	1260
CCCTCCTCTG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCC	CCCGCCGAGG	CCCTGTAGGG	1320
ACAGCATTG	AAGGACACAT	ATTGCAGTTG	CTTGGTTGAA	AGTGCCTGTG	CTGGAAGTGG	1380
CCTGTACTCA	CTCATGGGAG	CTGGCCCC				

Seq ID NO: 275 Protein sequence:

Protein Accession #: NP_003967.1

1	11	21	31	41	51	
MELGLGGLST	LSHCPWPRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	60
PAGHLPGGRT	ARWCSGRARR	PPPQPSRPAP	PPPAPPSALP	RGGRAARAGG	PGSRARAAGA	120
RGCLRLSQLV	PVRALGLGHR	SDELVRFRFC	SGSRRRARS	HDLSLASLLG	AGALRPPPGS	180
RPVSQPCCRP	TRYEAVSFMD	VNSTWRTVDR	LSATACGLG			

Seq ID NO: 276 DNA sequence

Nucleic Acid Accession #: NM_057091.1

Coding sequence: 783-1445

1	11	21	31	41	51	
ACTGGCCGCT	GAGAGAAGAA	TGGGTGGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
GGACCCCAAA	ATCTGCACGT	ACCAAGAGTC	AGCCGCCCCA	CGCAGGGACC	GGCTTACCCC	120
TCGCTCCCCG	CCCTCACTCA	CTTCTCCCG	CCCTCGGCC	GGCTTCCAG	CTCTCTACTT	180
CGCGTGTCTA	CAAACTCAAC	TCCCGGTTTC	CGTGCCTCTC	CACGCTCGA	GTTCTCTACT	240
CTCCATATCC	GAGGGGCCCC	TCCAGCATC	TACCCCTCTC	CCAACCTCGG	GGGACCTAGC	300
CAAGCTAGGG	GGGACTGGAT	CCGACGGGTG	GAGCAGCCAG	GTGAGCCCGG	AAAGGTGGGG	360
CGGGGCAGGG	GCGTCTCCAG	CCCCACCCCG	GGATCTGGTG	ACGCTGGGGG	TGGAATTTGA	420
CACCGGACGG	CTGCGGCGGG	GGGACGAGGG	CTGCTGAGGG	ATGGAGTTGG	GCCCGGCCCC	480
CAGACAAGGC	CGGGGGGCTC	CGCCAGCAGC	AGTCCCTCTG	GGCCCCAGCC	CTCGTGCACA	540

5
 10
 15
 20
 25

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CCCGGGCCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
TAAAAGAGGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
GCCCCAGCACT GGTCCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGCTGCC 720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GCGCTCCTG GTGTTGATAG 780
AGATGGAAGT TGGACTTGGG GGCCTCTCCA CGCTGTCCCA CTGCCCCTGG CCTAGGCGGC 840
AGCCTGCCCT GTGGCCCACT CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
CCCTGGGCTC CGCGCCCCGC AGCCTTGCCC CCGCGAAGG CCCCCGCTT GTCCTGGCGT 960
CCCCGCGCGG CCACCTGCGG GGGGGACGCA CGGCCCGCTG GTGCAGTGGG AGAGCCCGGC 1020
GGCGCGCGCC GCAGCTTCTT CGGCCCGCGC CCGCGCGGCC TGCACCCCA TCTGCTCTTC 1080
CCCGCGGGGG CCGCGCGGCG CGGGCTGGGG GCGCGGGCAG CCGCGCTCGG GCAGCGGGGG 1140
CGCGGGGCTG CCGCTGCGCG TCGCAGCTGG TGCCGGTGGC CGCGCTCGGC CTGGGCCACC 1200
GCTCCGACGA GCTGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC 1260
CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CCGCGACCG CCCCCGGGCT 1320
CCCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
AGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCGCG CACCGCCTGC GGTGCTCTGG 1440
GCTGAGGGCT CGCTCCAGGG CTTTGACAGG TGGACCCCTA CCGGTGGCTC TTCCTGCCTG 1500
GGACCTTCCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCGGA ACAGGTGAAG GGACAACTGA 1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG 1680
CTATGGAGCC CTTGCGAGCC ACTTCTACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
AGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
CTGGCCTGTA CTCACTCATG GGAGCTGGCC CC
  
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Seq ID NO: 277 Protein sequence:
Protein Accession #: NP_003967.1

30
 35

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1 11 21 31 41 51
| | | | |
MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
RGCRRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRRASP HDLSLASLLG AGALRPPPGS 180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG
  
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Seq ID NO: 278 DNA sequence
Nucleic Acid Accession #: NM_057160.1
Coding sequence: 1-714

40
 45
 50
 55
 60

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1 11 21 31 41 51
| | | | |
ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCCTTC TCCCCAAGCC 60
CACTTGGGTG CCTCTTTTCT CCCTGAGGCT CCACTTGCTC TCTCCGCGCA GCCTGCCCTG 120
TGGCCCAACC TGCCCGCTCT GGCTCTGCTG AGCAGCGCTG CAGAGGCTCT CCTGGGCTCC 180
GCGCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCCGCTG TCCTGGCGTC CCCCCCGGC 240
CACTTGCCTG GGGGACGAC GGGCCGCTGG TGCAGTGGAA GAGCCCGCG GAGCCCGCG 300
CAGCTTCTCT GCGCCGCGCC CCGCGCGCTG GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
CGCGCGGCGC GGGCTGGGGG CCGGGGCGAG CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
CGCTTGCCTC CCGAGCTGCT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
CTGGTGGGTT TCGCTTCTG CAGCGGCTCC TGCCGCGCG CCGCTCTCC ACACGACCTC 540
AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCGCGGGCTC CCGGCCCGTC 600
AGCCAGCCCT CCGTCCGACC CACCGGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
ACCTGGAGAA CCGTGGACCG CTTCTCCGCC ACCGCTCGG GCTGCCTGGG CTGAGGGCTC 720
GCTCCAGGGC TTTGACAGT GGACCTTAC CGGTGGCTCT TCCTGCCTGG GACCTCCCG 780
CAGAGTCCCA CTGCGGAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC 840
TACCGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
AGAGCCCTCA CCTTGGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
TTGGAACCCA CTTCTCAGC ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCT 1020
CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCGCCC AGGCCCTGTA GGGACAGCAT 1080
TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140
TCACTCATGG GAGCTGGCCC C
  
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Seq ID NO: 279 Protein sequence:
Protein Accession #: NP_476501.1

65
 70

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1 11 21 31 41 51
| | | | |
MPGLISARGQ PLLEVLPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SVAEASLGS 60
APRSPAPREG PPPVLASAPG HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
RAARAGPGS RARAAGARGC RLRSQLVVPR ALGLGHRSD E LVRFRFCSGS CRRARSPHDL 180
SLASLLGAGA LRPPPSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG
  
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Seq ID NO: 280 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29-715

75
 80
 85

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1 11 21 31 41 51
| | | | |
CTGATGGGCG CTCTGGTGT TGATAGAGAT GGAACCTGGA CTTGGAGGCC TCTCCACGCT 60
GTCCCACTGC CCTTGGCCTA GCGCGCAGGC TCCACTTGGT CTCTCGCGC AGCCTGCCCT 120
GTGGCCCACT CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCGTGGGCTC 180
CGCGCCCGCG AGCCCTGCCC CCGCGAAGG CCCCCGCTT GTCTTGGCGT CCGCCGCGG 240
CCACTGCGG GGGGACGCA CGGCCGCTG GTGCAGTGGG AGAGCCCGGC GCGCGCGCC 300
GCAGCTTCTT CGGCCGCGC CCGCGCGGCC TGCACCCCA TCTGCTCTTC CCGCGGGGG 360
CGCGCGGGG CGGGCTGGGG GCGCGGCGAG CCGCGCTCGG GCAGCGGGGG CGCGGGGCTG 420
CGCGCTGCGC TGCAGCTGG TGCCGGTGGC CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
GCTGGTGGCT TTCCGCTTCT GCAGCGGCTC CTGCCGCGC GCGCGCTCTC CACACGACCT 540
CAGCTGGCC AGCCTACTGG GCGCGGGGCG CCGTGCAGCG CCGCGGGGCT CCGCGCGCGT 600
CAGCCAGCCC TGCTGCCGAC CACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG 660
  
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CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
 CGCTCCAGGG CTTTGCAGAC TGGACCCCTA CCGGTGGCTC TTCTGCCTG GGACCCCTCC 780
 GCAGAGTCCC ACTAGCCAGC GGCTCTAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGGCC 840
 CTACCGGTGG CTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
 CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
 CTTCGGACCC ACTTCTCAG GACTCTGGCA CTGGCCAGGC CTGAACTCTG GGACCCCTCC 1020
 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGA CTGGCCTGTA 1140
 CTCATCATG GGAGCTGGCC CC

Seq ID NO: 281 Protein sequence:
 Protein Accession #: NP_476431.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPFVLASPA GHLPGGRTAR WSGRRARRPP PQPSRPAPPP PAPPSPALPRG GRAARAGGPG 120
 SRARAAGARG CRLRSQLFVQ RALGLGHRSD ELVRFRFCSG SCRRARSPHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 282 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 CTACTGCACC TGCCCTCTGT TTCCTTTGGA AATCTCTTAC CTTCATTAG GGTTCCTTTC 60
 ATAGCAATTT CCTTTGGTTT TTAAGACTTC TACATTGCTT TTCTTTTAT TATCTGTGCT 120
 CCGTGAACCT TATGAATGCT GCTTAAAAAT AATGTCAAAA TATGTTTAT CTGCCTACTC 180
 AGGTAACGTT TTCTTTTGTG CTCATCTTGG TTTCCATATA CTATTTTGG TTTTGTGTA 240
 GCTCTAATCA ATGATCTAGT CAGAGCTAC TTCCTGGCT AACAGTGATC ATGTTCATGT 300
 GCTAAAAATG AACTTGAAC ACAGGAGTAG TGGTTGGTCC AGTTTGAAG CTCTTATTAG 360
 TATCTTTCAT CCTGGCTGTA ATAATAGCCA TTATTTGTTA TGCTTTTGT ATGTAGCAGA 420
 CACTCTTAAG GATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA 480
 GAATCTCAGG ATACCTACAT TTATCACTTT TCAATATAT ATGTATTCT TATT

Seq ID NO: 283 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 564-1481

1 11 21 31 41 51
 GAGACTTTTA ATCATCTATC CCTTGTGCTT TACGCAGACC CTACAATACA CTAGAGGCTT 60
 CAAAGAGGTC AAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAGATG CCAGGCAAAAC 120
 GAAGTGCTAC CAAAACACGC AATGACTGTC CTAAGAGTGC GTTCTGGGAT ACACCTGTAA 180
 ACTTGATACA AGTTCCCTCC CCTCTCCTCA AAATATATCG ACTTGTGCTG AAAGAAATCA 240
 CGACCGATGC TCACAATTC GACCTCGTAA TTATATAGGG GGTGGTTTGT GTTCTGCGT 300
 CTTTCCCTGA TTCAGTGGCA GGTAAATAT TTCTGTGACA AAATGAACTG CAACACCACG 360
 GCAACAAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAAGTGGCGT 420
 GGGGAGACAC GGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCTGCC ACTGAGGAGG 480
 AAGGGCTGGC TAAGGGAGGC CGGGGCGGAG GAAGCCAAGC TCTGCAGGCC CTGACAAAGT 540
 CTCCCGGCC TCCACGCGTC GCCATGGCAA CGCGGGGTCT GTGCTGGCCG GGATTTGGCCG 600
 GCCTGGCGCG GCGACGTGGC GCTGGGAAAG CGCGTCCCG CGCGGCTCC GCCAGTTTGA 660
 ACTTGGCGGG CCAGATGTGG GCGGCGGGGC GCTGGGGGCC TACTTTTCCC TCTTCTACG 720
 CCGGTTTCTC TGCTGACTGC AGACCCAGGT CTCGGCCCTC CTGCGACTCC TGCTCAGTCC 780
 CTATGACGGG GCGACGTGGG CAGGGGCTGG AGGTGGTGGC CTCGCGTCC CCGCGCTGC 840
 CGCTGAGCTG CAGCAATTCC ACCAGGTGCG TGTGTGCTCC CCTTGGCCAC CAGAGCTTCC 900
 AGTTTGACGA GGACGACGGT GACGGGGAGG ATGAGGAAGA CGTGGATGAT GAGGAAGACG 960
 TGGATGAAGA GCTGCAATGAT TCAGAGGCCA AAGTGGCGAG CCTGAGAGGA ATGGAGTTAC 1020
 AGGGGTGCGC CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC 1080
 GCTTACCAGA AAGCCGCTCG ACACCATGGG AGGTGTGGTT TATTTGCAAA GAAAAAGAAG 1140
 AACGTGACCG GCTGCACTAG AAAGCTCTAG AGGAATTAAA TCAACAACTA GAAAAAGAA 1200
 AAGAAATGGA AGAAGCTGAA AAAAGAAAGA TAATTGCTGA AGAAAAGCAC AAGGAATGGG 1260
 TTCAGAAAAA GAATGAGCAA AAAAGAAAG AAAGAGACAA AAAAATTAAT AAAGAAATGG 1320
 AGGAAAAAGC AGCAAGAGAA CTGGAGAAAG AATACTTGCA AGAAAAAGCA AAAGAAAAAT 1380
 ATCAAGAATG GTTAAAGAAA AAAATGCTG AAGAATGTGA GAGGAAGAAG AAAGAAAAAG 1440
 AAAACAACAG CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAAA AGTTTCAAGA 1500
 ATGGTTGAAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA 1560
 TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACGAGCCT TTTATAATCC 1620
 AATTCCGTGG AAACCAATTC ATATGCCACC TCCCAAAGAA GCTAAGGATC TATCAGGAAG 1680
 GAAGAGTAAA AGDVCCTGTG TAAGTCAGCC ACACAAGTCA TCATCTCTGG TAATTCATAA 1740
 AGCCAGGAGC AATCTTTGCC TTGGAATCT GTGCAGAATA CAAGATAGC GTATGTGGAA 1800
 AATAACATGC TTTTATCTGG AGCTATTTAA TTTAAAAATC AGAAATTTGT TTTTACTGCT 1860
 CAGTCAATAA CTCACACTGT AATGTGATTA TTGACAAATA GCAATTTTGT CATTTGTATA 1920
 TGGAGTCTCT AGAGTTGAGG AAGATATTTT CTGGATTTTG GTTTTTATAA ACTTTTAAAG 1980
 GTTGATCTTG GCATGTTGTT TTGCAGAAATA AGTGGCTGAA TATGTAAGAA TTGTGTTTGT 2040
 ATTTAGCTTG TATTAAAAAGT AACTGTAAAT ACCAATAAAA CTAACAAATT TTCTTG

Seq ID NO: 284 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MATRGLCWPG LAGLARAGPA GKARPRRGS SLNLAGQMW AGRWGPFFPS SYAGFSADCR 60
 PRSRPSSDSC SVPMTGARQ GLEVVRSPP PLPLSCSNST RSLLSPLGHQ SFQFDEDDGD 120
 GEDEEDVDE EDVDEDAHDS EAKVASLRGM ELQGCSTQV ESENNQEEQ QVRLPESRLT 180
 PWEVWFIGKE KEERDRLQLE ALEELNQLE KRKEMEEREK RKI IAEKHK ENVQKQNEQK 240
 RKEREQKINK EMEERAAKEL EKEYLQEKAK EKYQEWLKKK NAECEKRRK EKNNSKLY 300

RRRRK

Seq ID NO: 285 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1-1746

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	1	11	21	31	41	51	
10	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCACC	120
	GGGGCACGCA	TGTGTGGCGT	GCCCAACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTCC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTCT	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
15	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGCT	GTTGCAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
20	GTCTCTCGGC	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACCTT	TGATGGGCTT	660
	GTTAACTGCG	AGGAACTGGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCAGCTG	780
	CCACCAGCA	TCTTCAATGA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
25	TATGACAACC	ACATCTCTTC	TCTACCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGATTTC	TAGCCGCGAA	TCAGATCAGC	TTCATCTCCC	CGGGTGCCTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACCTG	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCATGT	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCGAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAAACAG	1200
30	CTGGAGAATC	TGCCCTCTCG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	CGCTGCGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
	AACCAACGTA	GGTTAGGGAG	GGACACTGTA	CCTGTGTGTT	TCAGCCAGC	CAATGTCCGA	1380
	GGCCAGTCCC	CAATTCTCAT	CAATGTCAAC	GTGTCTGTTC	CAAGCGTCCA	TGTCCGTGAG	1440
	GTGCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
35	TCGCTCTCTT	CTACCACTGA	GCTAACCCAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTCAAGTCA	GCAAGTACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
	ATTGCCGCCA	TTGTAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGC	1680
	TGTTGCTGCT	GCAAGAAGAG	GAGCCAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAAGCTGGA	CAGGGCTGG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
40	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCCTAC	CTCTTCTCTG	CTTGCTGTAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTTCTCTACA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCOGA	TTCATACCCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTCTCA	AATCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTCGG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
45	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	CGCCCTCTCG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTGTGTTCT	CTTGTGTTGT	CTATGGCTTG	2220
	ACCCAGCATG	TCCCCTCAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGTCTCT	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAGTGA	GACTTCAAA	CATTTAAGTG	GTTTCTTAAG	AGCCCTCAAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAGAG	AGAAGGAAA	TCATGCCGCT	CAGTTCTCTG	2400
50	AGACAGAAGA	GCCGTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAGAAAAAC	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACTTTGCTT	2520
	TGAAAAGTTT	AGCCCTTTAA	GGAATGAAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
	AAAAATCAGT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCCTGGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTGTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGATC	GTGAGAAAA	2700
55	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCTGGGCT	TTTTCCCGAG	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGA	GCCAGGACGG	2880
	TCCCCCACA	GTCAGCTGT	GCAAAGGCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCTGAA	CAGGAGATT	TATTATATCT	GGAGACCTCG	3000
60	AGAGACCTCG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCCTC	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
	TCGCCCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTTAATT	TTCAATCTTC	3180
	ACTTAGGGGA	AGTGAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAACG	AAGTGTAACG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTCTGG	3360
65	GTCTGGGGGC	TCCCTGGAGC	TCCTCCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCCAGGGTTA	TTCTCCTCCT	CGAGTCACAG	TCACAGCAAT	ACCTGCCTTC	TCTGGCTTTC	3480
	GCTGTATACA	CATATTCACA	TGGCGCTCAA	GAAAGTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	CTGCCCCAGT	TTACAGTGAA	ATGGAGAAAT	TCAGGTCTCC	ACGTCTGCC	3600
70	AGGAAAGAAC	TTCAAGTGAC	TCCACGGGGA	TCTGGAAATC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TCGGCTCTTA	TTAGTCTCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCAACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGC	TGCTGACCAC	TTTTCCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
75	TGTTTGCAAA	CACATGTGCA	CTTTGTAGCT	TTTCCACCTC	TGTCCAGGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCATTTCCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCGCT	GATGGTGGCC	TGCTGTGCCT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGCCAC	AGACCTGTCT	4200
80	GGTGCTCCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCCTTA	4320
	GGTATTCCTG	GCAAGTAGCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCACT	GTCTCAGAT	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
85	GCCTCTTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCTTTTC	CAACAGGATG	ATGCATTGTC	TCAATCTCTA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAAGTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740

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 5 GGTGTTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
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 10 AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTTGGAAA 5280
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 15 CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTCTCACC AACCCGCTGC 5580
 CTTCATGCTG CTTTCAAAGC TAGATCATGT TTGCCTTGCT TAGAGAATTA CTGCAAATCA 5640
 GCGCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCCC TCAGGGTTTT GTAGAGTGTG 5700
 AGCCCTGGTG GGCAGGGTTG GGGGGTCTGT CTCTGCTGAG ATGCTGCTTG TAATCCATT 5760
 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 286 Protein sequence:
 Protein Accession #: NP_570843.1

1 11 21 31 41 51
 25 MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL 120
 FQGLDSLESL LLSSNQQLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFD HLVGLTKLNL 180
 GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQ NQIGLLSPGL 240
 30 PFNNHNLRL YLSNNHISGL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL 300
 YDNHISSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGDNV 360
 FRMLANLQNI SLQNNRLRLQ PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCLELRL 420
 YDNPWRCDSI ILPLRNWLLL NQPRLGTDIV PFCFSPANVR QSLIIINVN VAVPSVHVPE 480
 VPSYPETPWY PDTSPYPTDT SVSSTELTS PVEDYTDLT IQVTDDRSVW GMTQAQSGLA 540
 35 IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C

Seq ID NO: 287 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 1..954

1 11 21 31 41 51
 40 ATGTCTTCTG AGCAGAAGAG TCAGCACTGC AAGCCTGAGG AAGGCGTGA GGCCCAAGAA 60
 GAGGCCCTGG GCCTGGTGGG TGCACAGGCT CCTACTACTG AGGAGCAGGA GGCTGCTGTC 120
 TCCTCTCTCT CTCCTCTGGT CCCTGGCACC CTGGAGGAAG TGCCTGCTGC TGAGTCAGCA 180
 45 GGTCTCTCCC AGAGTCTCTA GGGAGCCTCT GCCTTACCCA CTACCATCAG CTTCACTTGC 240
 TGGAGGCAAC CCAATGAGGG TTCCAGCAGC CAAGAAGAGG AGGGGCCAAG CACCTGCGCT 300
 GACGCAGAGT CTTTGTTCGG AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT 360
 CTGCTCCGCA AGTATCGAGC CAAGGAGCTG GTCACAAAGG CAGAAATGCT GGAGAGAGTC 420
 50 ATCAAAATTT ACAAGCGCTG CTTTCTGTG ATCTTCGCA AAGCCTCCGA GTCCCTGAAG 480
 ATGATCTTTG GCAATTGAGT GAAGGAAGTG GACCCCGCCA GCAACACCTA CACCCTTGTC 540
 ACCTGCTGGG GCCTTTCCTA TGATGGCCTG CTGGGTAATA ATCAGATCTT TCCCAAGACA 600
 GGCTTCTGA TAATCGTCTT GGGCACAAAT GCAATGGAGG GCGACAGCGC CTCTGAGGAG 660
 GAAATCTGGG AGGAGCTGGG TGTGATGGGG GTGTATGATG GGAGGGAGCA CACTGTCTAT 720
 55 GGGGAGCCCA GGAACTGTCT CACCAAGAT TGGGTGCAGG AAAACTACCT GGAGTACCGG 780
 CAGGTACCGG GCAGTAATCC TGCAGCTGAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT 840
 GAAACCAAGT ATGTGAAGAT CCTGGAGCAT GTGGTCAGGG TCAATGCAAG AGTTGCAATT 900
 GCCTACCCAT CCCTGCGTGA AGCAGCTTTG TTAGAGGAGG AAGAGGGAGT CTGA

Seq ID NO: 288 Protein sequence:
 Protein Accession #: NP_002353.1

1 11 21 31 41 51
 65 MSSEQKSQHC KPEEGVEAQE EALGLVGAQA PTTEEQEAHV SSSSPLVPGT LEEVPAESA 60
 GPPQSPQAS ALPTTISFTC WRQPNEGSSS QEEEGPTSP DAESLFREAL SNKVDELAHF 120
 LLRKRYAKEL VTKAEMLERV IKNYKRCPPV IFGKASESLK MIFGIDVKEV DPASNTYTLV 180
 TCLGLSYDGL LGNNQIFPKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY 240
 70 GEPRKLLTQD WQENYLEYR QVPGSNPARY EFLWGPRALA ETSYVKVLEH VVRVNAVRI 300
 AYPSSLREAA LEEEBGV

Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 46..1344

1 11 21 31 41 51
 80 CGGCGGCCGC GCCCTGGTTG GGTCCCCACT GCTCTCGGGG GCGCCATGGA CGAGGCCGTG 60
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 CATCAGCGCG GCAGCAGCAC TGCAAGAAA GAAGACATAA ACCTGAGTGT TAGAAGCTA 180
 CTCAACAGAG ATAATATTGT GTTTGGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT 240
 85 TTGACCAGAA ATGTGCAGTC TGTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA 300
 CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACCTTACA TTTTCCAGCT GAATGAAGAT 360
 GGCCCCAGCA GTGAAAATCT GGAGGAAGAG ACAGAAAACA TAATTGCAGC AAATCACTGG 420
 GTTCTACCTG CAGCTGAATT CCATGGGCTT TGGGACAGCT TGGTATACGA TGTGGGAAGT 480
 AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTGACACAA GAACGTCAAC 540

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AGCAACCTCA TCACCTGGAA CCGGGTGGTG CTGCTCCACG GTCCTCCTGG CACTGGAAAA 600
ACATCCCTGT GTAAAGCCTT AGCCCAAGAA TTGACAATTA GACTTTCAAG CAGGTACCGA 660
TATGGCCAAT TAAATTGAAT AAACAGCCAC AGCCTCTTTT CTAAGTGGTT TTCGAAAAGT 720
GGCAAGCTGG TAACCAAGAT GTTTCAGAAG ATTCAGGATT TGATTGATGA TAAAGACGCC 780
CTGGTGTTCG TGCTGATTGA TGAGGTGGAG AGTCTCACAG CCGCCCGAAA TGCCCTGCAG 840
GCGGGCACCG AGCCATCAGA TGCCATCCGC GTGGTCAATG CTGTCTTGAC CCAAAATTGAT 900
CAGATTAATA GGCATTCCAA TGTGTGTGATT CTGACCACTT CTAACATCAC CGAGAAGATC 960
GACGTGGCCT TCGTGGACAG GGCTGACATC AAGCAGTACA TTGGGCCACC CTCTGCAGCA 1020
GCCATCTTCA AAATCTACCT CTCTGTGTTG GAAGAATGA TGAAGTGTCA GATCATATAC 1080
CCTCGCCAGC AGCTGCTGAC CCTCCGAGAG CTAGAGATGA TTGGCTTCAT TGAAAAACAC 1140
GTGTCAAAAT TGAGCCTTCT TTTGAATGAC ATTTCAAGGA AGAGCGAGGG CCTCAGCGGC 1200
CGGGTCTCTG AAAAACTCCC CTTTCTGGCT CATGCGCTGT ATGTCCAGGC CCCCACCGTC 1260
ACCATAGAGG GGTTCCTCCA GGCCCTGTCT CTGGCAGTGG ACAAGCAGTT TGAAGAGAGA 1320
AAGAAGCTTG CAGCTTACAT CTGATCCTGG GCTTCCCAT CTGGTGTCTT TCCCATGGAG 1380
AACACACAAC CAGTAAGTGA GGTTCGCCCA CACAGCCGTC TCCCAGGGAA TCCCTTCTGC 1440
AAACCAAGCG TTACTTAGAC TGCAAGCTAG AAAGCCACCA AGGCCAGGCT TTGTAAAAAG 1500
AAGTGTATTG TATTGTATTG GTTTTAAAT GCATACTGAG AGACAAACAT CTTGTCAATT 1560
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TTGCTTTCTG ATATCAGCTC GTTTGATTGA GTGCAAAAT GTTTTCAAGA CTATTTAATG 1860
GATGTAAAAA AGCCTATTTC TACATTATAC CAACTGAGAA AAAAAATGTC GGTAAGTGT 1920
TCTTTCATAA TAAATAATCA AGACATGGTC CCATTTGCAG GAAAAGTGCA GACTCTGAGT 1980
GTTCACAGGA AACACATCGT GGACATCCCT TGTAAACCGG TATGGGCGCC CCTGCATTGC 2040
TGGGATGTTT TGCCCAACGG TTTTGTGTTG GCAATAACGT TATCACATT CTAATGAGGA 2100
TTCACATTAA TATAATATAA AATAAATAGG TCAGTTACTG GTCTCTTCTC GCCGAATGTT 2160
ATGTTTGTCT TTTATCTCAC AGTAAATATA ATATAATTAA AAA

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Seq ID NO: 290 Protein sequence:

Protein Accession #: NP_004228

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1 11 21 31 41 51
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AANHWWLPAA EFHGLWDSLIV YDVEVKSHLL DYVMTTLFS DKNVNSNLIT WNRVLLHGP 180
PGTGTSLCKL TAGAGCTTCT TTTGAATGAC ATTTCAAGGA AGAGCGAGGG CCTCAGCGGC 240
DDKDALVFVL IDEVESLTAA RNACRAGTEP SDAIRVNAV LTQIDQIKRH SNVILITTSN 300
ITEKIDVAVF DRADIKQYIG PPSAAAIKFI YLSCLEELMK CQIIYPRQQL LTLRELEMIG 360
FIENNVSKLS LLLNISRKS EGLSGRVLRL LPFLAHLALYV QAPVTVTIEGF LQALSIAVDK 420
QFEERKKLAA YI

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Seq ID NO: 291 DNA sequence

Nucleic Acid Accession #: NM_002658.1

Coding sequence: 77-1372

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1 11 21 31 41 51
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GAGCGACTCC AAAGGCAGCA ATGAACCTCA TCAAGTTCCA TCGAAGCTGT ACTGTCTAAA 180
TGGAGGAACA TGTGTCTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA 240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
CTCTGCCACT TCTCCTCAGC AAACGTACCA TGCCCAAGA TCTGATGCTC TTCAGCTGGG 420
CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCCT GGTGCTATGT 480
GCAGGTGGGC CTAAAGCCCG TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
AAAGCCCTCC TCTCCTCAGC AAGAATTAAA ATTTCAAGT GTGCCAAAAGA CTCTGAGGCC 600
CCGCTTTAAG ATTATTGGGG GAGAATTCAC CACCATCGAG AACCAGCCCT GGTTCGCGC 660
CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
CCCTGTCTGG TGAATCAGG CCACACACTG CTTCAATTGAT TACCCAAGA AGGAGGACTA 780
CATCGTCTAC CTGGGTCGCT CAAGGCTTAA CTCCAACACG CAAGGGGAGA TGAAGTTTGA 840
GGTGGAAAAC CTCATCCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
CATTGCCTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCGGAATAT 960
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CACTGGCTTT GGAAAAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAAATGAC 1080
TGTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
CACCACCAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200
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CTGGGGCCGT GAGATGTGCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
CTTACCCTGG ATCCGCGAGC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
AGGGAGGAAA CGGGCACCAC CCGCTTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
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CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCAGGAT AGGCCTGGGT GCTGGCTGCC 1560
CAGACCTCTT GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620
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ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTGG 1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCTCT 1980
AAACTGTGTG CAGCTGTGATG CACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC 2040
CTGGGGCCTC TTGGGTCCCC CACGTGACAG TGCCTGGGAA TGTACTTATT CTGCAGCATG 2100
ACCTGTGACG AGCATGTGCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
ATCCCTTCCT TTTAGCTTAC TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCCT 2220
ACACTGAATA TTTATATTTC ACTATTTTAA TTTATATTTT TGTAATTTTA AATAAAAGTG 2280

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ATCAATAAAA TGTGATTTT CTGA

Seq ID NO: 292 Protein sequence:
Protein Accession #: NP_002649.1

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HCEIDKSKTC YEGNGHFYRG KASTDTMGRP CLPWSNATVL QQTYHAHRSD ALQLGLGKHN 120
YCRNPDNRRR PWCYVQVGLK PLVQECMVHD CADGKPKSSP PEELKFQCGQ KTLRPRFKII 180
GGFEFTIENQ PWFPAIYRRH RGGSVTVYCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240
RSRLNSNTQG EMKFEEVENLI LHKDYSADTL AHNNDIALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVVKLI SHRECCQPHY YGSEVITKML 360
CAADPQWKTD SCQGDSSGGL VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHFLPWIR 420
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Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_001498
Coding sequence: 93..2006

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TGAGCTGGGA GGAACCAAG CGCCATGCCG ACCACGTGCG GCGGCACGGG ATCTCCAGT 180
TCCTGCACAT CTACCACGCC GTCAAGGACC GGCACAAGGA CGTTCTCAAG TGGGGCGATG 240
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CTGGGGAGAA AGTTCTTGAA ACTCTGCAAG AGAAGGGGGA AAGGACAAAC CCAAACCATC 360
CTACCCTTTG GAGACCAGAG TATGGGAGTT ACATGATTGA AGGGACACCA GGACAGCCCT 420
ACGGAGGAAC AATGTCCGAG TTCAATACAG TTGAGGCCAA CATGCGAAAA CGCCGGAAGG 480
AGGCTACTTC TATATTAGAA GAAAATCAGG CTCTTTGCAC AATAACTTCA TTTCAGAT 540
TAGGCTGTCC TGGGTTTACA CTGCCCGAGG TCAAACCCAA CCCAGTGGAA GGAGGAGCTT 600
CCAAGTCCCT CTCTTTTCCA GATGAAGCAA TAAACAAGCA CCCTCGCTTC AGTACCTTAA 660
CAAGAAATAT CCGACATAGG AGAGGAGAAA AGGTTGTGAT CAATGTACCA ATATTTAAGG 720
ACAAGAATAC ACCATCTCCA TTTATAGAAA CATTTACTGA GGATGATGAA GCTTCAAGGG 780
CTTCTAAGCC GGATCATATT TACATGGATG CCATGGGATT TGGAAATGGG AATTGCTGTC 840
TCCAGGTGAC ATCTGAGCCA TGCAGTATAT CTGAGGCCAG ATACCTTTAT GATCAGTTGG 900
CTACTATCTG TCCAATTGTT ATGGCTTTGA GTGCTGCATC TCCCTTTTAC CGAGGCTATG 960
TGTCACAGAT TGATTGTCCG TGGGGAGTGA TTTCTGCATC TGTAGATGAT AGAACTCGGG 1020
AGGAGCGAGG ACTGAGGACA TGAAGAACA ATAACATAGG GATCAGTAAA TCCCGATATG 1080
ACTCAATAGA CAGCTATTTA TCTAAGTGTG GTGAGAAATA TAATGACATC GACTTGACGA 1140
TAGATAAAGA GATCTACGAA CAGCTGTGTC AGGAAGGCAT TGATCATCTC CTGGCCCGAGC 1200
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GAAGTAAAC TGACTCATCC AACTAGACAT TCTACAGAAA GAAAAATGCA TTATTGACGA 2040
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CAACCTACTG TCTAAGCACT TTTGTAATG TACTGGTAAT TGTACAATAC TTGCATTCCA 2340
GAGTTAAAT GTTTACTGTA AATTTTGTG CTTTAAAGA CTACCTGGGA CTTGATTTAT 2400
TGAAATTTT CTCTTAAAA ACATTTCTC TCGTTAATTT TCTTTGTGCA TTCTCTTTGT 2460
TGTCTACATT AAATCACTTG AATCCATTGA AAGTGCTTCA AGGGAATCT TGGGTTTCTA 2520
GCACCTTATC TATGATGTTT CTTTGTCAAT TGGAAATATC ACTTGGTCAC CTTGCCCCAA 2580
GCTTTCCCT CTGAATAAAT ACCCATTGAA CTCTGAAAAA AAAAAAAA AAAA

```

Seq ID NO: 294 Protein sequence:
Protein Accession #: NP_001489

```

1      11      21      31      41      51
|      |      |      |      |      |
MGLLSQGSPL SWEETKRHAD HVRRHGILQF LHIYHAVKDR HKDVLKWGDE VEYMLVSFDH 60
ENKKVRLVLS GEKVLETQGE KGERTNPNHP TLWRPEYGSY MIEGTPGQPY GGTMEFNTV 120
EANMRKRKE ATSSILEENQA LCTITSFPRL GCPGFTLPEV KPNPVEGGAS KSLFFDEAI 180
NKHPRFSTLT RNIRHRRGK VVINVPFKD KNTPSPIET FTEDDEASRA SKPDHIYMDA 240
MGFGMGNCLL QVTFQACSS EARLYDQLA TICPIVMALS AASPFYRGYV SDIDCRWGI 300
SASVDDRTRE ERGLEPLKNN NYRISKSRD SIDSYSKCG EKYNDIDLT DKEIYBQLLQ 360
EGIDHLLAQH VAHLFIRDPL TLFEEKIHL DANESDHFN IQSTNQWQTM FKPPPPNSDI 420
GWRVEFRPME VQLTDFENSA YVVFVLLTR VILSYKLDFL IPLSKVDENM KVAQRDAVL 480
QGMFYPRKDI CKGGNAVVDG CGKAQNSTEL AAEYTLMSI DTIINGKEGV FPGLIPILNS 540
YLENMEVDVD TRCSILNLYK LIKKRASGEL MTVARWMREF IANHPDYKQD SVITDEMNY 600
LILKCNQIAN ELCECEPELLG SAFRKVKYSG SKTDSSN

```

Seq ID NO: 295 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 247-816

5
1 11 21 31 41 51
| | | | |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCAGGTGC 120
10 CCTAGGGGGC ACATTTCCTCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
15 ATGACAGGAC ATGCTATTCC ACCAGCCAA TTGGATTCTC AGATTGATGA CTTCAGTGGT 480
TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCAAAAGC 600
CAACGAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
20 AAGCACCTTA AGAAGAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
CACACCCCAA ATGCATAATC TCGTTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAAAATAGC 960
CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTC TTTTCCCAA AGCATTTTAT 1020
25 TTGAAGGAT AACTTGTGTT TTGTTTATT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

Seq ID NO: 296 Protein sequence:

Protein Accession #: Eos sequence

30 1 11 21 31 41 51
| | | | |
MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
GHAIPPSQLD SQIDDFTFGS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQR 120
35 EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDFVKH 180
LKKKLKRLMI

Seq ID NO: 297 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 247-815

40 1 11 21 31 41 51
| | | | |
45 AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCAGGTGC 120
CCTAGGGGGC ACATTTCCTCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
50 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
ATGACAGGAC ATGCTATTCC ACCAGCCAA TTGGATTCTC AGATTGATGA CTTCAGTGGT 480
TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCAAAAGC 600
CAACAAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
55 CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
AAGCACCTTA AGAAGAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
CACACCCCAA ATGCATAATC TCATTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAACTGGC 960
60 CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTC TTTTCCCAA AGCGTTTAT 1020
TTGAAGGAT AACTTGTGTT TTGTTTATT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

Seq ID NO: 298 Protein sequence:

Protein Accession #: Eos sequence

65 1 11 21 31 41 51
| | | | |
70 MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
GHAIPPSQLD SQIDDFTFGS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDFVKH 180
LKKKLKRLMI

Seq ID NO: 299 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 247-815

75 1 11 21 31 41 51
| | | | |
80 AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCAGGTGC 120
CCTAGGGGGC ACATTTCCTCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
85 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCAGTGGT 480

TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC 600
 AACAAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TCGTGTGGAC 660
 AAAAAATATGA AAAAAATCTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
 ACACCCCAAA TGCATAATCT CATTAAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCAGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAAA GCGTTTTATT 1020
 TGAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 300 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKAKKLMT 60
 GHAIPPSQLD SQIDDPFGFS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
 EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIEKAA RCMRRDPVKH 180
 LKKKLKRLMI

Seq ID NO: 301 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 247-812

1 11 21 31 41 51
 | | | | |
 AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
 GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCAGGTGC 120
 CCTAGGGGGC ACATTTCCCA CAACCTCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
 GGGAGGGGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCACTGGTT 480
 TCAGCAAAGA TGGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA 540
 CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAAGCC 600
 AACAAGAAAT TAATGCTGAT ATAAAATGTC AAGTAGTGAA GGAAATCCGA TGCCCTGGAC 660
 AATATGAAA AATCTTCGAA ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC 720
 GATTTTITGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGACGAGAC TTTGTTAAGC 780
 ACCTTAAGAA GAAACTGAAA CGTATGATTT GAGAACTACT GTCCCTGGAG GATTATCACA 840
 CCCCAAATGC ATAATCTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT GCTGTTTCT 900
 ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC 960
 CAGAGGCTAA GAAATTTCTG TTAGTAAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTTGA 1020
 AAGGATAACT TGTGTTTGG TTATTTTGTA TTCCACCTG TGCTGCTAGA TATTATTAAAC 1080
 CCATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA

Seq ID NO: 302 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKLM 60
 GHAIPPSQLD SQIDDPFGFS KDRMMQKPGS NAPVGGNVTS NFSGDDLECR GIASSPKSQ 120
 EINADIKQV VKEIRCLGQY EKIFEMLEGV QGPTAVRKR FESIIEKAA RCMRRDPVKHL 180
 KKKLKRMI

Seq ID NO: 303 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 247-815

1 11 21 31 41 51
 | | | | |
 AGTGTTCGGC TGGGACAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTTCC ATCCCCCTTG 60
 GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCCA TGCACATCAC TCCAGATGC 120
 CCTAGGGGGC ACATTTCCCA CAACCTCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
 GGGAGGGGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCACTGGTT 480
 TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC 600
 AACAAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TCGTGTGGAC 660
 AAAAAATATGA AAAAAATCTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
 ACACCCCAAA TGCATAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCAGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAAA GCGTTTTATT 1020
 TGAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 304 Protein sequence:
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MTDKTEKVVAV	DPETVFKRPR	ECDSFSYQKR	QRMALLARKQ	GAGDSLIAGS	AMSKAKKLMT	60
GHAIPPSQLD	SQIDDFTFGS	KDRMMQKPGS	NAPVGGNVTS	SFSGDDLECR	ETASSPKSQQ	120
5	ENADIKRKL	VKELRCVGQK	YEKIFEMLEG	VQGPATAVRKR	FFESIIEKAA	180
	LKKKLKRLMI					

Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 87-689

1	11	21	31	41	51	
CGTGGAGGCA	GCTAGCGCGA	GGCTGGGGAG	CGCTGAGCCG	CGCGTCGTGC	CCTGCGCTGC	60
15	CCAGACTAGC	GAACAATACA	GTCAGGATGG	CTAAAGGTGA	CCCCAAGAAA	120
	AGATGTCCCG	TTATGCCCTC	TTTGTGCAGA	CATGCAGAGA	AGAACATAAG	180
	CAGAGGTCCC	TGTCATATTT	GCGGAATTTT	CCAAGAAAGT	CTCTGAGAGG	240
	TGTCCGGGAA	AGAGAAATCT	AAATTTGATG	AAATGGCAAA	GGCAGATAAA	300
	ATCGGGAAT	GAAGGATTAT	GGACCAGCTA	AGGGAGGCAA	GAAGAAGAAG	360
20	ATCCCAAAAG	GCCACCGTCT	GGATTCTTCC	TGTTCTGTTC	AGAATTCCGC	420
	AAATCCACAA	CCCCGCGATC	TCTATTGGAG	ACGTGGCAAA	AAAGCTGGGT	480
	ATAATTTAAA	TGACAGTGAA	AAGCAGCCTT	ACATCACTAA	GGCGGCAAG	540
	AGTATGAGAA	AGTATGTGCT	GACTATAAGT	CGAAGGAAA	GTTTGTAGGT	600
	CTGCTAAAGT	TGCCCGGAAA	AAGGTGGAAG	AGGAAGATGA	AGAAGAGGAG	660
25	AGGAGGAGGA	GGAGGAGGAG	GATGAATAAA	GAAACTGTTT	ATCTGTCTCC	720
	TTAGAGTAGG	GGAGGCGCGT	AATTGACACA	TCTCTTATTT	GAGAAGTGTC	780
	ATTAGTTTAA	ATTACAAAAT	TTGATCAGCA	TCATATTGTA	GTCTCTCAAA	840
	AATTGTCACT	GGTTTACATG	AAGTGGCCAT	GGGTGTCTGG	AGCACCTCTA	900
	AAGTTGTACA	TATTTCCAAA	CATTTTAAAA	ATGAAAAGGC	ACTCTCGTGT	960
30	CTGTGCACCT	TGCTGTTGGT	GTGACAAGGC	ATTTAAAGAT	GTTTCTGGCA	1020
	ATTTGTAAGG	TGGTGGTAAC	TATGGTTATT	GGCTAGAAAT	CCTGAGTTTT	1080
	TATCTATAGT	TTGTAAAGAG	AACAAAACAA	CCGAGACAAA	CCCTTGATGC	1140
	GCGTTGAGGC	TGTGGGGAAG	ATGCCCTTTG	GGAGAGGCTG	TAGCTCAGGG	1200
	GAGGCTGGAC	CTGTGACTCT	TGCAGGGGGC	ATCCATTAG	CTTCAGGTTG	1260
35	GTATATAGTG	ACATAGCATT	CTGCTGCCAT	CTTAGCTGTG	GACAAAGGGG	1320
	CATGAGAATA	TTTTTTTTTT	TAAGTGCGGT	AGTTTTTAAA	CTGTTTGTGT	1380
	TATAGAATCT	TTCAATGTCA	GCAAGACAAA	GAGTCACTGC	ATCAATGAAA	1440
	CTCCTGTACT	TAAACACGAT	TGCGCAACGT	CTGTTATTTT	TTTTGTATGT	1500
	GAAATGTTTT	TGAAGTTAAA	TAAACAGTAT	TACATTTTAA	AAACTCTTCT	1560
40	AGTCAATTTT	TGACTCACAG	CAGTGAACAA	ACCCCACTC	CATTGTATTT	1620
	CTCCCTATAA	TTTTTGTGCT	TTCTTTTATT	ACTCAGTGGC	CAGCTCACTT	1680
	TGAAGGAGAG	GGCTACTTGA	AGCTACTGTG	TGATTTTGT	TGTGTCTGAG	1740
	ATGAAGTCTG	GAGGAGTTAG	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	1800
	AGGAAGGTGG	GTTAGTTAGA	CTGAGGCTAT	CTAGGTTTAA	CTTTTGTCCC	1860
45	CCTATTTTGT	GGGGCCAAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGTAT	1920
	AAATTAAGGC	CTTATTTGTT	TTCTCTTTCA	CCCCTACCCC	CCGTGCTCCT	1980
	ACATTATTTG	TGGTGCCCAA	CATTTGGGGT	CTTGAGCCTG	CTGCTGGTCT	2040
	AGTGAGGGA	TGTGGGATGG	GGTGGTGGGG	TAGGGGACGG	TATCCTTTTT	2100
	TTGGAAACAC	CAAAACACCC	AAGGAAGATG	ATAGGCTCCA	TCTTGGGCCA	2160
50	AGGGCAGGCT	AATGGAATCA	ACCATTTCTG	AGCACTAAAT	GTATCATGAA	2220
	GCCTGCTCAT	AAGTTTAGCT	CATTCACTGG	AAATGTAGAT	TGATGTTCAA	2280
	GAAGGAGCTT	GGTTTGTGTG	TCAGTGGTTA	TATTAGTGGG	TAGTGTAAAC	2340
	GTTGGGGTGA	GGGGAGTAGC	CCACAGTAGC	AAGTGGTGAC	ACTAAATACC	2400
	CTGATGTGTA	TATACATCAT	TACTGTCCGT	AGCAATGAAG	GATACAGTAC	2460
55	GTGAGTGTG	CTATTGCCCA	GCATTAATAT	TTGGGTGTGT	ATGTTTGAGG	2520
	CGCAGGAGTG	TTTTTGTGCT	ATTAATTTTA	AGAGAAAGCA	GCTTTTCTCT	2580
	GTTGAGAAAC	TTGCATGTCT	GGAGGCGGTG	TCCTCTCCGC	CCTGTCCGGT	2640
	TAGGAGTTAT	GGTCACGGTC	ACAGCCTGAT	CTCTTATGTG	TTCAATAGCA	2700
	CATCAGAAT	GTTTGTCTCT	AATGTGTTCC	TCTAGTTCTA	GAAATGACC	2760
60	AAAACCTCGT	TGTGAGGTTT	GCCCAGAGGC	ACTTGTTCCT	GAATTTCCCC	2820
	GCCATGTCTT	TGTCACTTGG	CATTCTAAGC	TAAAGCTTTA	GCTTCCCAAT	2880
	CTAGGCCAAG	ATTCCGGAGC	TGTTGCCAGC	CTCGTCAAA	ATGGAAGAGA	2940
	GGTCAAAGG	GAGTGATTGG	TTAAGTGGTG	CGCGTCTATC	TCATAACTAG	3000
	CAGGGAAGGG	CCAAGGATGG	AAAGGGGTAA	CTTTTGTGCT	TCCAAAGTAG	3060
65	GTGGGGGAGC	AGTTTAGCCA	GATGATCTTT	GATTAGGCAA	ACATTGAGTT	3120
	TGTCAAGTTG	AGGCCACTTG	GTCCATTAGC	TGGGGCAGCA	AGATCACTAC	3180
	CACACTGTGG	CAAGATTGCT	CTTCTAGTGG	AATAATGCCC	TAGTTTCTCT	3240
	AAGTGGCATG	ATGTTTACCTA	AGGCTTAGGC	TTAGCTTGAT	TTCTGGGCCC	3300
	TTCTTAAGAT	GCCAACTGT	TGCTTTTTTT	TTTTTTTTTCC	CCCATTAAAA	3360
70	CTACTCCCTC	TAACCACTTC	ACCCCATTTCT	TGAATGACAT	TTTATCTCTC	3420
	AGGCTGTGAT	GTAGTGACTA	TTGTCTGTGT	CTCCTGTGTG	TGTCTGTCTC	3480
	GTATTTGGGG	ACGTTGGATG	CATTCAATTTT	CTGTAATAAA	G	

Seq ID NO: 306 Protein sequence:
Protein Accession #: NP_005333.1

1	11	21	31	41	51	
MAKGDPPKPK	GKMSAYAFV	QTCREEHKKK	NPEVPVNFAP	FSKKCSERWK	TMSGKEKSKP	60
80	DEMAKADKVR	YDREMKDYG	AKGGKKKKDP	NAPKRPPSGF	FLFCSEFRPK	120
	GDVAKKLGE	WNNLNDSEK	PYITKAALK	EKYEKDVADY	KSKGKFDGAK	180
	EEEEEEEEEE	EEEEEEEEEE				

Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_022342
Coding sequence: 1..2178

	1	11	21	31	41	51	
5	ATGGGTACTA	GGAAAAAAGT	TCATGCATT	GTCCTGTGCA	AACCCACCGA	TGACTTTGCT	60
	CATGAAATGA	TCAGATACGG	AGATGACAAA	AGAAGCATTG	ATATTCACCT	AAAAAAGAC	120
	ATTCCGAGAG	GAGTTGTCAA	TAACCAACAG	ACAGACTGGT	CGTTTAAGTT	GGATGGAGTT	180
	TTCAACGATG	CCTCCACGGA	CTTGGTTTAT	GAGACAGTTG	CAAAGGATGT	GGTTTCTCAG	240
	CCCTCGATG	GCTATAATGG	CACCATCATG	TGTTATGGGC	AGACGGGAGC	TGGCAAGACA	300
10	ACACCATGA	TGGGGGCAAC	TGAGAATTAC	AAGCACCAGG	GGATCCTCCC	TCGTGCCCTG	360
	AGCAGGTTT	TTAGGATGAT	CGAAGAACGC	CCACACATG	CCATCACTGT	GCGTGTTC	420
	ACTTGGAAA	TCTATAATGA	GAGCCTGTTT	GATCTCCTGT	CCACTCTGCC	CTATGTTGGA	480
	CCTCAGTCA	CACCAATGAC	CATCGTGGAA	AACCCCTCAAG	GAGTCTTCAT	TAAAGGGCTG	540
	CAGTTTACC	TCACAAGTCA	GGAGGAGGAT	GCATTACGCC	TCCTTTTGA	GGGTGAGACC	600
15	ACAGGATTA	TAGCCTCCCA	CACATGAAC	AAAACTCTT	CCAGATCACA	CTGCAATTTT	660
	CCATCTACT	TAGAGGCCCA	TTCCCGGACC	TTATCAGAGG	AAAAGTACAT	CACCTCCAAA	720
	TTAAGTTGG	TGGATCTGGC	AGGCTCAGAG	AGGCTGGGGA	AGTCTGGGTC	TGAGGGCCAA	780
	TCCTGAAGG	AAGCCACCTA	CATCAACAAA	TCGCTCTCAT	TCCTGGAGCA	GGCCATCATT	840
	CCCTTGGGG	ACCAGAACGG	GGACACATC	CCCTTTCGGC	AGTGCAAGCT	CACCCACGCT	900
	TGAAGGACT	CGTTAGGGGG	AAACTGCAAT	ATGGTCCTCG	TGACAAACAT	CTATGGAGAA	960
20	TCGCCAGT	TAGAAGAAAC	GCTATCTTCA	CTGAGATTG	CCAGCAGGAT	GAAGCTAGTC	1020
	CCACTGAGC	CTGCCATCAA	TGAAAAGTAT	GATGCTGAGA	GAATGGTCAA	GAACCTGGAG	1080
	AGGAAGTAC	CACACTCAA	GCAGGAGCTG	GCTATCCATG	ACAGCCTGAC	CAACCGCACC	1140
	TTGTGACCT	ATGACCCCAT	GGATGAAATC	CAGATTGCTG	AGATCAACTC	CCAGGTGGCG	1200
	GGTACCTGG	AGGGGACACT	GGACGAGATC	GACATAATCA	GCCTTAGACA	GATCAAGGAG	1260
25	GTTCACACC	AGTTCGGGT	GGTCTGAGC	CAACAGGAAC	AGGAAGTGA	GTCCACTTTG	1320
	GCAGGAAGT	ACACCTCTGA	TGACAGGAAT	GACTTTGCG	CCATTCTCTG	TATCCAGAAG	1380
	CGGGGCTTG	TGGATGTTGA	TGGCCACCTA	GTGGGTGAGC	CTGAAGGACA	AAACTTTGGA	1440
	TCGGAGTCG	CCCTTTCTC	TACCAACCT	GGGAAGAAAG	CCAAGTCCAA	GAAGACATTC	1500
30	AAGAGCCAC	TCAGGCCCGA	CACCCACCC	TCCAACCCAG	TGGCCTTTGA	GGAGTTTAA	1560
	ATGAGCAAG	GTAGTGAGAT	CAACCGAAT	TTCAAAGAAA	ACAAATCCAT	CTTGAATGAA	1620
	GGAGGAAAA	GGGCCACGCA	GACCACACAG	CACATCAATG	CCATCAAGCG	GGAGATTGAT	1680
	TGACCAAGG	AGGCCCTGAA	TTTCCAGAAG	TCACTACGGG	AGAAGCAAGG	CAAGTACGAA	1740
	ACAAGGGGC	TGATGATCAT	CGATGAGGAA	GAATTCCTGC	TGATCCTCAA	GCTCAAAGAC	1800
	TCAAGAGGC	AGTACCGCAG	CGAGTACCAG	GACCTGCGTG	ACCTCAGGGC	TGAGATCCAG	1860
35	ATTGCCAGC	ACCTAGTCGA	TCAGTGTGCG	CACCGCTCTG	TCATGGAATT	TGACATCTGG	1920
	ACAATGAGT	CCTTTGTCT	CCCTGAGGAC	ATGCAGATGG	CACTGAAACC	AGGCGGCAGC	1980
	TCCGGCCAG	GCATGGTCCC	TGTGAACAGG	ATTGTGTCTC	TGGGAGAAGA	TGACCAGGAC	2040
	AATTGAGCC	AGCTGCAGCA	GAGGGTGCTT	CCTGAGGGCC	CTGATTCCAT	CTCCTTCTAC	2100
40	ATGCCAAAG	TCAAGATAGA	GCAGAAGCAT	AATTACTTGA	AAACCATGAT	GGGCTCCAG	2160
	AGGCACATA	GAAATATG					

Seq ID NO: 308 Protein sequence:

Protein Accession #: NP_071737

45	1	11	21	31	41	51	
	MGTRKKVHAF	VRVKPTDDFA	HEMIRYGDDK	RSIDIHLKKD	IRRGVVNNQQ	TDWSFKLDGV	60
	LHDASQDLVY	ETVAKDVVSQ	ALDGVNGTIM	CYGGTQAGKT	YTMGATENY	KHRGILPRAL	120
50	QQVFRMIEER	PTHATVVRVS	YLEIYNESLF	DLSTLPYVG	PSVTPMTIVE	NPQGVFIKGL	180
	SVHLTSQEEED	AFSLLFEGET	NRIIASHTMN	KNSRSRHCIF	TIYLEAHSRT	LSEKYITSK	240
	INLVDLAGSE	RLGKSGSEQG	VLKEATYINK	SLSFLEQAI	ALGDQKRDHI	PFRQCKLTHA	300
	KDLSLGGNCN	MVLVTNIYGE	AAQLEETLSS	LRFASRMKLV	TTEPAINEKY	DAERMVKNLE	360
	KELALLKQEL	AHDSLTNRT	FVTYDPMDEI	QIAEINSQVR	RYLEGTILDEI	DIISLRQIKE	420
55	VFNQFRVVL	QQEQEVESYL	RRKYTLIDRN	DFAAISAIQK	AGLVDVDGHL	VGEPEGQNF	480
	LGVAFFSTKP	GKKAISKKT	KEPLRPDTPP	SKPVAFEEFK	NEQGSEINRI	FKENKSILNE	540
	RRKRASETQ	HINAIKREID	VTKEALNFQK	SLREKQKQYE	NKGLMIIDEE	EPFLILKLD	600
	LKKQYRSEYQ	DLRLDRAEQ	YQHLVDQCR	HRLLEMEFIW	YNESFVIPED	MQMALKPGGS	660
	IRPGMVPVNR	IVSLGEDDQD	KFSQLQQRVL	PEGPDSISFY	NAKVKIEQKH	NVLKTMMLQ	720
60	QAHRK						

Seq ID NO: 309 DNA sequence

Nucleic Acid Accession #: CAT cluster

65	1	11	21	31	41	51	
	TTTTTTTTTT	TTTTTTTAA	TGCCTGCTGT	CATGCTCTGT	CTACCAGGGT	GAATTTCCAA	60
	AAATTTCTGC	ATAGCAATTT	TAGCCAAAAC	TATATATGTT	CTGGGGAGGA	TAGGCATAGG	120
	CACATTGAAG	ACCAAAGGAA	AGAGTGAAGA	AGTGTAGTTG	GGTCATTGTG	AATGGATGTT	180
70	TAGATTGTCA	AGAAAAGTGG	GCCAGAGGCC	CCACCTCACA	CTAGGACGGC	AATGCCTCT	240
	CATTAGTATC	TCAGGCACCA	TGGGTCTTAT	TTGGTGTCTAT	AAGAAACACC	CTCAACAAAG	300
	TAATGAACCC	TCAGCCTCCA	GCTTCTCTTC	TTCGGGATTC	TTCTTAGGGC	CTCCTTTTTC	360
	CTTTTATGTT	TCCAGTACCC	TGAATTTCTT	ATTCCCATCC	CCCATTAATA	TCTGCTTCAA	420
75	AGAAAAACA	AGAAGGACAC	ATTCACCTTA	AGATCCAAAT	GAATGATAAG	AGCTTAAAC	480
	ATTATACCTA	TCAGTATTAT	TGCAATTTT	ATAGAAACCA	AAACCATATT	TCACCAAC	

Seq ID NO: 310 DNA sequence

Nucleic Acid Accession #: NM_018622.2

Coding sequence: 1-1140

80	1	11	21	31	41	51	
	ATGGCGTGGC	GAGGCTGGGC	GCAGAGAGGC	TGGGGCTGCG	GCCAGGCGTG	GGGTGCGTGG	60
	GTGGGCGGCC	GCAGCTGCCA	GGAGCTCACT	GCGGTCTTAA	CCCCGCGCGA	GCTCCTCGGA	120
85	CGCAGGTTTA	ACTTCTTTAT	TCAACAAAAA	TGCGGATTCA	GAAAGCACC	CAGGAAGGTT	180
	GAACCTCGAA	GATCAGACCC	AGGGACAAGT	GGTGAAGCAT	ACAAGAGAAG	TGCTTTGATT	240
	CCTCCTGTGG	AAGAAACAGT	CTTTTATCCT	TCTCCCTATC	CTATAAGGAG	TCTCATAAAA	300
	CCTTTATTTT	TTACTGTTGG	GTTTACAGGC	TGTGCATTG	GATCAGCTGC	TATTTGCGAA	360

TATGAATCAC TGAAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTTG 420
 GATAGCATAA GACCACAAAA AGAAGGAGAC TTCAGAAAGG AGATTAACAA GTGGTGGAAAT 480
 AACCTAAGTG ATGGCCAGCG GACTGTGACA GGTATTATAG CTGCAATGT CCTTGTATTTC 540
 TGTATTGGA GAGTACCTTC TCTGCAGCGG ACAATGATCA GATATTTCAC ATCGAATCCA 600
 GCCTCAAAGG TCCTTTGTTC TCCAATGTTG CTGTCAACAT TCAGTCACTT CTCCTTATTT 660
 CACATGGCAG CAAATATGTA TGTTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG 720
 GGTCAAGAGC AGTTTCATGCG AGTGTAACCTA TCTGCAGGTG TTATTTCCAA TTTTGTTCAGT 780
 TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGCATC 840
 ATGACAGTCC TCGCAGCTGT CTGCACTAAG ATCCCAAGAG GGAGGCTTGC CATTATTTTC 900
 CTTCGGATGT TCACGTTTAC AGCAGGGAAT GCCCTGAAAG CCATTATCGC CATGGATACA 960
 GCAGGAATGA TCTTGGGATG GAAATTTTTT GATCATGCGG CACATCTTGG GGGAGCTCTT 1020
 TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACTGATTT GGAAGAACAG GGAGCCGCTA 1080
 GTGAAATCT GGCATGAAAT AAGGACTAAT GGCCCCAAAA AAGGAGGTGG CTCTAAGTAA

Seq ID NO: 311 Protein sequence:
 Protein Accession #: NP_061092.2

1 11 21 31 41 51
 MAWRGWAQRG WCGGQAWGAS VGGRSCEELT AVLTPPQLLG RRFNFFIQK CGFRKAPRKV 60
 EPRRSDPGTS GEAYKRSALI PPVEETVFYP SPYPIRSLIK PLFFTUVGFTG CAFGSAAIWQ 120
 YESLKSRLVQS YFDGKADWL DSIRPQKEGD FRKEINKWNN NLSDGQRTVT GIIAANVLVF 180
 CLWRVPQLQR TMIRYFTSNP ASKVLCSPLM LSTFSHFSLF HMAANMYVLW SPSSSIVNIL 240
 GQEQFMAVYL SAGVISNFVS YLKVATGRY GPSLGAAGAI MTVLAAVCTK IPEGRILAIIF 300
 LPMFTFTAGN ALKAIAMDT AGMILGWKFF DHAHLGGLAL FGVYVYTYGH ELIWNKREPL 360
 VKIWHBIRTN GPKKGGGSK

Seq ID NO: 312 DNA sequence
 Nucleic Acid Accession #: NM_000625
 Coding sequence: 195..3656

1 11 21 31 41 51
 CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG 60
 CACAGGTCTC TTCCTGGTTT GACTGTCTTT ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA 120
 GCCCACAGT GAAGAACATC TGAGCTCAAA TCCAGATAAG TGACATAAGT GACCTGCTTT 180
 GTAAAGCCAT AGAGATGGCC TGTCTTGGGA AATTTCTGTT CAAGACCAAA TTCCACCAGT 240
 ATGCAATGAA TGGGGAAAAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT 300
 CCAGTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT 360
 CCCCAGCAGC CCTCGTGGAG ACGGGAAAGA AGTCTCCAGA ATCTCTGGTC AAGCTGGATG 420
 CAACCCCATT GTCTTCCCA CCGCATGTGA GGATCAAAAA CTGGGGCAGC GGGATGACTT 480
 TCCAAGACAC ACTTCACCAT AAGGCCAAAG GGATTTTAACT TGCAGGTCC AAATCTTGCC 540
 TGGGTCCAT TATGACTCCC AAAAGTTTGA CCAGAGGACC CAGGGACAAG CCTACCCCTC 600
 CAGATGAGCT TCACTCTCAA GCTATCGAAT TTGTCAACCA ATATTACGGC TCCTCAAAG 660
 AGCAAAAAAT TCGCCGGAAT CTGGCCAGGG TGGAGCGGT AACAAAGGAG ATAGAAACAA 720
 CAGTAACCTA CCAACTGACG GGAGATGAGC TCATCTTCGC CACCAAGCAG GCCTGGCGCA 780
 ATGCCCCAGC CTGCATTGGG AGGATCCAGT GGTCCAACCT GCAGGTCTTC GATGCCCGCA 840
 GCTGTTCCAC TGCCTGGGAA ATGTTTGAAC ACATCTGCAG ACACGTGCGT TACTCCACCA 900
 ACAATGGCAA CATCAGGTGC GCCATCACCG TGTTCCTCCA GCGGAGTGAT GGCAAGCAG 960
 ACTTCGGGT GTGGAATGCT CAGCTCATCC GCTATGTCTG CTACCAGATG CCAGATGGCA 1020
 GCATCAGAGG GGACCTTGCC AACGTGGAAT TCATCTAGCT GTGCATCGAC CTGGGCTGGA 1080
 AGCCCAAGTA CGGCCGCTTC GATGTGGTCC CCCTGGTCTT GCAGGCCAAT GGCCGTGACC 1140
 CTGAGCTCTT CGAAATCCCA CCTGACCTTG TGCTTGAGGT GGCCATGGAA CATCCCAAAT 1200
 ACGATGGGT TCGGGAACAT GAGCTAAAGT GGTACGCCCT GCCTGCAGTG GCCAACATGC 1260
 TGCTTGAGGT GGGCGGCTGC GAGTTCCAG GGTGCCCTT CAATGGCTGG TACATGGGCA 1320
 CAGAGATCGG AGTCCGGGAC TTCTGTGATG TCCAGCGCTA CAACATCCTG GAGGAAGTGG 1380
 GCAGGAGAA TGGCCTTGGA ACGCACAAAG TGGCTCGCT CTGGAAGAGC CAGGCTGTGC 1440
 TTGAGATCAA CATTGCTGTG CTCCATAGTT TCCAGAAGCA GAATGTGACC ATCATGGACC 1500
 AACCATCGGC TGCAGAACTC TTCTGAAAGT ACATGCAGAA TGAATACCGG TCCCGTGGGG 1560
 GCTGCCCGGC AGACTGTGAT TGGCTGGTCC CTCCATGTC TGGGAGCATC ACCCCGTGT 1620
 TTCACCAGGA GATGCTGAAC TACGTCTGT CCCCTTTCTA CTACTATCAG GTAGAGGCCT 1680
 GGAAGAACCA TGTCTGGCAG GACGAGAAGC GGAGACCCAA GAGAAGAGAG ATTCCATTGA 1740
 AAGTCTTGGT CAAAGCTGTG CTCCTTGCCT GTATGCTGAT GCGCAAGACA ATGGCGTCCC 1800
 GAGTCAGAGT CACCATCTCT TTTGCGACAG AGACAGGAAA ATCAGAGGCG CTGGCCTGGG 1860
 ACCTGGGGGC CTTATTCAGC TGTGCCTTCA ACCCAAGGT TGTCTGCATG GATAAGTACA 1920
 GGCTGAGCTG CTTGGAGGAG GAACGGCTGC TGTGGTGGT GACCAGTACG TTTGGCAATG 1980
 GAGACTGCCC TGGCAATGGA GAGAACTGA AGAAATCGCT CTTTCATGCTG AAAGAGCTCA 2040
 ACAACAAAT CAGGTACGCT GTGTTTGGCC TCGGCTCCAG CATGTACCCT CGGTTCTGCG 2100
 CCTTTGCTCA TGACATTGAT CAGAAGCTGT CCCACCTGGG GGCTCTCAG CTCACCCCGA 2160
 TGGGAGAAGG GGATGAGCTC AGTGGGCAGG AGGACGCTT CCGCAGCTGG GCCGTGCAAA 2220
 CCTTCAAGGC AGCCTGTGAG ACCTTTGATG TCCGAGGCAA ACAGCAGCAT CAGATCCCCA 2280
 AGCTCTACAC CTCCTAATGT ACCTGGGACC CGCACCACTA CAGGCTCGTG CAGGACTCAC 2340
 AGCCTTTGGA CCTCAGCAAA GCCCTCAGCA GCATGCATGC CAAGAACGTG TTCACCATGA 2400
 GGCCTAAATC TCGGCAGAA CTACAAAGTC CGATCCAGC CCGTGCCACC ATCCTGGTGG 2460
 AACTCTCCTG TGAGGATGGC CAAGGCCTGA ACTACCTGCC GGGGGAGCAC CTTGGGGTTT 2520
 GCCCAGGCAA CCAGCCGGCC CTGGTCCAAG GCATCCTGGA GCGAGTGGTG GATGGCCCCA 2580
 CACCCACCA GGCAGTGGCC CTGGAGGCC TGGATGAGAG TGGCAGTAC TGGGTCAAGT 2640
 ACAAGAGGCT GCCCCCTGC TCACTAGCC AGGCCCTCAC CTACTTCTG GACATACCA 2700
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 GCCCACAATT CCTGGAGGTG CTAGAGGAGT TCCCGTCCCT GCGGGTGTCT GCTGGCTTCC 2880
 TGCTTTCCCA GCTCCCCATT CTGAAGCCCA GGTCTACTC CATCAGCTCC CCCCGGGATC 2940
 ACACGCCAC GGAGATCCAC CTGACTGTGG CCGTGGTCC CATACCACAC CGAGATGGCC 3000
 AGGGTCCCTG GCACACGGC GTCTGCAGCA CATGGCTCAA CAGCCTGAAG CCCCAGACC 3060
 CAGTGCCTG CTTTGTGCGG AATGCCAGCG GCTTCCACCT CCCCAGGAT CCTTCCATC 3120

CTTGCATCCT CATCGGCGCT GGCACAGGCA TCGCGCCCTT CCGCAGTTTC TGGCAGCAAC 3180
 GGCTCCATGA CTCCCAGCAC AAGGGAGTGC GGGGAGGCGG CATGACCTTG GTGTTTGGGT 3240
 GCGCGCGCCC AGATGAGGAC CACATCTACC AGGAGGAGAT GCTGGAGATG GCCCAGAAAG 3300
 GGGTGTCTGCA TCGGCTGCAC ACAGCCTATT CCGCCTGCGC TGGCAAGCCC AAGGTCTATG 3360
 5 TTCAGGACAT CCTGCGGCG CAGCTGGCCA GCGAGGTGCT CCGTGTGCTC CACAAGGAGC 3420
 CAGGCCACCT CTATGTTTGC GGGGATGTGC GCATGGCCCG GGACGTGGCC CACACCCTGA 3480
 AGCAGCTGGT GGCCTGCCAAG CTGAAATTGA ATGAGGAGCA GGTGAGGAC TATTCTTTC 3540
 AGCTCAAGAG CCAGAAGCGC TATCACGAAG ATATCTTTGG TGCTGTATTT CCTTACGAGG 3600
 CGAAGAAGGA CAGGGTGGCG GTGCAGCCCA GCAGCTGGA GATGTCAGCG CTCTGAGGGC 3660
 10 CTACAGGAGG GGTAAAGCT GCCGGCACAG AACTTAAGGA TGGAGCCAGC TCTGCATTAT 3720
 CTGAGGTCAC AGGGCCTGGG GAGATGGAGG AAAGTGATAT CCCCCAGCCT CAAGTCTTAT 3780
 TTCTCAACG TTGCTCCCA TCAAGCCCTT TACTTGACCT CCTAACAAAGT AGCACCCCTG 3840
 ATTGATCGGA GCCTC

Seq ID NO: 313 Protein sequence:
 Protein Accession #: NP_000616

1 11 21 31 41 51
 | | | | |
 MACPWKFLFK TKFHQYAMNG EKGINNVEK APCATSSPVT QDDLQYHNLS KQNESPOPL 60
 VETGKSPES LVKLDATPLS SPRHVRIQNW GSGMTFQDTL HHKAKGILTC RSKSCLGSIM 120
 TPKSLTRGPR SWAGVTGKAL PQAIEFVNQY YGSLKEAKIE EHLARVEAVT KEIETTITYQ 180
 25 LTGDELIFAT KQAWRNAPRC IGRIQWSNLQ VFDARSCSTA REMFEHICRH VRYSTNNGNI 240
 RSAITVFPQR SDGKHDFRVW NAQLIRYAGY QMPDGSIRGD PANVEFTQLC IDLGWPKPYG 300
 RFDVPLVLQ ANGRDPLEFE IPPDLVLEVA MEHPKYEWFR ELELKWYALP AVANMLLEV 360
 GLEFPFGCFN GWYMGTEIGV RDFCDVQRYN ILEEVGRRMG LETHKLASLW KDQAVVEINI 420
 AVLHSFQKQN VTIMDHSSAA ESFMKYMONE YRSRGGCPAD WIWLVPPMSG SITPVFHQEM 480
 30 LNVVLSPPFY YQVEAWKTHV WQDEKRRPKR REIPLKVLVK AVLFACMLMR KTMASRVVVT 540
 ILFATETGKS EALAWDLGAL FSCAFNPKVV CMDKYRLSCL EEERLLLVT STFGNGDCPG 600
 NGEKLLKSLF MLKELNNKFR YAVFGLGSSM YPRFCAPAH IDQKLSHLGA SOLTPMGEGD 660
 ELSGQEDAFR SWAVQTFKAA CTDFDVRGKQ HIQIPKLYTS NVTWDPHYR LVQDSQPLDL 720
 35 SKALSSMHAK NVFTMLKSR QNLQSPSSR ATILVELSCE DGQGLNLYLF EHLGVCPGNQ 780
 PALVQGILER VVDGPTPHQA VRLEALDESG SYWVSDKRLP PCSLSQALTY FLDITTPPTQ 840
 LLLQKLAQVA TESEPERQLE ALCQPSSEYSK WKFTNSPTFL EVLEEFPSLR VSGFLLSQL 900
 PILKPRFYSI SSPRDHTPTE IHLTVAVVTY HTRDQGGPLH HGVCSTWLNS LKQDPVPCF 960
 VRNAGSFLPL EDPSPHCILI GPGTGIAPFR SFWQORLHDS QHKGVRRGGM TLVFGCRRPD 1020
 EDHIYQEEML EMAQKGVHLHA VHTAYSRLPG KPKVYVQDIL RQQLASEVLR VHLKEPGHLY 1080
 40 VCGDVRMARD VAHTLKQLVA AKLKLNEBQV EDYFFQLKSQ KRYHEDIFGA VFPYEAKKDR 1140
 VAVQPSSELM SAL

Seq ID NO: 314 DNA sequence
 Nucleic Acid Accession #: XM_087254
 Coding sequence: 47..2332

1 11 21 31 41 51
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 50 AGAGTACGCTG TTTACAGATA AAACCTGGTAC ACTGACAGAA AATGAGATGC AGTTTCGGGA 60
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 AACACCAGAC TCTTCAGAAG GAAACTTATC TTATCTTAGT AGTTTATCCC ATCTTAACAA 180
 CTTATCCCAT CTTACAACCA GTTCTCTTT CAGAACCACT CCTGAAATG AAACCTGAACT 240
 AATTAAAGAA CATGATCTCT TCTTTAAAGC AGTCAGTCTC TGTACACTG TACAGATTAG 300
 CAATGTTCAA ACTGACTGCA CTGGTGATGG TCCCTGGCAA TCCCACTGG CACCATCGCA 360
 55 GTTGAGTATC TATGCTCTT CACCAGATGA AAAGGCTCTA GTAGAAGCTG CTGCAAGGAT 420
 TGTATTTGTG TTTATTGGCA ATTCTGAAGA AACTATGGAG GTTAAAACTC TTGGAAGAAC 480
 GGAACGGTAC AAACCTGCTC ATATTCTGGA ATTTGATTCA GATCGTAGGA GAATGAGTGT 540
 AATGTTTCAG GCACCTTCAG GTGAGAAGTT ATTATTGCT AAAGGAGCTG AGTCATCAAT 600
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 60 TTTGAAAGGG CTAAGAACTC TGTGTATAGC ATATAGAAAA TTTACATCAA AAGAGTATGA 720
 GGAATATAGT AAACGCATAT TTGAAGCCAG GACTGCCTTG CAGCAGCGGG AAGAGAAATT 780
 GGCAGCTGTT TTCCACTTCA TAGAGAAAGA CCTGATATTA CTTGGAGCCA CAGCAGTAGA 840
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 65 AGTATGGGTG CTTACTGGGG ATAAACATGA AACAGCTGTT AGTGTGAGTT TATCATGTGG 960
 CCATTTTCAT AGAACCATGA ACATCCTTGA ACTTATAAAC CAGAAATCAG ACAGCGAGTG 1020
 TGCTGAACAA TTGAGGCAGC TTGCCAGAAG AATTACAGAG GATCATGTGA TTCAGCATGG 1080
 GCTGGTAGTG GATGGGACCA GCCTATCTCT TGCATCTCAG GAGCATGAAA AACTATTTAT 1140
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 70 AAAAGTAATA AGACTAATAA AAATATCACC TGAGAAACCT ATAACATTGG CTGTTGGTGA 1260
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 AGAAGGAAGA CAGGCTGCAA GAAACAGTGA CTATGCAATA GCCAGATTTA AGTTCCCTCTC 1380
 CAAATTGCTT TTGTTTCATG GTCAATTTTA TTATATTAGA ATAGCTACCC TTGTACAGTA 1440
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 75 GTTTTCTCAG CAAACATGTT ATGACAGCGT GTACCTGACT TTATACAATA TTTGTTTATC 1560
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 80 TGGCACTTTG GTCTTCACAG TCATGGTTAT TACAGTCACA GTAAAGATGG CTCTGGAAAC 1860
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 85 CTGTTTCCCG GAAGGAGAAG CAGCGTGTGC ATCTGTTGGA AGAATGCTGG AACGAGTTAT 2220
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 CAACGACAGG AGCATCTTGA CTCTCTCCAC AATGACTCA TCTACTTGT AAAGGGGCAG 2340

		TAGTACTTTG	TGGGAGCCAG	TTCACTCTCT	TTCTAAAAAT	TCAGTGTGAT	CACCTGTGTA	2400
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5		TGAATCTGAA	CATGTTAAAA	TTTGAGAATA	AAGAGACATT	TTTCATCTCT	TTGTCTGGTT	2580
		TGTCCTCTGT	GCCTATGGGA	CTCTTAATAG	CTTTTCAGTC	TGTTGCTGAG	GCCATTATAT	2640
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10		ATACTGAGGA	TTTTTGGTCC	CTCAGTGACC	TGTTGTGTTA	ATTCAATATT	GCATCTGAGT	2880
		TTTACAGAGC	AAATTAGGAG	AATCATTTC	AACCATTAAT	TACTGCAGTA	TGGGGAGTAA	2940
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		CAAGGGTATA	TCATATATAT	AATCAGGAAA	TACGGTCCGT	TACCGCAAGT	TCAAATTGAT	3060
		GTTTACTAAT	ATTTTGTGTA	CAGAGTATAA	AGACCTTATA	GTGGGTAAT	TAGATACTAT	3120
		TAGCATATTA	TTAATTTAAT	CTCTTTATCA	TTGGATCTTT	TGCACTGCTT	AATCTGGTTA	3180
		ACATATTTAA	ATTTGCTTTT	TTTTCTTTTA	CCTGAAGGCT	CTGTGTATAG	TATTTCTATG	3240
		CATCGTTGTA	CAGTTTAACT	ATATCAATAA	AAAGTTTGGA	CAGTATTTAA	ATATTGCAAA	3300
		CTGTTTAAAT	TATACAATTC	AGAAATGAT	GGGTAAATTA	ATGAATAACA	AAAGAAAGAC	3360
		CTCTTTCTGC	AGCGCAATTC	GACATGCTCT	TCCTTTCTTA	TAAAGTAGAT	TTTGAATAAT	3420
		AGGGTTTCAG	TTAATAATCT	TATTTTCAGG	TTATGTCATC	TAACTTATAG	CAAACCTACCA	3480
		CAATACAGTG	AGTTCTGCCA	ATGTCGCCAG	ACAAGGCATA	TTTCAGGTGT	GGCTGTGGAA	3540
		TGTAATAATG	CTCAACTTGT	ATCGAGTAAT	GTTAGCAATG	AATTAATATG	TAAAGATGAT	3600
		TAATCGGTA	CATGTTACTG	TAATTAACCT	ATTGCACTTC	AAAACCTAAC	TTCCATCTCG	3660
		AATTTATCAA	TGAGTTCAGT	ATTGTCATTT	GTTTTGTGTT	TATTTGAAAG	TAATGTTGTC	3720
25		TTAAGATTAA	GAGGTGATTA	TTAGCTTATG	AACATATTACC	CAGCTCTAAG	CAAAATAATG	3780
		TGTATACAT	ATTAAGATAA	TGGTTAAATG	CGGTTTTACC	AAGTTTTCCC	TTGAAATGTT	3840
		AATTCCTTTA	TGGAGATTTA	TTTGTGCAGC	CTAAGCTTCC	TTCCCAATTC	ATGAATATAA	3900
		GGCTCTAGAA	ATTTGGACTG	CAGGGGAAAG	AATGGTAGAG	ACCAAAATTA	AGACTTTATC	3960
		CTTGTTTGCT	TGTAACATAT	TATTTTCTTG	CTAATGTAAC	ATTTGTCCTG	TCCAGTGATG	4020
30		TAAGGATATT	AAGTTATTTAA	GCTAAATATT	AATTTTCAAA	AATAGTCCCT	CTTTAACTTA	4080
		GATATTTACT	ACGTGGATTT	AGGAAGATAT	GTTATTCTGG	AGTAGCTAAA	AGAAATAATA	4140
		CAACGTACAA	TGCTGTCATT	CACATAATCA	TGTTCCAGAA	GAGGAAATTA	TGAAGATATA	4200
		CTCAGTAGAG	TACTAGGTGG	GAGGATATGG	AAATTTGCTC	ATAAAACTTC	TTATAAAACG	4260
		TGCATATAAC	AAATAGCAC	CCAGTAGGCC	TGCATTACAT	TTACATGACC	GTGTTTATTT	4320
		GCCATCAAT	AACTGAGTAA	CTGACACGAG	ACAAAGACTC	CRAAGTCTAA	AAATAGCATA	4380
35		TGACCAACTG	CAGCAAGACA	GGAGGTCAAG	TCGCCTATAA	TGGTGCTTAA	AGTGTGATTG	4440
		ATGTAAATTT	CTGTACTCAC	CATTGGAAGT	TAGTTAAGGA	GAACTTTATT	TTTTTAAAAA	4500
		AAGTAAATGG	CAACCACTAG	TGTGCTCATC	CTGAACGTGT	ACTCCAAATC	CACCTCGGTT	4560
		TTAAAGCAAA	ATTATCTTGT	GATTTTAAAG	AAAGAGTTT	CTATTTATT	AAGAAAGTAA	4620
40		CAATCGAGTC	TGCAAGCTTT	CAGTAGTTTT	CTAGTGCAT	ATTCTCTCTG	TAAACTCTTT	4680
		ACTACGTAA	CAGTAATCAC	AAGGAAAGTG	TCCTCTTTGC	ATATTTCTTT	AAATTTCTTT	4740
		CTTTGGAAAG	TATGATGTAT	ATTAAATCT	TACCTTATAT	TGCCAAAACC	AGAGCAAAAT	4800
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		AGGTCACTTC	TACTGGA AAA	GATTTGTAGA	TGGAACCTAT	CTGATCGCTT	GAGACTCCCTA	5280
50		ATAGGCAAGG	CTCAAGGCCA	CTGAGAAATT	GACAGCTTAAG	AGCCAAAAGT	TTTTTAAAAA	5340
		TGCTACTCTG	AAAAATCTCG	TGAAGGCTGT	AGGAAAAGGG	AGAATCTTCC	ATGTTGGTGT	5400
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		TGTGAAATPA	CTTGAATGTT	GTTCTCTATA	AAAAATAGAT	ATAAATCATG	ATATGTTTGT	5640
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		GGTTTAAAAAT	TTTGAGCCTG	AGACACTGTG	CGTGTCTAAT	GTAATCCTTT	AAAAATCTC	5760
		TGCAATTGTCA	GTAATATGTAG	TATATTATG	TACAGCTACT	CATAATTTTT	TAAAGTTTAT	5820
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Seq ID NO: 315 Protein sequence:
Protein Accession #: XP_087254

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70	AAARIGIVFI	GNSBETMEVK	TLGKLERYKL	LHLEFPDSR	RMMSVIVQAP	SGEKLLFAKG	180
	AESSLKPCI	GGEIEKRIH	VDEFALKGLR	TLCIAYRKFT	SKAYEEDIKR	IDFEARTALQ	240
	REEKLAAVFQ	PIEKDLILLG	ATAVEDRLQD	KVRETIEALR	MAGIKWVVL	GDKHETAVSV	300
	SLSCGCFHRT	MNLELINCKM	SDSECAQLRL	QLARRITEDH	VIQHGLVDV	TSLSALALRE	360
	EKLFMVEHNR	CSAULNCRKA	PLQKACVQLR	IKISKEPKIT	LAVGDDGND	SMQEAHVGI	420
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	MALETHFNTW	INHLVTWGSI	IFYFVFLSFY	GGILWPFLGS	QNNMYFVFIQL	LSSGSAAWPAI	660
	ILMVVTCLEF	DIKKVVDPRH	LHPSTSEBAQ	LTLETNAGIK	LDSMCCFPFG	EAACASVGRM	720
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Seq ID NO: 316 DNA sequence
Nucleic Acid Accession #: NM_004473
Coding sequence: 661..1791

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 5 GGCACTAATC TFAAACTAGC GGGCACCACA GACCAGCTGC AGCCACCCCA ACCCAGGGAT 300
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 25 ACCACCGGCT ACCAGCGCGC AGGCTGCACC GGGGCGCGCC CGGCCAACCC CTCTGCTTAT 1500
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 35 CGGGATGCTT TCTGGCATTC TATCGGGGAG GGTCTTGGC GGTAAACAGA GGGCAGCGTA 2100
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 AA

Seq ID NO: 317 Protein sequence:
Protein Accession #: NP_004464

1 11 21 31 41 51
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 PFYRDNPKKW QNSIRHNLTL NDCFLKIPRE AGRPGKGNWY ALDPNAEDMF ESGSFLRRRK 180
 RFKRSDLSTY PAYMHDAAAA AAAAAAATAA AAAAAIIPGA VPAARPPYPG AVYAGYAPPS 240
 70 LAAPPVYVYP AASPGFCRVF GLVPERPLSP ELGPAPSGPG GSCAFASAGA PATTTGYQPA 300
 GCTGARPNP SAYAAAYAGP DGAYPQAGS AIFAAAGRLA GPASPPAGGS SGGVETTVDF 360
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Seq ID NO: 318 DNA sequence
Nucleic Acid Accession #: NM_005688
Coding sequence: 126..4439

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 85 GGAGAACTCG ACCGTGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA GCCAGGGGCC 300
 TCTCTCTGA TGCTTCAATG CATTCTCAGC TCAGAACTCT GGATGAGGAG CATCCCAAGG 360
 GAAAGTACCA TACTGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACCAGC 420
 ACCCAGTGA CAATGCTGGG CTTTTTCTCT GTATGACTTT TTCGTGGCTT TCTTCTCTGG 480

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	AAGTTGGGCC	AGACGTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
5	TCATCTGTGC	CATCTGTGTC	GTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCCAGCT	720
	TCATGTGTAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCCCT	CTCCTGACGG	AAATCGTGGC	GTCTTGGTCG	CTTGCACTGA	840
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	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
10	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTTATGATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCCCTGG	ATCAGCTGTT	TTTATCCTCT	TTTACCCAGC	AATGATGTTT	GCATCAGGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
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15	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
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	CTGTTTCATAT	GACCCCTGGG	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
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20	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
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25	ACAGCATCGA	CTTGAGATTC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
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	ACCTCAGGTT	GCTGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAAACCCC	TTTGTGCTGT	5640
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5

Seq ID NO: 319 Protein sequence:
 Protein Accession #: NP_005679

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 15 ALNRYRTGVR RLGAITMAFK KILKLNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
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 30 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWQPE GEVTFENAEM 1200
 RYRENPLVL KKVSTFKPK EKIGIVGRTG SGKSSLMGAL FRLVELSGG IKIDGVRISD 1260
 IGLADLRSL SIIPQEPVLF SGTVRSLNDP FNQYTEDQIW DALERTHME CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380
 35 MLTIAHRLHT VLGS DRIMVL AQGQVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKG

Seq ID NO: 320 DNA sequence
 Nucleic Acid Accession #: AK022089.1
 Coding sequence: 181-1488

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 TGGGAGCTCA GCCCAGCAAA CTACATGAAG ACTTTACCAC CAGATAAACA AAAAAAGATA 660
 55 GTCAGGAAAA CTTTCGGGAA ACTGGCTAAA ATTAAGCAGG ACACAGTTTC TCATGATCGA 720
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 GTCAGAGAAA TGGAAGAGCT GGATCTGGAA ATTGAAAGT GTGAAGCTAA GTTCCATCTT 840
 GATCGAGTAG AAAATGATGG AGAAAACTAT GTTCAGGATG CATATTTAAT GCCCAGTTTC 900
 AGTGAAGTTG AGCAAAATCT AGACTTGCAG TATGAGGAAA ACCAGACTCT GGAGGACCTG 960
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 AGAGCGAAGG AATCTHAGT TCCAGTAGC AATGGGGAGA TTCCTCCCTT TACTCAAAGA 1380
 GTATTAGCA ATTACACAAA TGACACAGAC TCGACACTG GTATCAGTTC TAACCACAGT 1440
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Seq ID NO: 321 Protein sequence:
 Protein Accession #: NP_005438.1

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 80 LPVPLWRTAE AKLVQNTKEL WELSPANYM TLPPDKQKRI VRKTFRKLAK IKQDTVSHDR 180
 DNMTLVHLI ISQDHTIHQ VKRMKELDL IEKCEAKFHL DRVENDGENY VQDAYLMPSP 240
 SEVEQNLDLQ YEENQTLDEL SESDIEQLE ERLKYRILI DKLSAEIEKE VKSVCIDINE 300
 DAEGEAASEL ESSNLESVK DLEKSMKAGL KIHSHLSGIQ KEIKYSDSL QMKAKEYELL 360
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Seq ID NO: 322 DNA sequence
 Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

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	CTGGTGGTGG	TAGTGGGCGT	TTATATTTGC	GTTCTCTTTC	ATTCAATTCT	AAATCTCTTA	240
10	AAAATTTTGG	GTTGGGGGTA	TTGGGGAAGG	CAGGAAAGGG	AAAAGGAGAG	TAGTAGCTGA	300
	AGAGCAAGAG	GAGGACATGG	AGATGAAGAA	GAAGATTAAC	CTGGAGTTAA	GGAACAGATC	360
	CCCGGAGGAG	GATGACAGAT	TAGTCCTTGA	TAATTGCTCG	TGTGTCAATG	GGGAAATTGA	420
	AGGCCTGAAT	GATACTTTCA	AAGAACTAGA	ATTTCTGAGT	ATGGCTAATG	TGGAACCTAAG	480
	TTGCTGGGCC	CGGCTTCCCA	GCTTAAATAA	ACTTCGAAAA	TTGGAGCTTA	GTGATAATAT	540
15	AATTTCTGGA	GCTTGGGAAG	TCCTGGCAGA	GAAATGTCCA	AATCTTACCT	ACCTCAATCT	600
	GAGTGGAAAC	AAAATAAAG	ATCTCAGTAC	AGTAGAAGCT	CTGCAAAATC	TTAAAAATTT	660
	GAAAACTCTT	GACCTGTTTA	ACTGTGAGAT	CACAAACCTG	GAAGATTATA	GAGAAAGTAT	720
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	GCCGGAATCT	GAAGAGGAGG	ATGATGAGGA	TGGAGATGAA	GATGATGAAG	AGGAAGAGGA	840
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	TGAGGATGAG	GATGAAGATG	AAGATGAAGC	AGGTTCAAGG	TTGGGAGAGG	GAGAAGAGGA	960
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	GAAACGAGAT	GCTTGAAGAC	ATGGAGAGGA	AGAAGATGAC	TAGATCATTG	TAAGACCAGA	1140
25	TTCTCTAATG	TTTCTGGGTG	TGCAATAGAG	TGATCACATC	TTTGTTCCTT	CATGTACGAT	1200
	AGCTATCCCT	ACAGAAGATA	ATGTGTAAC	TTTTATAGGA	AAAGTGTGGT	TTTACTATTT	1260
	TTGCTTATC	ATTCCAAATA	AGAACTAGTC	TGTTAATGAT	CATATTGTAT	GTAGAGAAAA	1320
	ATTTTCATG	ACTCCCATG	TGGAATCCC	TAGCAATTTA	TTTAGACTTA	ATTTTTTAAA	1380
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30	GGTGTAGTAT	GGTGCAATTC	ATTCCTTATT	TATAGATTAA	CTGAAATTAC	AGTTTGTCTAT	1500
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	TTCAAGCAAC	TAGTTCATGG	ATTTTGTGGA	GGTTCTATTC	AGTAATATGG	TTTATGGATT	1740
35	TAGTGGTGAC	TGATAAGATT	TTATTTTGA	AGGAAAAATT	GCTTATACTA	AGTCCAGAGA	1800
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	GTTTCACTCC	CTCCCGCTCT	CTCAAAAGGA	ACTTGGGAAA	CTTGTGAAAC	CCAGGAAAAAC	1980
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45	TAATAGCATT	TAATTTGAA	ATACTAGGCA	GCTGGAAGAA	TATTTGAAAC	TAAATTGACA	2400
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55	ATTTTAAAA	TGAAATCTAT	ATATTGACTT	TCTTATCAAT	CATCTTACTG	TGCAATCAAA	3000
	ATTAGAGTAC	TTTGGTTTGA	AAACAACACT	TAGAGCCTCC	AGATAACTTT	TAAGACTTAT	3060
	TTAGCTTTGT	GGGTGCTGCT	TTCTGCAAAA	TAAAGTAAAGG	TGGGTTTAT	ATTTTGTAGA	3120
	AGTTTTCGGT	CCTATTTTAA	TGCTCTTTGT	ATGGCAGTAT	GTATATATTG	TGTTAAGTTC	3180
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Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

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	FNCEITNLED	YRESIFELLQ	QITYLDGFDQ	EDNEAPDSEE	EDDEDGDEDD	EEEEENEAGP	180
70	PEGYEEEEEE	EEEEDEDEDE	DEDEAGSELG	EGEEVGLSY	LMKEEIQDEE	DDDDVVEEGE	240
	EEEEEEBGL	RGEKRRDAE	DDGEEEDD				

Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224..2722

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80	CCATGCGCGC	GAGCGCGGCT	TGACCGGCTC	CGCCCGCGGC	CGCCCCGCGC	CTAGCCCGGC	180
	GCTCTGCGCG	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCAGCAG	240
	CAGCTGCGCG	CAGCGGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCTT	GCGGCCCCCA	300
	ACGCGGCCCC	GCCGCGCTGG	TGCCTGCCAG	CGCCCCGGCC	CGCACGCGCG	CCTGCGCGCT	360
	GCTTCTGCTC	CTTCTCTGCG	TGCCTCCGCT	CGCCGCTCG	TCCCGGCCCC	GCGCCTGGGG	420
85	GGCTGCTGCG	CCCAGCGCTC	CGCATTTGAA	TGAAACTGCA	GAAAAAATTT	TGGGAGTCTT	480
	GCGAGATGAA	GACATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
	AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600

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Seq ID NO: 325 Protein sequence:
Protein Accession #: NP_003803

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INQDSESPYH VLDTKARHQ KHNKAVHLAQ ASFQIEAPGS KFILDILINN GLLSSDYVEI 180
HYENGKPYQS KGEHCYHYH SIRGVKDSKV ALSTCNGLHG MFEDDTFVYM IEPLELVHDE 240
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LELMIVNDHK TYKKHRSSHA HTNPFASV V NLVDSIYKEQ LNTRVVLVAV ETWTEKDQID 360
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LPMAVAQVLS QSLAQNLAGT WEPSSRKPKC DCTESWGCCI MEETGVSHSR KFSKCSILEY 480
RDFLRQGGGA CLFNRPRTKL EPTGCGNGYV EAGEECDGPF HVECYGLCKC KCSLSNGAHC 540
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Seq ID NO: 326 DNA sequence
Nucleic Acid Accession #: AK074418.1
Coding sequence: 244-1515

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10	CCTGAAAATG	CCAGACAGTG	ACAGGCACCT	GAGCAGCCAT	TTC AACCTCA	GAATGAAGGG	1680
	AAGCCCTTCA	GAACATGGCT	CCCAACAAAG	CATTTTCAAC	AGATATGCTC	AGCAGGTATG	1740
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15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
	ACCCCGTGAA	ACCTTTCCCT	CTCCTACTCG	GCCACCTCCC	ACCAACCTGG	CATCGTTCCT	2100
	CCCGGGAGCT	AGCCAGCTTC	AGAAAGCACA	TACAGCATCC	TTGCTGCCAA	ACCACTATG	2160
	TGCACACAGG	ATTTCCTTAA	TGGCTTAATA	AACTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
20	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCCTCT	TACCGTTAAA	AAAAAAAATA	2280
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Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

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	QYAGIFRFRF	WQCGQWVEVV	IDDRLPVQGD	KCLFVRPRHQ	NQEFWPCLE	KAYAKLLGSY	180
30	SDLHYGFLED	ALVDLTGGVI	TNIHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
	MENGLVSLHA	YVTVTGAEQIQ	YRRGWEEIIS	LWNPNWGWET	EWGRWSDGS	QWEETCDPR	300
	KSQLHKKRED	GEFWMSCQDF	QOKFIAMPIC	SEIPITLDHG	NTLHEGWSQI	MFRKQVILGN	360
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35	KLK						

Seq ID NO: 328 DNA sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74-2788

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45	GCCTCGGCGA	GGCAATGATC	CTCTCACCTC	CAGCCCTGGC	CGAAGCTCCC	GGCGTACTGA	180
	TGCCCTCACC	TCCAGCCCTG	GCCGTGACCT	TCCACCATTT	GAGGATGAGT	CCGAGGGGCT	240
	CCTAGGCACA	GAGGGGCCCC	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGGAGATGG	300
	CATGGAAGG	GACTACCGCG	CCATCCACAG	GCTGGACGCC	TATGAGCCCG	AGGGACTGGC	360
50	TCTGGATGAT	GAGGACGTAG	AGGAGCTGAC	GGCCAGTCAG	AGGGAGGCAG	CAGAGCGGGC	420
	CATGCGGCAG	CGTGACCGGG	AGGCTGGCGG	GGCCCTGGGC	CGCATGCGCC	GTGGGCTCCT	480
	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCCTGCCCGC	AAGCGCCGCC	AGGTGGAGCG	540
	GGCCACGGAG	GACGCGAGG	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	ACCTGGAGGA	600
	TCTCAAGAGC	CACCTCTGTG	GCGAGTGGGT	GAGCATGGCG	GGCCCCGGCG	TGGAGATCCA	660
55	CCACCGCTTC	AAGAACTTCC	TGCGCACTCA	CGTCGACAGC	CACGGCCACA	ACGTCTTCAA	720
	GGAGCGCATC	AGCGACATGT	GCAAAGAGAA	CCGTGAGAGC	CTGGTGGTGA	ACTATGAGGA	780
	CTTGGCAGCC	AGGGAGCAGC	TGCTGGCCCTA	CTTCTGCCT	GAGGCACCGG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCATCTC	CCACCTGCCT	CTGGTGGAGG	AGCTGCGCTC	960
60	GCTGAGGCAG	CTGCATCTGA	ACCAGCTGAT	CCGACCCAGT	GGGGTGGTGA	CCAGCTGCAC	1020
	TGGCGTCTCT	CCCCAGCTCA	GCATGGTCAA	GTACAACATG	AACAAGTGCA	ATTTCTGTCT	1080
	GGGTCTCTTC	TGCCAGTCCC	AGAACCAGGA	GGTGAAACCA	GGCTCTGTGC	CTGAGTGCCA	1140
	GTGGGCGGCG	CCCTTTGAGG	TCAACATGGA	GGAGACCATC	TATCAGAACT	ACCAGCGTAT	1200
	CCGAATCCAG	GAGAGTCCAG	GCAAAGTGGC	GGCTGGCCGG	CTGCCCGGCT	CCAAGGACGC	1260
65	CATTCTCCTC	GCAGATCTGG	TGGACAGCTG	CAAGCCAGGA	GACGAGATAG	AGCTGACTGG	1320
	CATCTATCAC	AACAACATATG	ATGGCTCCCT	CAACACTGCC	AATGGCTTCC	CTGTCTTTGC	1380
	CACCTGTATC	CTAGCCAAAC	ACGTGGCCAA	GAAGGACAAC	AAGGTTGCTG	TAGGGGAACT	1440
	GACCGATGAA	CATGTGAAGA	TGATCACTAG	CCTCTCCAAG	GATCAGCAGA	TCCGAGAGAA	1500
	GATCTTTGCC	AGCATTGTCT	CTTCCATCTA	TGGTCATGAA	GACATCAAGA	GAGGCTGGGC	1560
70	TCTGGCCCTG	TTCCGAGGGG	AGCCCAAAAA	CCCAGGTGGC	AAGCACAAGG	TACGTGGTGA	1620
	TATCAACGTG	CTCTTGTGCG	GAGACCCCTG	CACAGCGAAG	TCCGAGTTTC	TCAAGTATAT	1680
	TGAGAAAGTG	TCCAGGCCAG	CCATCTTCAC	CACCTGGCCAG	GGGGCGTCGG	CTGTGGGCCT	1740
	CACGGCGTAT	GTCCAGCGCG	ACCCTGTGAG	CAGGGAGTGG	ACCTTGGAGG	CTGGGGCCCT	1800
	GGTCTTGGCT	GACCGAGGAG	TGTGTCTCAT	TGATGAATTT	GACAAGATGA	ATGACCAAGGA	1860
75	CAGAAACGAG	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
	CGTCACTTCC	CTGCAGGCTC	GCTGCACGGT	CATTGCTGCC	GCCCAACCCA	TAGGAGGGCG	1980
	CTACGACCCC	TGCTGACTTT	TCTCTGAGAA	CGTGGACCTC	ACAGAGCCCA	TCATCTCACG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGACG	AGATGTGGGC	2100
	CCGCTTCGTG	GTGGGCGAGC	ACGTGACACA	CCACCCGAGC	AACAAGGAGG	AGGAGGGGCT	2160
80	GGCCAATGGC	AGCGCTGCTG	AGCCCGCCAT	GCCCAACACG	TATGGCGTGG	AGCCCTTGCC	2220
	CCAGGAGGTC	CTGAAGAAAT	ACATCATCTA	CGCCAAGGAG	AGGGTCCACC	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAGAT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	CACAGGCAGC	ATCCCATTTA	CGGTGCGGCA	CATCGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CCACGCGCGC	ATCCATCTGC	GGGACTATGT	GATCGAAGAC	GACGTCAACA	TGGCCATCCG	2460
	CGTGATGCTG	GAGAGCTTCA	TAGACACACA	GAAGTTGAGC	GTCTATGCGCA	GCATGCGCAA	2520
85	GACTTTTGCC	CGCTACCTTT	CATTTCGGCG	TGACAACAAT	GAGCTGTGTC	TCTTCATACT	2580
	GAAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCCAGCAGGA	2640
	CACTATTGAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

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 TTCTGTTTGG GGGTGGTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA 2880
 TGAATCGGG GTACTAGGGT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC 2940
 5 TGTTTGTTC TCCAAGCCTG CTTTGTGCTT CTCACCTTGG GGTGGGATGC CTGGCCAGTG 3000
 TGCTTACTT GGTGTCTGAA CATCTTGCCA CCTCCGAGTG CTTTGTCTCC ACTCAGTACC 3060
 10 TTGGATCAGA GCTGCTGAGT TCAGGATGCC TGCCTGTGGT TTAGGTGTTA GCCTTCTTAC 3120
 ATGGATGTCA GGAGAGCTGC TGCCCTCTTG GCGTGAGTTG CGTATTCAGG CTGCTTTTGC 3180
 TGCCCTTGGC CAGAGAGCTG GTTGAAGATG TTTGTAATCG TTTTCAGTCT CTGTCAGGTT 3240
 TCTGTGCCCC TGTGTGGGAA GAGGGCACGA CAGTGCCAGC GCAGCGTTCT GGGCTCCTCA 3300
 GTCGAGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA 3360
 TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCATT CGGTTTGGTT TCTGTAGTTT 3420
 TAATTTTAA TAAAGTTGAA TAAATATAA AAAAAAAAAA AAAAAA

Seq ID NO: 329 Protein sequence:
 Protein Accession #: AAH17490.1

1 11 21 31 41 51
 20 MAESSESFTM ASSPAQRRRG NDPLTSSPGR SSRRTDALTS SPGRDLPPFE DESEGLLGTE 60
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 DREAGRGLGR MRRGLLYDS EDEERPARK RROVERATED GEDEEMIES IENLEDLKGH 180
 SVREWVSMA GPRLEIHRFK NFLRTHVDSH GHNVFKERIS DMCKENRESL VVNYEDLAAR 240
 25 EHVLAFLPE APAELQIFD EAALEVVLAM YPKYDRITNH IHVRISHLPL VEELRSLRQL 300
 HLNQLIRTSG VVTSCGTGVL QLSMVKYN CNFVLGPFQ SQNQEVKPG SCPEQCSAGP 360
 FEVNMETIY QNYQRIQIE SPGKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGSILNAN GFVPVFATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QQIGEKIFAS 480
 IAPSIYGHED IKRGLALALF GGEFKNPFGK HKVRGDINVL LCGDPGTAKS QPLKYIEKVS 540
 30 SRAIFTTGGQ ASAVGLTAYV QRHPVSREW TLEAGALVLAD RGVCLIDEFD KMNDQDRTSI 600
 HEAMEQQSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL 660
 CVVRDVTDPV QDEMLARFV GSHVRHPSN KEEBGLANGS AEAPAMPNTY GVEPLPQEV 720
 KYIYIYAKER VHPKLNQMDQ DKVAKMYS DL RKESMATGSI PITVRHIESM IRMAEAHARI 780
 HLRDVIYIED VNMALIRVME SFIDTQKFSV MRSMRKTFAR YLSFRDNN E LLLFILKQLV 840
 35 AEQVYIYQRN PGAQQTIEV PEKDLVDKAR QINIHNLSAF YDSELFMRNK FSHDLXKRM 900
 LQOF

Seq ID NO: 330 DNA sequence
 Nucleic Acid Accession #: M17254
 Coding sequence: 257-1645

1 11 21 31 41 51
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 AAAGATGGCA GAACCAAGGC CAACTAAAGC CGTCAGGTTT TGAACAGCTG GTAGATGGGC 240
 50 TGCTTACTG APAGGATGTA TTCAGACTGT CCCGACCCCA GCAGCTCATA TCAAGGAAGC 300
 CTTATCAGTT GTGAGTGAAG ACCAGTCGTT GTTGTAGTGT GCCTACGGAA CGCCACACCT 360
 GGCTAAGACA GAGATGACCG CGTCTCTCTC CAGCGACTAT GGACAGACTT CCAAGATGAG 420
 CCCACGCGCT CCTACGACAG ATTGGCTGTC TCAACCCCCA GCCAGGGTCA CCATCAAAAT 480
 GGAATGTAA CCTAGCCAGG TGAATGGCTC AAGGAACCTC CCTGATGAAT GCAGTGTGGC 540
 CAAAGGCGGG AAGATGGTGG GCAGCCCAAG CACCGTTGGG ATGAACACAG GCAGCTACAT 600
 GGAGGAGAAG ACATGCGCAC CCCCACCAAC GACACGCAAG GAGCGCAGAG TTATCGTGCC 660
 55 AGCAGATCCT ACCTATGGA GTACAGACCA TGTGCGGACG TGGCTGGAGT GGGCGGTGAA 720
 AGAATATGGC CTTCACAGC TCAACATCTT GTTATTCAG AACATCGATG GGAAGGAAC 780
 GTGCAAGATG ACCAAGGACG ACTTCCAGAG GCTCACCCCC AGCTACACAG CCGACATCCT 840
 TCTCTACAT CTCCACTACC TCAGAGAGAC TCCTCTTCCA CATTTGACTT CAGATGATGT 900
 TGATAAAGCC TTACAAAAC CTCCACGGTT AATGCATGCT AGAAACACAG ATTTACCATA 960
 60 TGAGCCCCC AGGAGATCAG CTTGGACCGG TCACGGCCAC CCCACGCCCC AGTCGAAAGC 1020
 TGCTCAACCA TCTCTTCCA CAGTGCCCAA AACTGAAGAC CAGCGTCTC AGTTAGATCC 1080
 TTATCAGATT CTTGGACCAA CAAGTAGCCG CCTTGCAAAT CCAGGCAGTG GCCAGATCCA 1140
 GCTTTCGAG TCTCTCTGG AGCTCCTGTC GGACAGCTCC AACTCCAGCT GCATCACCTG 1200
 GGAAGGCACC AACCGGGAGT TCAAGATGAC GGATCCCGAC GAGGTGGCCC GGGCTGGGG 1260
 65 AGAGCGGAAG AGCAAAACCA ACATGAACCTA CGATAAGCTC AGCCCGCCCC TCCGTTACTA 1320
 CTATGACAAG AACATCATGA CCAAGGTCCA TGGGAAGGCG TACGCCTACA AGTTGCACTT 1380
 CCACGGGATC GCCCAGGCC TCCAGCCCCA CCCCCCGGAG TCATCTCTGT ACAAGTACCC 1440
 CTCAGACCTC CCGTACATGC GCTCCTATCA CGCCCAACCA CAGAAGATGA ACTTTGTGGC 1500
 CCCCCACCTC CCGACCTTCC CCGTGACATC TTCCAGTTT TTTGCTGCCC CAAACCCATA 1560
 70 CTGGAATTCA CCAACTGGGG GTATATACCC CAACACTAGG CTCCCCACCA GCCATATGCC 1620
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 CACCAGCCCA TCGCCACAAA CTCTATCGGA GAACATGAAT CAAAAGTGCC TCAAGAGGAA 1740
 TGAAAAAAGC TTTACTGGGG CTGGGGAAGG AAGCCGGGGA AGAGATCCAA AGACTCTTGG 1800
 GAGGGAGTTA CTGAAGTCTT ACTACAGAAA TGAGGAGGAT GCTAAAAATG TCACGAATAT 1860
 75 GGACATATCA TCTGTGGACT GACCTTGTA AAGACAGTGT ATGTAGAAGC ATGAAGTCTT 1920
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 AATCCCACTA ATGCAAACTG GGATGAACT AAAGCAATAG AAACAACACA GTTTTGACCT 2040
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 80 ACTGCATGGC ATGTGCTGTT TTGGTTGAAA TCAAAATACAT TCCGTTTGAT GGACAGCTGT 2220
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 85 GTAATGAGAA AAGGAAAGTA GTAGAATTCA GAAACAAAAA TGCGCATCTC TTTCTTTGTT 2580
 GTCAAAATGA AAATTTTAA TGAATTTGTC TGAATTTTAA GAGAAACATT CAGGACCTCA 2640
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ACAATCAGAA ATCACGCAGG CATTTTGGGT AGGCGGCCTC CAGTTTTCCT TTGAGTCGCG 2760
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 ATAATTATAT AACTTATGCA TTTATACACT ACGAGTTGAT CTCGGCCAGC CAAAGACACA 2880
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 TAGCATGGCA AATCAGATTT ATACAGGAGT CTGCATTGTC ACTTTTTTTA GTGACTAAAG 3060
 TTGCTTAATG AAAACATGTG CTGAATGTTG TGGATTTTGT GTTATAATT ACTTTGTCCA 3120
 TGAACCTGTG CAAGGGAGAG CCAAGGAAAT AGGATGTTTG GCACCC

Seq ID NO: 331 Protein sequence
 Protein Accession #: AAA52398

1 11 21 31 41 51
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 QDWLSQPPAR VTIKMECNPS QVNGSRNSPD ECSVAKGGKM VGSPDTVGMN YGSYMEEKHM 120
 PPPNMTTNER RVIIVPADPTL WSTDHVRQWL EWAVKEYGLP DVNILLFQNI DGKELCKMTK 180
 DDFQRLTPSY NADILLSHLH YLRETPPLHL TSDDVDKALQ NSPRLMHARN TDLPEYPPRR 240
 SAWTGHGHPT PQSKAAQPSF STVPKTEDQR PQLDPYQILG PTSSRLANPG SQGIQLWQFL 300
 LELLSDSSNS SCITWEGTNG EFKMTDPDEV ARRWGERKSK PNMNYDKLSR ALRYYDYKNI 360
 MTKVHGKRYA YKFDHFHQAQ ALQPHPPSS LYKYPSDLPY MGSYHAHPQK MNFVAPHPPA 420
 LPVTSSSFFA APNPYWSNPT GGIYPNTRLP TSHMPSHLGT YY 462

Seq ID NO: 332 DNA sequence
 Nucleic Acid Accession #: NM_000020
 Coding sequence: 283-1794

1 11 21 31 41 51
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 GAGCGAGCCC CTCGCCGGCT CCAGCCCGGT CCGGGGCGCG GCCGACCCC AGCCCGCGT 180
 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240
 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CCATGACCTT GGGCTCCCCC 300
 AGGAAAGGCC TCTGATGCT GCTGATGGCC TTGGTGACCC AGGGAGACCC TGTGAAGCCG 360
 TCTCGGGGCC CGCTGGTGAC CTGCACTGT GAGAGCCAC ATTGCAAGGG GCCTACCTGC 420
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 CAACCTCCTT CGGAGCAGCC GGGAACAGAT GGCAGCTGG CCCTGATCCT GGGCCCCGTG 660
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 5 GCAGTGAAGA AAGCTCTCCC CGCTCCTGCT GTAATGACCC AGAGTAGCCT CCCCAGGCGG 3720
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 10 GGAACAACT CCTGCTGAGA CCCACAGCC AGAAACTGAA AGCAGCAGCT CCCCAGGCC 4020
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 15 ATGGTTAAAT CCTGAAAAA AAAAAAAA

Seq ID NO: 333 Protein sequence
 Protein Accession #: NP_000011

1 11 21 31 41 51
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 20 MTLGSPRKGL LMLLMALVTQ GDPVKPSRGP LVTCTCESPH CKGPTCRGAW CTVVLVREEG 60
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 LILGPVLALL ALVALGVLLG WHVRRRQEQ RGLHSELGES SLILKASEQG DTMGLDLLDS 180
 25 DCTTSGSGSL PFLVQRTVAR QVALVECVGK GRYGEVVRGL WHGESVAVKI FSSRDEQSWF 240
 RETEIYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSYDFLQ RQTLPHLAL 300
 RLAVSAACGL AHLHVEIFGT QGKPAIAHRD FKSRLVLVKS NLQCCIADLG LAVMHSQSGD 360
 YLDIGNPRV GTKRYMAPEV LDEQIRTDCE ESYKWTDIWA FGLVLWEIAR RTIVNGIVED 420
 YRPPFYDVVP NDPSFEDMKK VVCVDQQTPT IPNRLAADPV LSLGLAQMMRE CWYPNPSARL 480
 30 TALRIKKTLO KISNSPEKPK VIQ

Seq ID NO: 334 DNA sequence
 Nucleic Acid Accession #: NM_004126.1
 Coding sequence: 108-329

1 11 21 31 41 51
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 40 ACATCGAAGA TTGCCAGAG AAGGAAAAAC TGAAATGGA AGTTGAGCAG CTTGCAAG 180
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 45 TGAAATTAAG AGGAGACTTT CTTAAGCACC ATATAGATAG GGTATATAT AAAAGCATAT 480
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Seq ID NO: 335 Protein sequence
 Protein Accession #: NP_004117.1

1 11 21 31 41 51
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 55 MPALHIEDLP EKEKLKMEVE QLRKEVKLQR QVSKCEEI KNYIEERSGE DPLVKGIPED 60
 KNPFKEKGC VIS

Seq ID NO: 336 DNA sequence
 Nucleic Acid Accession #: NM_005795
 Coding sequence: 555-1940

1 11 21 31 41 51
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 65 GCACGAGGGA ACAACCTCTC TCTCTSCAGC AGAGAGTGTC ACCTCCTGCT TTAGGACCAT 60
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 70 AAGAAATCTT TAAAGACAAT GTCAAATATG ATCCAAGAGA AAATGTGATT TGAGTCTGGA 300
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 GAATAATAAA AACCCATACT AGCCTATAGA AAACAATATT TGAAAGATTG CTACCACTAA 420
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 75 TTATGATTCT TGTACAGCA GAATTAGAAG AGAGTCCTGA GGACTCAATT CAGTTGGGAG 660
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 80 CAAGCAACAG AACTGGACA AATTATACC AGTGTAATGT TAACACCCAC GAGAAAGTGA 960
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 85 AGTTCATTCA TCTTACCTG ATGGGCTGTA ATTACTTTTG GATGCTCTGT GAAGGCATTT 1260
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5 TATATTACAA TGACAAATTCG TGGATCAGTT CTGATACCCA TCTCCTCTAC ATTATCCATG 1440
 GCCCAATTGT TGCTGCTTTA CTGGTGAATC TTTTTCCTT GTTAAATATT GTACGCGTTC 1500
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 10 CTGAAGGAAA GATTGCAGAG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACTTCC 1680
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 20 CTATGAAAAG CAATGAGTA CAATTGTTAT GATCTACTCA TTTGCTGACA CATCAGTTAT 2580
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 ATTTTCTTGG AATTTGTAA AAAGAAATG TGAAAAATGA GCTTGTAAT ACTCCATTAT 2880
 TTTATTTTAT AGTCTCAAT CAAATACATA CAACCTATGT AATTTTAA GCAATATAT 2940
 AATGCAACAA TGTGTGTATG TTAATATCTG ATACTGTATC TGGGCTGATT TTTTAAATAA 3000
 AATAGAGTCT GGAATGCT

Seq ID NO: 337 protein sequence
 Protein Accession #: NP_005786.1

35 1 MEKKTLYFL VLLPFFMILV TAELESPED SIQLGVTRNK IMTAQYECYQ KIMQDPIQQA 60
 EGVVCRNTWD GWLCWNDVAA GTESMQLCPD YFQDFDPSEK VTKICDQDGN WFRHPASNRT 120
 WTNYTQCNVN THEKVKTALN LPYLTIIHGH LSIALLLISL GIFFYFKSL SQRITLHKNL 180
 FFSFVNCNSV TIIHLTAVAN NQALVATNPV SKVSVQFIHL YLMGCNPFWM LCEGIYHLTL 240
 40 IVVAVFAEKQ HLMWYFELGW GFPLIPACIH AIARSLYND NCWISSDTHL LYIIHGPICA 300
 ALLVNLFPFL NIVRVLTIKL KVTHQAESNL YMKAVRATLI LVPLLGIIEFV LIPWRPEGKI 360
 AEEVYDYIMH ILMHFQQLLV STIFCFNGE VQAILRRNWN QYKIQFNGSF SNSEALRSAS 420
 YTVSTISDGP GYSHDCPSEH LNKSIHDIE NVLLKPEPLY N

Seq ID NO: 338 DNA sequence
 Nucleic Acid Accession #: NM_001795
 Coding sequence: 25-2379

50 1 GCACGATCTG TTCTCTCTGG GAAGATGCAG AGGCTCATGA TGCTCCTCGC CACATCGGGC 60
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 CGGGACACCC ACAGCCTGCT GCCCACCCAC CGGCGCCAAA AGAGAGATTG GATTTGGAAC 180
 CAGATGCACA TTGATGAAGA GAAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG 240
 TCAAGCGTGA GTCGCAAGAA TGCCAAGTAC CTGCTCAAAG GAGAATATGT GGGCAAGGTC 300
 55 TTCCGGGTGG ATGCAGAGAC AGGAGACGTG TTCGCCATTG AGAGGCTGGA CCGGGAGAAT 360
 ATCTCAGAGT ACCACCTCAC TGTGTCTATT GTGGACAAGG ACACCTGGTG AAACTGGGAG 420
 ACTCCTTCCA GCTTCACCAT CAAAGTTCAT GACGTGAAAG ACAACTGGCC TGTGTTCAAG 480
 CATCGGTGTT TCAATGCGTC CGTGCCTGAG TCGTCGGCTG TGGGGACCTC AGTCATCTCT 540
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 ATCTGTAAGG GGAAGAGATA TTTTGCCATC GATAATTCTG GACGTATTAT CACAATAACG 660
 AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGAAGC GCGAGATGCC 720
 CAGGGCCTCC GGGGGGACTC GGGCAGGCC ACCGTGCTGG TCACTCTGCA AGACATCAAT 780
 GACAACCTCC CCTTCTTAC CAGACCAAG TACACATTG TCGTGCCTGA AGACACCGT 840
 65 GTGGGCACCT CTGTGGGCTG TCTGTTTGTG GAGGACCCAG ATGAGCCCA GAACCGGATG 900
 ACCAAGTACA GCATCTTGGG GGGCGACTAC CAGGACGCTT TCACCATGTA GACAAACCC 960
 GCCCACAACG AGGCATCAT CAAGCCCATG AAGCCTCTGG ATTATGAATA CATCCAGCAA 1020
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 70 CAGCAGCCTT TCTACCACTT CAGCTGAAG GAAAACCAAG AGAAGCCTCT GATTGGCACA 1200
 GTGCTGGCCA TGGACCTCTG TCGGGTAGG CATAGCATG GATACTCCAT CCGCAGGACC 1260
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 75 AATGACAATG CCCCGGAGTT TGCCAGCCCC TACCAGCCCA AAGTGTGTGA GAACGCTGTC 1500
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 AAGTTCAAA TCACTTGAA TACTGAGAAC AACTTTACCC TCACGGATAA TCACGATAAC 1620
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 CAGTGGGCGG TAGCATACGA GGCAGTGGTA GCCATCTTAC TCTGATCCT CATCATCA 1860
 GTGATCACCC TGCTCATCTT CTGCGGCGG CGGCTCCGGA AGCAGGCCCG CGCGCACGGC 1920
 AAGAGCGTGC CGGAGATCCA CGAGCAGCTG GTCACTACG ACGAGGAGGG CGGCGCGGAG 1980
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 85 CCCCAGCGGC CCGCGCTGGA CGCCCGGCT TCCCTCTATG CGCAGGTGCA GAAGCCACCG 2100
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 AAGGACGAGG GAGACACGCA CGGCGACGGC CCCCCTACG ACACGTGCA CATCTACGGC 2220
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	TCTGACGTGG	ATTAGCATTT	CCTTAAACGAC	TGGGGACCCA	GGTTTAAAGAT	GCTGGCTGAG	2340
	CTGTACGGCT	CGGACCCCGG	GGAGGAGCTG	CTGTATTAGG	CGGCCGAGGT	CACTCTGGGC	2400
	CTGGGGACCC	AAACCCCTCG	CAGCCAGGC	CAGTCAGACT	CCAGGCACCA	CAGCCTCCAA	2460
5	AAATGGCAGT	GACTCCCCAG	CCCAGCACC	CTTCTCTGTG	GGTCCCAGAG	ACCTCATCAG	2520
	CCTTGGGATA	GCAAACTCCA	GGTTCCTGAA	ATATCCAGGA	ATATATGTCA	GTGATGACTA	2580
	TTCTCAATG	CTGGCAATC	CAGGCTGGTG	TTCTGTCTGG	GCTCAGACAT	CCACATAACC	2640
	CTGTACCCA	CAGACCGCG	CTTAACCTCA	AGACTTCTCT	TGGCTCCCA	AGGCTGCAA	2700
	GCAAAACAGA	CTGTGTTTAA	CTGCTGCAGG	GTCTTTTCT	AGGGTCCCTG	AACGCCCTGG	2760
10	TAAGGCTGGT	GAGGTCCCTG	TGCCTATCTG	CCTGGAGGCA	AAGGCCTGGA	CAGCTTGACT	2820
	TGTGGGGCAG	GATTCTCTGC	AGCCCATTC	CAAGGAGAG	TGACCATCAT	GCCCTCTCTC	2880
	GGGAGCCCTA	GCCCTGCTCC	AACTCCATAC	TCCACTCCAA	GTGCCCCACC	ACTCCCCAAC	2940
	CCCTCTCCAG	GCCTGTCAAG	AGGGAGGAAG	GGGCCCCATG	GCAGCTCCTG	ACCTTGGGTC	3000
	CTGAAGTGAC	CTCACTGGCC	TGCCATGCCA	GTAACCTGTG	TGTACTGAGC	ACTGAACCAC	3060
15	ATTCAGGGAA	ATGCTTATTA	AACTTGAAG	CAACTGTGAA	TTCATTCTGG	AGGGGCGAGT	3120
	GAGATCAGGA	GTGACAGATC	ACAGGGTGAG	GGCCACCTCC	ACACCCACCC	CCTCTGGAGA	3180
	AGGCCTGGAA	GAGCTGAGAC	CTTGCTTTGA	GACTCCTCAG	CACCCCTCCA	GTTTTCCTCG	3240
	AGAAGGGGCA	GATGTTCCCG	GAGATCAGAA	GACGTCTCCC	CTTCTCTGCC	TCACCTGGTC	3300
	GCCAATCCAT	GCTCTCTTTC	TTTTCTCTGT	CTACTCTCTA	TCCCTTGTTT	TAGAGGAACC	3360
20	CAAGATGTGG	CCTTTAGCAA	AACTGACAAT	GTCCAAACCC	ACTCATGACT	GCATGACGGA	3420
	GCCGAGCATG	TGCTTTTACA	CCTCGCTGTT	GTCACTCTCT	AGGGAACTGA	CCCTCAGGCA	3480
	CACCTTGCGA	AAGGAAGGCC	CTGCCCTGCC	CAACCTCTGT	GGTCACCCAT	GCATCATTC	3540
	ACTGGAACGT	TTCATGCAA	ACACACCTTG	GAGAAGTGGC	ATCAGTCAAC	AGAGAGGGGC	3600
	AGGGAAGGAG	ACACCAAGCT	CACCCCTCGT	CATGGACCGA	GGTTCCCACT	CTGGCAAAGC	3660
	CCCTCACACT	GCAAGGGATT	GTAGATAACA	CTGACTTGTT	TGTTTTAACC	AATAACTAGC	3720
25	TTCTTATAAT	GATTTTTTTA	CTAATGATAC	TTACAAGTTT	CTAGCTCTCA	CAGACATATA	3780
	GAATAAGGGT	TTTTGCATAA	TAAGCAGGTT	GTTATTTAGG	TTAACAATAT	TAATTCAGGT	3840
	TTTTTAGTTG	GAAAAACAAT	TCCTGTAAAC	TTCTATTTTC	TATAATTGTA	GTAATTGCTC	3900
	TACAGATAAT	GTCTATATAT	TGGCCAAACT	GGTGCATGAC	AAGTACTGTA	TTTTTTTATA	3960
30	CCTAAATAAA	GAAAAATCTT	TAGCCTGGGC	AACAAAAAAA			

Seq ID NO: 339 Protein sequence

Protein Accession #: NP_001786

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35	MORLMMLLAT	SGACLGLLAV	AAVAAAGANP	AQRDTHSLLP	THRRQKRWDI	WNQMHIIDEK	60
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	VIVVDKDTGEN	LETPSSFTIK	VHDVNDNWPV	PTHRLFNASV	PSSAVGTSV	ISVTAVDADD	180
40	PTVGDHASVM	YQILKGEYF	AIDNSGRIIT	ITKSLDREKQ	ARYEIVVEAR	DAQGLRGDSG	240
	TATVLVLTQD	INDNFFFTQ	TKYTFVVPED	TRVGTSVGS	FVEDPDEPQN	RMTKYSILRG	300
	DYQDAFTIET	NFAHNELI	PMKPLDYEYI	QYSFIVEAT	DPTIDLRYMS	PPAGNRAQVI	360
	INITDVDEPP	IFQQPFYHFQ	LKENQKKPLI	GTVLAMPDPA	ARHSIGYSIR	RTSDKGQFFR	420
	VTKKGDYINE	KELDREVYPW	YNLTVEAKEL	DSTGTPGKE	SIVQVHIEVL	DENDNAPEFA	480
45	KPYQPKVCEN	AVHGLVLQI	SAIDKDIPTP	NVKFKFTLNT	ENNFPLTDNH	DNTANITVKY	540
	GQFDREHTKV	HPLPVVISDN	GMPSTRGTST	LTVAVCKCNE	QGEFTFCEDM	AAQGVGSIIQA	600
	VVAILLCILIT	ITVITLLIFL	RRRLRKQARA	HGKSVPEIHE	QLVTYDEEGG	GEMDTTSYDV	660
	SVLNSVRRRG	AKPPPRALDA	RPSLYAQVQK	PPRHAPGAHG	PGGEMAAMIE	VKKDEADHDE	720
	DGPPYDTLHI	YGYEGSESIA	ESLSLSLGTDS	SDSDVDYDFL	NDWGRPFKML	AELYGSDPRE	780
50	ELLY						

Seq ID NO: 340 DNA sequence

Nucleic Acid Accession #: NM_003088

Coding sequence: 112-1593

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60	AACGGCAGAG	CCGAGGCGGT	GCAGATCCAG	TTCGCGCTCA	TCAACTGCGG	CAACAAGTAC	180
	CTGACGGCGG	AGGCGTTCCG	GTTCAAGGTG	AACGCGTCCG	CCAGCAGCCT	GAAGAAGAAG	240
	CAGATCTGGA	CGCTGCTGAC	GCCCCCTGAC	GAGGCGGGCA	GCGCGGCGGT	GTGCTGCGCG	300
	AGCCACCTGG	GCCGTACCT	GCGGCGGAC	AAGGACGGCA	ACGTGACCTG	CGAGCGCGAG	360
65	GTGCGCGGTC	CGACTGCGCG	TTTCTCATC	GTGCGGCACG	ACGACGGTCG	CTGGTCTGCTG	420
	CAGTCCGAGG	CGCAGCGGCG	CTACTTCGGC	GGCACCAGAG	ACCGCTGTCT	CTGCTTCGCG	480
	CAGACGGTGT	CCCCCGCCGA	GAAGTGGAGC	GTGCACATCG	CCATGCACCC	TCAAGTCAAC	540
	ATCTACAGTG	TCACCCGTAA	GCGCTACGCG	CACCTGAGCG	CGCGGCGGGC	CGACGAGATC	600
	GCCGTGGACC	GCGACGTGTC	CTGGGGCGTC	GACTCGCTCA	TCACCTCTCG	CTTCCAGGAC	660
70	CAGCGCTACA	GCGTGCAGAC	CGCCGACCAC	CGCTTCTGCG	GCCACGACGG	GCGCCTGGTG	720
	GCGCGCCCCG	AGCCGGCCAC	TGGCTACACG	CTGGAGTTCC	GCTCCGGCAA	GGTGGCCTTC	780
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	AAGGCCACCA	AGGTGGGCAA	GGACGAGCTC	TTTGCTCTGG	AGCAGAGCTG	CGCCAGGTC	900
	GTGCTGCAGG	CGGCCAACGA	GAGGAACGTG	TCCACGCGCC	AGGGTATGGA	CCTGTCTGCC	960
75	AATCAGGAGG	AGGAGGAGCC	CCAGGAGACC	TTCAGCTGG	AGATCGACCG	GCACACCAAA	1020
	AAGTGTGCCT	TCCGTACCCA	CACGGGCAAG	TACTGGACGC	TGACGGCCAC	CGGGGCGGTG	1080
	CAGTCCACCG	CCTCCAGCAA	GAATGCCAGC	TGCTACTTTG	ACATCGAGTG	GCGTGACCGG	1140
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	GCCGCTCCGG	TGAGACAGC	AGGGGACTCA	GAGCTCTTCC	TCTAGAGCT	CATCAACCGC	1260
80	CCCATCATCG	TGTTCCGCGG	GGAGCATGGC	TTCATCGGCT	GCCGCAAGGT	CACGGGCACC	1320
	CTGGACGCCA	ACCGCTCCAG	CTATGACGTC	TTCAGCTGG	AGTTCAACGA	TGGCGCCTAC	1380
	AACATCAAAG	ACTCCACAGG	CAAATACTGG	ACGGTGGGCA	GTGACTCCGC	GGTCACCAGC	1440
	AGCGGCGACA	CTCCTGTGGA	CTTCTTCTTC	GAGTTCTGCG	ACTATAACAA	GGTGGCCATC	1500
	AAGGTGGGCG	GCGCTACTCT	GAAGGGCGAC	CACGCAAGCG	TCTGGAAGGC	CTCGGCGGAA	1560
85	ACCGTGGACC	CGCCTCGCT	CTGGGAGTAC	TAGGGCCGGC	CCGTCTTCTC	CGGCCCTGTC	1620
	CCCATGTCGG	GCTCTGCGCA	ACCTTCCCTG	CTAACCCCTT	CTCCGCCAGG	TGGGCTCCAG	1680
	GGCGGAGGCG	AAGCCCCCTT	GCCTTTCAAA	CTGGAACCCC	CAGAGAAAC	GGTGCCCCCA	1740
	CCTGTGCCCC	CTATGGACTC	CCCACTCTCC	CCTCCGCCCG	GGTTCCTTAC	TCCCTCGGG	1800

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 ACAGGGTCTG CCGCTGCGAC GTTCTGCCAA GGTGTGTGTG GCGGGCGGGT AGGGGTGTGG 2280
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 TCCCAACTAT GCATCTCACT CTGGGTGTCT TGGTCTTTTA TTTTGTGTA GTGTCAATTG 2700
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Seq ID NO: 341 Protein sequence
 Protein Accession #: NP_003079

1 11 21 31 41 51
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 CFAQTVSPAE KWSVHIAMHP QVNIYSVTRK RYAHLSARPA DEIAVDRDVP WGVDSLITLA 180
 FQDQRYSVQT ADHRFLRHDG RLVARPEPAT GYTLFEFRSGK VAFRDCGGRY LAPSGPSGTL 240
 KAGKATKVKG DELFALEQSC AQVVLQAANE RNVSTRQGM DLSANQDEETD QETFOLEIDR 300
 DTKKCAFRTH TGYKWLITAT GGVSSTASSK NASCYFDIEW RDRRITLRAS NGKFVTSKKN 360
 GQLAASVETA GDSLFILMKL INRPIIVFRG EHGFIGCRKV TGTLDANRSS YDVQLEFND 420
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 SAETVDPASL WEY

Seq ID NO: 342 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence:660..1705

1 11 21 31 41 51
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 CACCCCACTG CCGACCGTGC TGGCTGCTCG GCCTCGGGGG CCTGTACAG CCTGCACCAC 360
 GCTACCATGA AGCGCGAGGC GGCCGAGGAG GCCTGCATCC TCGAGGTTGG GCGCTCAGC 420
 ACCGTGCGTG CGGCGCGCGA GCTGCGCGCT GTGCTCGCGC TCCTGCGGGC AGGCCAGGG 480
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 TGCGCGGTAC TCCAGGCCAC CGGTGGGGTC GAGCCCGCAG CTGGAAGGAG ATGCGATGCC 720
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Seq ID NO: 343 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 KFSFKGMCRL LALGGPGQVT YTFPQTSS SLEAVPFASA ANVACGEGDK DETQSHYFLC 240
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	MQDGNFLLSA	LQPEAGVCSL	ALPSDLQLDR	RGAEGPEAER	LRAARVQEQV	RARLLQLGQQ	60
	PRHNGAAEPE	PEAETARGTS	RGQYHTLQAG	FSSRSQGLSG	DKTSGFRPIA	KPAYSPASWS	120
5	SRSAYDLSCS	RRLSAHNGG	SAFGAAGYGG	AQPTPPMPTR	PVSFHERGGV	GSRADYDTLS	180
	LRSLRLGPGG	LDDRYSLVSE	QLEPAATSTY	RAFAYERQAS	SSSSRAGGLD	WPEATEVSPS	240
	RTIRAPAVRT	LQRFQSSHRS	RGVGGAVPGA	VLEPVARAPS	VRSLSLSLAD	SGHLPDVHGF	300
	NSYGSHTRLQ	RLSSGDDID	LPSAVKYLMA	SDPNLQVLGA	AYIQHKCYSD	AAAKQARS	360
	QAVPRLVKLF	NHANQEVQRH	ATGAMRNLIY	DNADNKLALV	EENGIFELLR	TLREQDDDEL	420
10	KNVTGILWNL	SSSDHLKDR	ARDTLEQLTD	LVLSPLSGAG	GPPLIQNAS	EAEIFYNATG	480
	FLRNLSSASQ	ATRKQMRCH	GLVDALVTSI	NHALDAGKCE	DKSVENAVCV	LRNLSYRLYD	540
	EMPPSALQRL	EGRRGRDLAG	APPGEVVGC	TPQSRRLREL	PLAADALTFA	EVSKDPKGLE	600
	WLWSPQIVGL	YNRLLRCEL	NRHTTEAAAG	ALQNTAGADR	RWAGVLSRLA	LEQERILNPL	660
	LDVRVTTADHH	QLRSLTGLIR	NLSRNARNKD	EMSTKVVS	IEKLPGSVGE	KSPPAEVLVN	720
15	IIAVLNNLVV	ASPLAARDLL	YFDGLRKLIF	IKKKRDS	PKSSRAASSL	LANLWQYNKL	780
	HRDFRAKGYR	KEDFLGP					

Seq ID NO: 352 DNA sequence

Nucleic Acid Accession #: M31469

Coding sequence: 1-651

	1	11	21	31	41	51	
	ATGGCTGCGC	AGGGAGAGCC	CCAGGTCCAG	TTCAAACCTG	TATTGGTTGG	TGATGGTGGT	60
25	ACTGGAAAAA	CGACCTTCGT	GAAACGTCAT	TTGACTGGTG	AATTTGAGAA	GAAGTATGTA	120
	GCCACCTTGG	GTGTTGAGGT	TCATCCCTTA	GTGTTCCACA	CCAACAGAGG	ACCTATTAAAG	180
	TTCAATGTAT	GGGACACAGC	CGGCCAGGAG	AAATTCGGTG	GACTGAGAGA	TGGCTATTAT	240
	ATCCAAGCCC	AGTGTGCCAT	CATAATGTTT	GATGTAACAT	CGAGAGTTAC	TTACAAGAAT	300
30	GTGCTAACT	GGCATAGAGA	TCTGGTACGA	GTGTGTGAAA	ACATCCCAT	TGTGTTGTGT	360
	GGCAACAAAG	TGGATATTAA	GGACAGGAAA	GTGAAGCGCA	AATCCATTGT	CTTCCACCGA	420
	AAGAAGAAAT	TTCACTACTA	CGACATTTCT	GCCAAAAGTA	ACTACAACCT	TGAAAAGCCC	480
	TTCTCTGGC	TTGCTAGGAA	GCTCATTGGA	GACCTAACT	TGGAATTTGT	TGCCATGCCT	540
	GCTCTCGCC	CACCAGAAAT	TGTCATGGAC	CCAGCTTTGG	CAGCACAGTA	TGAGCACGAC	600
35	TTAGAGGTTG	CTCAGACAAC	TGCTCTCCCG	GATGAGGATG	ATGACCTGTG	A	

Seq ID NO: 353 Protein sequence

Protein Accession #: AAA36546

	1	11	21	31	41	51	
	MAAQGEPOVQ	FKLVLVGDGG	TGKTTFVKRH	LTGEFEKKYV	ATLGVEVHPL	VFHTNRGPIK	60
40	FNWVDTAGQE	KFGGLRDGY	IAQCAIIMF	DVTSRVTYKN	VPNWHRDVLR	VCENIPIVLC	120
	GNKVDIKDRK	VKAISIVFHR	KKNLQYYDIS	AKSNYNFEKP	PLWLARKLIG	DPNLEFVAMP	180
45	ALAPEVVMDD	PALAAQYEH	LEVAQTALP	DEDDDL			

Seq ID NO: 354 DNA sequence

Nucleic Acid Accession #: NM_002820

Coding sequence: 304-831

	1	11	21	31	41	51	
	CCGGTTCCGA	AAGAAGCTGA	CTTCAGAGGG	GGAAACTTTC	TTCTTTTAGG	AGGCGGTTAG	60
55	CCCTGTTCCA	CGAACCCAGG	AGAACTGCTG	GCCAGATTAA	TTAGACATTG	CTATGGGAGA	120
	CGTGTAACAA	CACACTACTAT	CATTGATGCA	TATATAAAAC	CATTTTATT	TGCTATTAT	180
	TTCAAGAGGAA	GCGCCTCTGA	TTTGTCTCTT	TTTTCCTTTT	TTGCTCTTTC	TGGCTGTGTG	240
	GTTTGGAGAA	AGCACAGTTG	GAGTAGCCGG	TTGCTAAATA	AGTCCCAGAG	GCGAGCGGAG	300
	ACGATGACAG	CGAGACTGGT	TCAGCAGTGG	AGCGTCGCGG	TGTTCTGCT	GAGCTACGCG	360
60	GTGCCCTCCT	GCGGCGCTC	GTTGGAGGGT	CTCAGCCGCC	GCCTCAAAAG	AGCTGTGTCT	420
	GAACATCAGC	TCCTCCATGA	CAAGGGGAAG	TCCATCCAAG	ATTTACGCGG	ACGATTCTTC	480
	CTTCACCATC	TGATCGCAGA	AATCCACACA	GCTGAAATCA	GAGCTACCTC	GGAGGTGTCC	540
	CCTAACTCCA	AGCCCTCTCC	CAACACAAAG	AACCACCCCG	TCCGATTGGG	GTCTGATGAT	600
	GAGGGCAGAT	ACCTAACTCA	GGAAACTAAC	AAGGTGGAGA	CGTACAAGA	GCAGCCGCTC	660
65	AAGACACCTG	GGAGAGAAAA	GAAAGGCAAG	CCCGGGAAAC	GCAAGGAGCA	GGAAAGGAAA	720
	AAACGGCGAA	CTGCTCTGCG	TCTGGTAGAC	TCTGGAGTGA	CTGGGAGTGG	GCTAGAAGGG	780
	GACCACCTGT	CTGACACCTC	CACAACGTCG	CTGGAGCTCG	ATTACCGGTA	ACAGGCTTCT	840
	CTGGCCCGTA	GCCTCAGCGG	GGTGCTCTCA	GCTGGGTTTT	GGAGCCTCCC	TTCTGCCTTG	900
	GCTTGGACAA	ACCTAGAATT	TTCTCCCTTT	ATGTATCTCT	ATCGATTGTG	TAGCAATTGA	960
70	CAGAGAATAA	CTCAGAATAT	TGTCTGCCTT	AAAGCAGTAC	CCCCCTACCA	CACACACCCC	1020
	TGTCTCTCAG	CACCATAGAG	AGGCGCTAGA	GCCCATTCCT	CTTCTCTCAC	CGTCACCCAA	1080
	CATCAATCCT	TTACCACTCT	ACCAATAAAT	TTCATATTCA	AGCTTCAGAA	GCTAGTGACC	1140
	ATCTTCATAA	TTTGTCTGGAG	AAGTGTATTT	CTTCCCTTAA	CTCTCACACC	TGGGCAAACT	1200
	TTCTTCAGTG	TTTTCATTCT	CTTACGTTCT	TTCACTTCAA	GGGAGAAATAT	AGAAGCATTT	1260
75	GATATTATCT	ACAAACACTG	CAGAACAGCA	TCATGTCATA	AACGATTCTG	AGCCATTAC	1320
	ACTTTTATT	TAATTAATG	TATTTAATTA	AATCTCAAAT	TTATTTTAAT	GTAAGAAGCT	1380
	TAAATATATG	TTTAAACACA	TGCTTAAAT	TTGTTTAAAT	AAATTTAACT	CTGTTTCTCA	1440
	CCAGCTCATA	CAAAATAAAT	GGTTCTGAA	AATGTTTAA	TATTAACCTA	CAAGGATATA	1500
80	GGTTTCTCTC	ATGTATCTTT	TTGTTCTATTG	GCAAGATGAA	ATAATTTTTC	TAGGGTAATG	1560
	CCGTAGGAAA	AATAAACTT	CACATTTAAA	AAAAA			

Seq ID NO: 355 Protein sequence

Protein Accession #: NM_002820

	1	11	21	31	41	51	
85	MORRLVQQWS	VAVFLLSYAV	PSCGRSVEGL	SRRLKRAVSE	HQLLHDKGKS	IQDLRRRFFL	60
	HHLIAEIHIA	EIRATSEVSP	NSKPSPTNKN	HPVRFGSDDE	GRYLTQETNK	VETYKEQPLK	120

TPGKKKKGKPF GKRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSDR

Seq ID NO: 356 DNA sequence

Nucleic Acid Accession #: NM_017522

Coding sequence: 1-2100

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1	11	21	31	41	51	
ATGGGCTCC	CCGAGCCGGG	CCCTCTCCGG	CTTCTGGCGC	TGCTGCTGCT	GCTGCTGCTG	60
CTGCTGCTGC	TGCGGCTCCA	GCATCTTGCG	GCGGCAGCGG	CTGATCCGCT	GCTCGGCGGC	120
CAAGGGCCGG	CCAAAGGATG	CGAAAAGGAC	CAATTCCAGT	GCCGGAAACGA	GCGCTGCATC	180
CCCTCTGTGT	GGAGATGCGA	CGAGGACGAT	GACTGTCTAG	ACCACAGCGA	CGAGGACGAC	240
TGCCCCAAGA	AGACCTGTGC	AGACAGTGAC	TTCACCTGTG	ACAAACGGCCA	CTGCATCCAC	300
GAACGGTGA	AGTGTAGCGG	CGAGGAGGAG	TGTCCTGATG	GCTCCGATGA	GTCCGAGGCC	360
ACTTGACCA	AGCAGGTGTG	TCCTGCAGAG	AAGCTGAGCT	GTGGACCCAC	CAGCCACAAG	420
TGTGTACCTG	CCTCGTGGCG	CTGCGACGGG	GAGAAGGACT	GCGAGGGTGG	AGCGGATGAG	480
GCCGGCTGTG	CTACCTCACT	GGGCACCTGC	CGTGGGACG	AGTTCAGTG	TGGGATGGG	540
ACATGTGTCC	TTGCAATCAA	GCATGTCAAC	CAGGAGCAGG	ACTGTCCAGA	TGGGAGTGAT	600
GAAGCTGGCT	GCCTACAGGG	GCTGAACGAG	TGTCTGCACA	ACAATGGCGG	CTGCTCACAC	660
ATCTGCACTG	CTAGCTCACT	TGGCTTTGAA	TGCACGTGCC	CAGCAGGCTT	CCAGCTCCTG	720
GACCAGAAGA	CTTGTGGCGA	CATTGATGAG	TGCAAGGACC	CAGATGCCTG	CAGCCAGATC	780
TGTGTCAATT	ACAAGGGCTA	TTTAAAGTGT	GAGTGTACC	CTGGCTGCGA	GATGGACCTA	840
CTGACAAGA	TCTATAGCGG	TGCTGTGGC	AAGAGCCCAT	CCCTAATCTT	CACCAACCGC	900
ACGAGTGGCG	AGGATCGACC	TGTGAAGCGG	AACATTCAC	GCCTCATCCC	CATGCTCAAG	960
AATGTCGTGG	CACAGATGAT	GGAAGTTGCC	ACCAATCGCA	TCTACTGGTG	TGACCTCTCC	1020
TACCGTAAGA	TCTATAGCGG	CTAGATGGAC	AAGGCCAGTG	ACCCGAAAGA	GCGGGAGGTC	1080
CTCATTGACG	AGCAGTTGCA	CTCTCCAGAG	GGCTTGGCAG	TGGACTGGGT	CCACAAGCAC	1140
ATCTACTGGA	CTGACTCGGG	CAATAAGACC	ATCTCAGTGG	CCACAGTTGA	TGGTGGCCGC	1200
CGACGCACTC	TCTTCAAGCT	TAACCTCAGT	GAACCCCGGG	CCATCGCTGT	TGACCCCTCG	1260
CGAGGGTTCA	TGTATTGGTC	TGACTGGGGG	GACCAGGCCA	AGATTGAGAA	ATCTGGGCTC	1320
AACGGTGTGG	ACCGGCAAAAC	ACTGGTGTCA	GACAATATTG	AATGGCCCAA	CGGAATCACC	1380
CTGGATCTGC	TGAGCCAGCG	CTTGTACTGG	GTAGACTCCA	AGCTACACCA	ACTGTCCAGC	1440
ATTGACTTCA	GTGGAGGCAA	CAGAAAGACG	CTGATCTCCT	CACTGACTTT	CCTGAGCCAC	1500
CCTTTTGGGA	TAGCTGTGTT	TGAGGACAAG	GTGTTCTGGA	CAGACCTGGA	GAACGAGGCC	1560
ATTTTTCAGT	CAAACTCGCT	CAATGGCCTG	GAAATCTCCA	TCCTGGCTGA	GAACCTCAAC	1620
AACCCACATG	ACATTGTCTAT	CTTCCATGAG	CTGAAGCAGC	CAAGAGCTCC	AGATGCCTGT	1680
GAGCTGAGTG	TCCAGCCTAA	TGGAGGCTGT	GAATACCTGT	GCCTTCCTGC	TCCTCAGATC	1740
TCCAGCCACT	CTCCCAAGTA	CACATGTGCC	TGTCCTGACA	CAATGTGGCT	GGGTCCAGAC	1800
ATGAAGAGGT	GCTACCGAGA	TGCAAAATGAA	GACAGTAAGA	TGGGCTCAAC	AGTCACTGCC	1860
GCTGTTATCG	GGATCATCGT	GCCCATAGTG	GTGATAGCCC	TCCTGTGCAT	GAGTGGATAC	1920
CTGATCTGGA	GATGTGAGAG	GCGGAAGAAC	ACCAAAAGCA	TGAATTTTGA	CAACCCAGTC	1980
TACAGGAAAA	CAACAGAAGA	AGAAGATGAA	GATGAGCTCC	ATATAGGGAG	AACTGCTCAG	2040
ATTGGCCATG	TCTATCCTCG	ACGAGTGGCA	TTAAGCCTTG	AAGATGATGG	ACTACCCTGA	2100
GGATGGGATC	ACCCCTTCG	TGCCTCATGG	AATTCAGTCC	CATGCACTAC	ACTCCGATG	2160
GTGTATGACT	GGATGAATGG	GTTTCTATAT	ATGGGTCTGT	GTGAGTGTAT	GTGTGTGTGT	2220
GATTTTTTTT	TTTAAATTTA	TGTTGCGGAA	AGGTAACCCAC	AAAGTTATGA	TGAACTGCAA	2280
ACATCCAAAG	GATGTGAGAG	TTTTTCTATG	TATAATGTTT	TATACACTTT	TAACTGGTTT	2340
GCACTACCCA	TGAGGAATTC	GTGGAATGGC	TACTGCTGAC	TAACATGATG	CACATAACCA	2400
AATGGGGGCC	AATGGCACAG	TACCTTACTC	ATCATTAAAA	AACTATATTT	ACAGAAGATG	2460
TTTGGTTGCT	GGGGGGCTTT	TTTAGGTTTT	GGGCATTGTG	TTTTTGTAAT	TAAGATGATT	2520
ATGCTTTGTG	GCTATCCATC	AACATAAGT				

Seq ID NO: 357 Protein sequence

Protein Accession #: NP_059992

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70

1	11	21	31	41	51	
MGLPEPGPLR	LLALLLLLLL	LLLLRLQHLA	AAAADPLLGG	QGPKECEKD	QFQCRNERCI	60
PSVWRCEDD	DCLDHSDEDD	CPKKTCDSD	FTCDNGHCIH	ERWKCDEEEE	CPDGSDESEA	120
TCTKQVCPAE	KLSCGPTSHK	CVPASWRCDG	EKDCGEGADE	AGCATSLGTC	RGDEFQCGDG	180
TCVLAIKHCN	QEQDCPDGSD	EAGCLQGLNE	CLHNNGGCSH	ICTDLKIGFE	CTCPAGFQLL	240
DQKTCGDIDE	CKTCCAGSQI	CVNYKGYFKC	ECYPGCEMDL	LTNCKCAAAG	KSPSLIFTNR	300
TSAEDRPVKR	NYSRLIPMLK	NVVALDVEVA	TNRIYWCDLS	YRKIYSAYMD	KASDPKEREV	360
LIDEQLHSPE	GLAVDWVHKH	IYWTDSGNKT	ISVATVDGGR	RRTLFNRNLS	EPRAIADVPL	420
RGFMYWSDWG	DQAKIEKSGL	NGVDRQTLVS	DNIEWPNGIT	LDLLSQRLYW	VDSKLHQLSS	480
IDFSGGNRKT	LISSTDFLSH	PFGIAVPEDK	VFWTDLNEA	IFSANRLNGL	EISILAENLN	540
NPHDIVIFHE	LKQPRAPDAC	ELSVQPNNGC	EYLCLPAPQI	SSHSPKYTCA	CPDTMWLPGD	600
MKRCYRDANE	DSKMGSTVTA	AVIGIIIVIV	VIALLCMSGY	LIWRNWKRN	TKSMNFDNEV	660
YRKTTEEDE	DELHIGRTAQ	IGHVYPARVA	LSLEDDGLP			

Seq ID NO: 358 DNA sequence

Nucleic Acid Accession #: M27826

Coding sequence: <1-503

75
80
85

1	11	21	31	41	51	
AGCCCAAGAA	ACATCTCACC	AATTTCAAAT	CTGATCTATT	CGGCTTAGCG	ACTGAAGATT	60
GACGCTGCCC	GATCGCCTCG	GAAGTCCCTT	GGACCATCAC	AGAAGCCGAG	CTTCGGGTAA	120
CTCTCACAGT	GGAGGGTAAG	TCCATCCCCT	GTTTAAATCGA	TACGGGGGCT	ACCCACTCCA	180
CGTTGCCCTT	TTTTCAAGGG	CCTGTTTCCC	TGCCCCCAT	AACTGTTGTG	GGTATTGACG	240
GCCAAAGCTTC	AAAACCCCTG	AAAACCTCCC	CACCTCTGGT	CCAACCTTGA	CAACACTCTT	300
TTATGCACTC	TTTTTTAGTT	ATCCCCACCT	GCCCCACTTC	CTTATTAGGC	CGAAATATTT	360
TAACCAAAAT	ATCTGCTTCC	CTGACTATTC	CTGGAGTACA	GCTACATCTC	ATTGCTGCC	420
TTCTTCCCAA	TCCAAAGCCT	CCTTTGTGTC	CTCTAACATC	CCCAATATAT	CAGCCCTTAC	480
CACAAGACCT	CCCTTCAGCT	TAATCTCTCC	CACCTCTAGG	TCCACGCGCG	CCCCTAATCC	540
CACTTGAAGC	AGCCCTGAGA	AACATCGCCC	ATTCTCTCTC	CATACCAACC	CCCAAAATTT	600
TTGCGCGCTC	CAACACTTCA	ACACTATTTT	GTTTTATTGT	TCTTATTAAT	ATCAGAAGGC	660

AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCACGTAT 720
 ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAACCTG 780
 ATGACATTCC ACCATTGTGA TTTGTTCTCG CCCACCCCTA ACTGATCAAT GTACTTTGTA 840
 ATCTCCCCCA CCTTAAGAA GGTTCCTTTGT AATTCTCCCC ACCCTTGAGA ATGTACTTTG 900
 TGAGATCCAC CCCTGCCAC CAGAGAACAA CCCCCTTTGA TTGTAATTTT TTATTACCTT 960
 CCCAATCCT ATAAACAGC CCCACCCCTA TCTTCCTTCA CTGACTCTCT TTTCGGACTC 1020
 AGCCACGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC

Seq ID NO: 359 Protein sequence
 Protein Accession #: AAA65999

1 11 21 31 41 51
 PKKHLTNFKS DLFLGLATEDW RCPIASEVPW TITEAELRVT LTVEGKSIPC LIDTGATHST 60
 LPSFGQPVSL APITVVGIDG QASKPLKTPP LWCQLGQHSF MHSFLVIPTC PLPLLLGRNII 120
 TKLSASLTIP GVQLHLIAAL LPNPKPLCP LTSPQYQPLP QDLPSA

Seq ID NO: 360 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 162-5582

1 11 21 31 41 51
 AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTC CCCTCTCCCT CCCCAATGGC 60
 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 TTCGTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCTCTTA 180
 GGTGGAAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCTCGCA TTGACCTTCC 240
 TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG TCACAGTTGA TGTACTAAAA GCAC TAGATT 300
 TTCACAAATC TCCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAAAT 360
 CTAAAGGCTC AGATACTGCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCAACAA 420
 AACAGTTATT TCCAGGTGGA ACTTCCCTCAG AAGACTTTTC AATACTATT ACAGTAAAAAC 480
 CAAAAAAGG AATTCAGTCT TTCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA 540
 TTGGTGTGTA GGTGGGAGA TCACCTGTTT TTCTGTTTGA AGACCACACT GGAAAACTCTG 600
 CCCAGAAGA CTATCCCTC TCCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CCGAGGAGAA AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAAACA 720
 CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTGTATAC CAATGGAATC ACGGTTTTTG 780
 GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGACAT TCAGCAGTTT TTGATCACAG 840
 GTGATCCCAA GGCAGCGATG GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTCAG 900
 CACCAAGGC TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCCACA GAGGATATAA 960
 TCGAATATGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020
 GACCCACTGA AACTGGAGAA ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
 AAGAATACAA CTATGGAACA ATGGAAGATT ACCAGACAGA AGCTCCTAGG CATGTTCTG 1140
 GGACAAATGA CCCAAATCCA GTTGAAGAAA TATTACTGA AGAATATCTA ACGGAGAGG 1200
 ATTATGATTG CCGAGGAGAA AATCTGAGG ATACACTATA TGAACACAA GAAATAGACG 1260
 GCAGGGATTG TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA 1320
 AAGAATATGA AGATAAACCA ACAAGCCCC CTAAATGAAGA ATTTGGTCCA GGTGTACCAG 1380
 CAGAAACTGA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCAATGGA GAGAAAGGAC 1440
 AGAAAGGAGA ACCAGCAGTG GTTGAGCCTG GTATGCTTGT CGAAGGACCA CCAGGACCAG 1500
 CAGGACCTGC AGGTATTATG GGTCTCCAG GTCTACAAGG CCCCCTGGA CCCCCTGGTG 1560
 ACCCTGGCGA TGGGGGCC CCGAGACGTC CTGGCTTACC AGGGGCTGAT GGTCTACCTG 1620
 GTCCTCCTGG TACTATGTTG ATGTTACCGT TCCGTTATGG TGGTGTATGG TCCAAAGGAC 1680
 CAACCATCTC TGCTCAGGAA GCTCAGGCTC AAGCTATTCT TCAGCAGGCT CGGATTGCTC 1740
 TGAGAGGCC ACCTGGGCCA ATGGGTCTAA CTGGAAGACC AGGTCTCTGT GGGGGGCTG 1800
 GTTCATCTGG GGCACAAAGT GAGAGTGGTG ATCCAGGTCC TCAGGGCCCT CGAGGCGTCC 1860
 AGGGTCCCC TGGTCCAACG GGAACCTG GAAAAAGGG TCGTCCAGGT GCAGATGGAG 1920
 GAAGAGGAAT CCGAGGAGAA AGGGGACG AGGGTTGAT GGACTTCCGG 1980
 GTCTGCCAGG TGACAAAGGT CACAGGGTG AACGAGGTCC TCAAGGTCTC CCAGGTCTC 2040
 CTGGTGATGA TGGAAATGAG GGAGAAGATG GAGAAATTGG ACCAAGAGGT CTTCCAGGTG 2100
 AAGCTGGCCC ACGAGGTTTG CTGGGTCCA GGGGAACCTC AGGAGCTCCA GGGCAGCCTG 2160
 GTATGGCAGG TGATAGATGG CCCCAGGAC CAAAAGGGAA CATGGTCCC CAAGGGGAGC 2220
 CTGGGCCCTC AGGTCAACAA GGAATCCAG GACCTCAGGG TCTTCTGTG CCACAAGGTC 2280
 CAATTGGTCC AATTGGTGAA AAGGACCA AAGGAAACC AGGACTTGCT GGACTTCTG 2340
 GTGCTGATGG GCCTCCTGGT CATCTGGGA AAGAAGGCCA GTCTGGAGAA AAGGGGGCTC 2400
 TGGGTCCCC TGGTCCACAA GGTCTATTG GATNCCGGG CCCCCTGGGA GTAAAGGGAG 2460
 CAGATGGTGT CAGAGGTCTC AAGGGATCTA AAGGTGAAAA GGGTGAAGAT GGTTTCCAG 2520
 GATTCAAAGG TGACATGGGT CTAAAAGGTG ACAGAGGAGA AGTTGGTCAA ATTGGCCCAA 2580
 GAGGNAAGA TGGCCCTGAA GGACCCAAAG GTCGAGCAGG CCAACTGGA GACCAGGTG 2640
 CTTCAGGTCA AGCAGGAGAA AAGGGAAAAC TTGGAGTTCC AGGATTACCA GGATATCCAG 2700
 GAAGACAAGG TCCAAAGGGT TCCACTGGAT TCCTGGGTT TCCAGGTGCC AATGGAGAGA 2760
 AAGGTGACG GGGAGTAGCT GGCACACAG GCCTCGGGG TCAGCGTGGT CCAACGGGTC 2820
 CTCGAGGTTC AAGAGGTGCA AGAGGTCCA CTGGGAAACC TGGGCCAAG GGCATTCTAG 2880
 GTGGCGATGG CCCTCCTGGC CTTCCAGGTG AAAGAGGTCC TCAAGGACCT CAGGGTCCAG 2940
 TTGGATTCCC TGGACCAAAA GGCCTCCTG GACCACCAGG AAGGATGGGC TGCCACGGAC 3000
 ACCCTGGGCA ACGTGGGGAG ACTGGATTTC AAGGCAAGAC CGGCCCTCT GGGCAGGGG 3060
 GAGTGGTTGG ACCACAGGGA CCAACCGGTG AGACTGGTCC AATAGGGGAA CGTGGGTATC 3120
 CTGTCCTTCC TGGCCCTCTT GGTGAGCAAG GTCTTCTGTG TGCTGCAGGA AAAGAAGGTG 3180
 CAAAGGGTGA TCCAGGTCTT CAAGGTATCT CAGGGAAGA TGGACACGA GGATTACGTG 3240
 GTTTCCACAG GGAAGAGGT CTTCTGGAG CTCAGGTGTC ACCTGGACTG AAAGGAGGGG 3300
 AAGGTCCCCA GGGCCACCA GGTCCAGTTG GCTCACCAGG AGAAGTGGG TCAGCAGGTA 3360
 CAGCTGGCCC AATTGGTTTA CAGGGGCGCC CGGACCTCA GGTCTCTCT GGTCCAGCTG 3420
 GAGAGAAAGG TGCTCCTGGA GAAAAAGGTC CCAAGGGGCC TGACGGGAGA GATGGAGTTC 3480
 AAGGTCTGT TGGTCTCCCA GGGCCAGCTG GTCTGCCGG CTCCTCTGGG GAAGACGGAG 3540
 AACAGGGTGA AATTGGTGG CCGGACAAA AAGGCAGCAA GGGTGGCAAG GGAGAAAATG 3600
 GCCCTCCCGG TCCCCAGGT CTTCAAGGAC CAGTTGGTGC CCTTGGAAAT GCTGGAGGTG 3660
 ATGGTGAACC AGGTCTTAGA GGACAGCAGG GGATGTTTGG GCAAAAAGGT GATGAGGGTG 3720
 CCAGAGGCTT CCTGGACCT CTTGGTCCA TAGGTCTTCA GGGTCTGCCA GGCCACCTG 3780
 GTGAAAAAGG TGAATGGG GATGTTGGTC CATGGGGGCC ACCTGTCTCT CCAGGCCCAA 3840

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GAGGCCCTCA AGGTCCTCAAT GGAGCTGATG GACCACAAGG ACCCCCAGGT TCTGTGTGGT 3900
CAGTTGGTGG TGTGGAGAA AAGGGTGAAC CTGGAGAAGC AGGAAACCCA GGGCCTCCTG 3960
GGGAAGCAGG TGTAGGCGGT CCCAAAGGAG AAAGAGGAGA GAAAGGGGAA GCTGGTCCAC 4020
CTGGAGCTGC TGGACCTCCA GGTGCCAAGG GGCCGCCAGG TGATGATGGC CCTAAGGGTA 4080
ACCCGGGTCC TGTGGTMTT CTGGAGATC CTGGTCTCTC TGGGGAACCT GGCCTGTCAG 4140
GTCAAGATGG TGTGGTGGT GACAAGGGTG AAGATGGAGA TCCTGGTCAA CCGGGTCTCT 4200
CTGGCCCATC TGGTGAGGCT GGCCCAACAG GTCCTCTCTG AAAACGAGGT CCTCTGGAG 4260
CTGCAGGTGC AGAGGGAAGA CAAGGTGAAA AAGGTGCTAA GGGGAAGCA GGTGCAGAAG 4320
GTCCTCTGGG AAAAACCGGC CCAGTCCGTC CTCAGGGACC TGCAGGAAAG CTTGGTCCAG 4380
AAGGTCTTCG GGGCATCCCT GGTCTGTGG GAGAACAAGG TCTCCCTGGA GCTGCAGGCC 4440
AAGATGGACC GCAAGTCCCT ATGGGACCTC CTGGCTTACC TGGTCTCAA GGTGACCCTG 4500
GCTCCAAGGG TGAAAAGGGA CATCTGGTT TAATTGGCCT GATTGGTCTC CCAGGAGAAC 4560
AAGGGGAAAA AGGTGACCGA GGGCTCCCTG GAACCTCAAG ATCTCCAGGA GCAAAGGGG 4620
ATGGGGGAAT TCCTGTCTCT GCTGGTCCCT TAGGTCCACC TGGTCTCCA GGTCTACCAG 4680
GTCCTCAAGG CCCAAGGGT AACAAAGGCT CTACTGGACC CGCTGGCCAG AAAGGTGACA 4740
GTGGTCTTCC AGGGCTCTCT GGGCTCCAG GTCACCTGG TGAAGTCATT CAGCCTTTAC 4800
CAATCTTGTG CTCCTCAAAA ACGAGAAGAC ATACTGAAG CATGCAAGCA GATGCAGATG 4860
ATAATATTCT TGATTACTCG GATGGAATGG AAGAAATATT TGGTTCCTCT AATTCCCTGA 4920
AACAGACAT CGAGCATATG AAATTTCCAA TGGGTACTCA GACCAATCCA GCCCGAACTT 4980
GTAAGACCT GCAAGTCCAG CATCTGACT TCCAGATGG TGAATATTGG ATTGATCCTA 5040
ACCAAGGTTG CTCAGGAGAT TCCTTCAAAG TTTACTGTAA TTTACATCT GGTGGTGAGA 5100
CTTGCAATTA TCCAGACAAA AAATCTGAGG GAGTAAGAAT TTCATCATGG CCAAAGGAGA 5160
AACCAGGAAG TTGGTTTACT GAATTAAGA GGGGAAACT GCTTTCATAC TTAGATGTG 5220
AAGGAAATTC CATCAATATG GTGCAATGA CATTCCTGAA ACTTCTGACT GCCTCTGCTC 5280
GGCAAAATTT CACCTACCAC TGTCAATCAGT CAGCAGCCTG GTATGATGTG TCATCAGGAA 5340
GTTATGACAA AGCACTTCGC TTCCTGGGAT CAAATGATGA GGAGATGTCC TATGACAAAT 5400
ATCCTTTTAT CAAAACACTG TATGATGGTT GTACGTCCAG AAAAGGCTAT GAAAAAAGT 5460
TCATTGAAAT CAATACACCA AAAATTGATC AAGTACCTAT TGTGATGTG ATGATCAGTG 5520
ACTTTGGTGA CCAAGTCCAG AAGTTCGGAT TTGAAGTTGG TCCTGTGTTT TTTCTTGGCT 5580
AAGATTAAGA CAAAGACAT ATCAAATCAA CAGAAATGT ACCTTGTGTC CACCAACCCA 5640
TTTTGTGCCA CATGCAAGTT TTGAATAAGG ATGTATGGAA AACAACGCTG CATATACAGG 5700
TACCATTTAG GAAATACGTA TGCCTTTGTG GGGGCAGAAAT CACAGACAAA AGCTTTGAAA 5760
ATCATAAAGA TATAAGTTGG TGTGGCTAAG ATGGAACAG GGCTGATTCT TGATCCCAA 5820
TTCTCAACTC TCCTTTTCTT ATTTGAAATTT CTITGGTGTG GTAGAAAACA AAAAAAGAAA 5880
AATATATATT CATAAAATAT ATGGTGCTCA TTCTCATCCA TCCAGGATGT ACTAAACAG 5940
TGTGTTAAT AAATTGTAAT TATTTTGTGT ACAGTTCTAT ACTGTTATCT GTGTCCATT 6000
CCAAACTTGG CAGGTGTCCC TGAATTCGCG TGACTCTAAT TTATGAGGAT GCCGAAGTCT 6060
GATGGCAATA ATATATGTAT TATGAAATG AAGTTATGAT TTCCGATGAC CTTAAGTCCC 6120
TTTCTTGGT TAATGATGAA ATTCCTTTGT GTGTGTTT

Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

45
50
55
60
65
70
75

1 11 21 31 41 51
MEPSSRWKT KRWLWDFVT TLALTFLFQA REVRGAAPVD VLKALDFHNS PEGISKTTGF 60
CTNRKNSKGS DTAYRVSKQA QLSAPTKQLF PGGTFPEDFS ILFTVVKPKKG IQSFLLSIYN 120
EHGIQQIGVE VGRSPVLFPE DHTGKPAPED YPLFRTVNIA DGKWHRAVIS VEKKTVMIV 180
DCKKTKTKPL DRSERAIVDT NGITVFGTRI LDEEVFEGDI QQFLITGDPK AAYDYCEHYS 240
PDCDSSAPKA AGTAQEPQIDE YAPEDIIEYD YEYGEAEYKE AESVTEGPTV TEETIAQTEA 300
NIVDDFQEYN YGTMSYQTE APRHVSQNE PNPVEEIFTE EYLTGEDYDS QRKNS EDTLY 360
ENKEIDGRDS DLLVDGLDGE YDFYKEYEY DKPTSPPNEE FPGVPVPAETD ITETSINGHG 420
AYGEGKGQGE PAVVEPGLMV EGPPPGAGPA GIMGPPGLQG PTGPPGDPGD RGPGRPLGL 480
GADGLPGPPG TMLMLPFRYG GDGSKGPTIS AQEAQAQAIL QQARIALRGP PGPMLTGRP 540
PVGPGPGSSG AKGESGDPGP QGPRGVQGGP GPTGKPGKRG RPDAGGGRGM PGEFPAKGRD 600
GFDGLPLPLG DKGHRGEPG QGPPGPPGDD GMRGEDGEIG PRGLPGEAGP RGLLGRPTG 660
GAPGQPMAG VDGPPPGKGN MGPPQGEPPG GQQGNPFPQG LPPGQGPFGP PGEKGPQKGP 720
GLAGLPGADG PPGHPGKEQG SGEGKALGPP GPQGPFGKPG PRGVKADGV RGLKGSKEGK 780
GEDGFPFGKG DMGLKGDRGE VQIGPRGXG GPEGPKGRAG PTGDPGPGSG AGEKGLGVP 840
GLPGYPGRQG PKGSTGPPGF PGANGKGRG GVAGKPGPRG QRGPTGPRGS RGARGPTGKP 900
GPKGTSGGDD PPGPPGERGP QGPQGPVGFPG GPKGPPGPPG RMGCPGHFGP RGETGPFQKT 960
GPPGPGGVVG POGPTGTETG IGERGYPGPP GPPGEGQLPG AAGKEGAKGD PGPQGISGKD 1020
GPAGLRGFPG ERGLPGAQGA PGLKGEGEPQ GPPGPVGSFG ERGSAGTAGP IGLRGRFGPQ 1080
GPPGPAGEKG APGEKGPQGP AGRDGVQGPV GLPGPAGPAG SPGEDGDKGE IGEPPGQKGS 1140
GKGENGPPG PPGLPQPVGA PGIAGGDGEP GPRGQGMFG QKDEGARGF PGPPGPIGLQ 1200
GLPGPPGEKG ENGDDVPWGP PGPPGPRGPQ GPNAGDGPQG PPGSVGSVGG VGEKGEFGEA 1260
GNPGPPGEAG VGGPKGERGE KGEAGPPGAA GPPGAKGPPG DDGPKGNPFP VGFPGDPGPP 1320
GELGPAGQDG VGGDKGEDGD PGQPPGPPGS GEAGPPGPPG KRGPPGAAGA EGRQGEKGA 1380
GEAGBEGPPG KTGVPVGPQG AGKPGPEGLR GIPGVPGEQG LPGAAGQDGP PGPMGPPLG 1440
GLKGDPSKG EKGHPGLIGL IGPPGEQGEK GDRGLPGTQG SPGAKGDGGI PGPAAGPLGP 1500
GPPGLPGPQG PKGNKSGTGF AGQKGDGSLP GPPGPPGPPG EVIQPLPLS SKKTRRHTEG 1560
MQADADDNII DYSDGMEEIF GSLNSLKQDI EHMKFPMGTQ TNPARTCKDL QLSHPDFPDG 1620
EYWDIPNQGC SGDSFKVYCN FTSGGETCIY PDKKSEGVRI SSWPKEKPGS WFSEFKRGKL 1680
LSYLDVEGNS INMVMTFLK LITASARQNF TYHCHQSAAW YDVSSGSYDK ALRFLGSNDE 1740
EMSYDNNPFI KTYLDGCTSR KGYEKTVEI NTPKIDQVPI VDVMSDFDQ QNPKFGFEVG 1800
FVCFLG

80
85

Seq ID NO: 362 DNA sequence
Nucleic Acid Accession #: NM_003107
Coding sequence: 351-1775

1 11 21 31 41 51
TTCCCCAGCA TTCGAGAAAC TCCTCTCTAC TTTAGCACGG TCTCCAGACT CAGCCGAGAG 60
ACAGCAAACCT GCAGCGCGGT GAGAGAGCGA GAGAGAGGGA GAGAGAGACT CTCCAGCCTG 120
GGAACATAA CTCCTCTGCG AGAGGCGGAG AACTCCTTCC CCAATCTTT TGGGGACTTT 180

	TCTCTCTTTA	CCCACCTCCG	CCCCTGCGAG	GAGTTGAGGG	GCCAGTTCGG	CCGCCGCGCG	240
	CGTCTTCCCG	TTCGCGGTGT	GCTTGGCCCG	GGGAACCGGG	AGGGCCCGGC	GATCGCGCGG	300
	CGGCGCGCGC	GAGGGTGTGA	GCGCGCGTGG	GCGCCCGCGG	AGCCGAGGCC	ATGGTGCAAG	360
5	AAACCAACAA	TGCGGAGAAC	ACGGAAGCGC	TGCTGGCCGG	CGAGAGCTCG	GACTCGGGCG	420
	CCGGCCTCGA	GCTGGGAATC	GCCTCTCTCC	CCACGCCCGG	CTCCACCGCC	TCCACGGGCG	480
	GCAAGGCCGA	CGACCCGAGC	TGGTGCAAGA	CCCCGAGTGG	GCACATCAAG	CGACCCATGA	540
	ACGCTTCAT	GGTGTGTGCG	CAGATCGAGC	GGCGCAAGAT	CATGGAGCAG	TGCGCCGACA	600
	TGCACAAAGC	CGAGATCTCC	AAGCGGCTGG	GCAAAACGCTG	GAAGCTGTCT	AAAGACAGCG	660
10	ACAAGATCCC	TTTCATTGGA	GAGGCGGAGC	GGCTGCGCCT	CAAGCACATG	GCTGACTACC	720
	CCGACTACAA	GTACCGGCCC	AGGAAGAAGG	TGAAGTCCGG	CAACGCCAAC	TCCAGCTCCT	780
	CGGCGCGCGC	CTCTCTCAAG	CCGGGGGAGA	AGGGAGACAA	GGTCGTGGC	AGTGGCGGGG	840
	GCGGCCATGG	GGGCGGCGGC	GGCGCGGGGA	GCAGCAACGC	GGGGGGAGGA	GGCGCGGTG	900
	CGAGTGGCGG	CGGCGCCAAC	TCCAAACCGG	CGCAGAAAAA	GAGCTGCGCG	TCCAAAGTGG	960
	CGGGCGGCGC	GCGCGGTGGG	GTTAGCAAAAC	CGCACGCCAA	GCTCATCTCTG	GCAGGCGGCG	1020
15	GCGGCGGCGG	GAAAGCAGCG	GCTGCGCGCG	CCGCTCTCTT	CGCCGCGGAA	CAGGCGGGGG	1080
	CCGCGCGCCT	GCTGCCCTTG	GGCGCGCGCG	CCGACCACCA	CTCGCTGTAC	AAGGCGCGGA	1140
	CTCCGAGCGC	CTCGGCTCTG	GCCTCTCTCG	CAGCCTCGGC	CTCCGAGCG	CTCGCGGCC	1200
	CGGGCAAGCA	CCTGGCGGAG	AAGAAGGTGA	AGCGCGTCTA	CCTGTTGCGC	GGCTGGGCA	1260
20	CGTCGTCTG	GCCCGTGGGC	GGCGTGGGCG	CGGGAGCGGA	CCCCAGCGAC	CCCCTGGGCC	1320
	TGTACGAGGA	GGAGGGCGAG	GGCTGTCTGC	CCGACGCGCC	CAGCCTGAGC	GGCGCGACGA	1380
	GCGCGCGCTC	GTCGCCCGCC	GCGGGCGGCT	CGCCGCGCGA	CCACCGCGGC	TACGCCAGCC	1440
	TGCGCGCGCG	CTCGCCCGCC	CCGTCCAGCG	CGCCCTCGCA	CGCGTCTCTC	TGCGCTCTCT	1500
	CCCACTCTCT	CTCTCTCTCT	TCTCTGGGCT	CCTCGTCTCT	CGACGACGAG	TTCGAAGACG	1560
25	ACCTGCTCGA	CCTGAACCCC	AGCTCAAACT	TTGAGAGCAT	GTCCCTGGGC	AGCTTCAGTT	1620
	CGTCGTCTGC	GCTCGACCGG	GACCTGGATT	TTAACTTCGA	GCCCGGCTCC	GGCTCGCACT	1680
	TCGAGTTCCC	GAGACTCTGC	ACGCGCGAGG	TGAGCGAGAT	GATCTCGGGA	GACTGGCTCG	1740
	AGTCCAGCAT	CTCCAACCTG	GTTTTACCT	ACTGAAGGGC	GCGCAGGCAG	GGAGAAGGGC	1800
	CGGGGGGGGT	AGGAGAGGAG	AAAAAAAAG	TGAAAAAAG	AAACGAAAAG	GACAGACGAA	1860
30	GAGTTTAAAG	AGAAAGAGGA	AAAAAGTAAG	CAAGGCTCGT	TGCGCCCGCT	TGCGCCCGCT	1920
	TCTCGTCTGC	GGATCAAGGA	GCGGGCGGCG	GTTTTGGACC	CGCGCTCCCA	TCCCCACCT	1980
	TCCCCGGGCG	GGGACCACT	CTGCCAGCC	GGAGGGACGC	GGAGGAGGAA	GAGGGTAGAC	2040
	AGGGGCGACC	TGTGATTGTT	GTTATTGATG	TTGTTGTTGA	TGGCAAAAAA	AAAAAGCGAC	2100
	TTGAGTTTG	CTCCCTTTTG	CTTGAAGAGA	CCCCCTCCCC	CTTCCAACGA	GCTTCCGAC	2160
35	TTGTCTGCAC	CCCCAGCAAG	AAGGCGAGTT	AGTTTTCTAG	AGACTTGAAG	GAGTCTCCCC	2220
	CTTCTGTCAT	CACCACCTTG	GTTTTGTTT	ATTTTGCTTC	TTGGTCAAGA	AAGGAGGGGA	2280
	GAAACCAGCG	CACCCCTCCC	CCCCTTTTT	TAAACGCGTG	ATGAAGACAG	AAGGCTCCGG	2340
	GGTGACGAAT	TTGGCCGATG	GCAGATGTTT	TGGGGGAACG	CCGGGACTGA	GAGACTCCAC	2400
40	GCAGGCGAAT	TCCCGTTTGG	GGCCTTTTT	TCTCCCTCT	TTTCCCTTGG	CCCCCTCTGC	2460
	AGCCGGAGGA	GGAGATGTTG	AGGGGAGGAG	GCCAGCCAGT	GTGACCGGCG	CTAGGAAATG	2520
	ACCCGAGAAC	CCCGTTGGAA	GCGCAGCAGC	GGGAGCTAGG	GGCGGGGGCG	GAGGAGGACA	2580
	CGAAGTGGAA	GGGGGTTTCA	GGTCAAACTG	AAATGGATT	GCACGTTGGG	GAGCTGGCGG	2640
	CGGCGGCTGC	TGGGCTCTCG	CCTTCTTTTC	TACGTGAAAT	CAGTGAGGTG	AGACTTCCCA	2700
45	GACCCCGGAG	GCGTGGAGGA	GAGGAGACTG	TTTGATGTGG	TACAGGGGCA	GTCAGTGGAG	2760
	GGCGAGTGGT	TTCGGAAGAA	AAAAAGAA	AAAAGG			

Seq ID NO: 363 Protein sequence

Protein Accession #: NP_003098

	1	11	21	31	41	51	
50	MVQQTNNAE	TEALLAGESS	DSGAGLELGI	ASSPTPGSTA	STGGKADDPS	WCKTPSGHIK	60
	RPMNAFMVWS	QIERRKIMEQ	SPDMHNAEIS	KRLGKRWKLL	KDSDKIPFIR	EAERLRLKHM	120
	ADYDPYKYRP	RAKKVSGNAN	SSSSAAASSK	PGEKGDVKG	SGGGHGGGGG	GGGSSNAGGG	180
55	GGGASGGGAN	SKPAQKSCG	SKVAGGAGGG	VSKPHAKLIL	AGGGGGGKAA	AAAAASFPAE	240
	QAGAAALLPL	GAAADHHSly	KARTPSASAS	ASSAASASAA	LAAPGKHLAE	KVKRVYLFPG	300
	GLGTSSSPVG	GVGAGADPSD	PLGLYEEEGA	GCSFDAPSLs	GRSSAASSPA	AGRSADHRG	360
	YASLRAASPA	PSSAPSHASS	SASSHSSSSS	SSGSSSSDDE	FEDDLLDLNP	SSNFESMSLG	420
	SFSSSSALDR	DLDFNFEPGS	GSHPFEPDYC	TPEVSEMISG	DWLESSISNL	VFTY	

Seq ID NO: 364 DNA sequence

Nucleic Acid Accession #: U10860

Coding sequence: 123-2204

	1	11	21	31	41	51	
65	TGCCGGCTGC	TCCTCGACCA	GGCCTCCTTC	TCAACCTCAG	CCCGCGGCGC	CGACCCTTCC	60
	GGCACCCCTCC	CGCCCGCTCT	CGTACTGTGC	CCGTCAACGC	CGCGGCTCCG	GCCCTGGGCC	120
70	CGATGGCTCT	GTGCAACGGA	GACTCCAAGC	TGGAGAATGC	TGGAGGAGAC	CTTAAGGATG	180
	GCCACCACCA	CTATGAAGGA	GCTGTTGTCA	TTCTGGATGC	TGGTGCTCAG	TACGGGAAAG	240
	TCATAGACCG	AAGAGTGAAG	GAACGTGTCG	TGCAGTCTGA	AATTTTCCCC	TGGAAACAC	300
	CAGCATTGCG	TATAAAGGAA	CAAGGATTCC	GTGCTATTAT	CATCTCTGGA	GGACCTAATT	360
	CTGTGTATGC	TGAAGATGCT	CCCTGGTTTG	ATCCAGCAAT	ATTCACTATT	GGCAAGCCTG	420
75	TTCTPGGAAT	TTGCTATGGT	ATGCAGATGA	TGAATAAGGT	ATTTGGAGGT	ACTGTGCACA	480
	AAAAAAGTGT	CAGAGAAGAT	GGAGTTTTC	ACATTAGTGT	GGATAATACA	TGTTTATTAT	540
	TCAGGGGCGT	TCAGAAGGAA	GAAGTTGTTT	TGCTTACACA	TGGAGATAGT	GTAGACAAAG	600
	TAGCTGATGG	ATTCAAGGTT	GTGGCAGGTT	CTGGAACAT	AGTAGCAGGC	ATAGCAATG	660
	AATCTAAAAA	GTTATATGGA	GCACAGTTCC	ACCCTGAAGT	TGGCCTTACA	GAAATGGAA	720
80	AAGTAATACT	GAAGAATTTC	CTTTATGATA	TAGCTGGATG	CAGTGGAAAC	TTCACCGTGC	780
	AGAACAGAGA	ACTTGAGTGT	ATTGAGAGAG	TCAAAGAGAG	AGTAGGCAGC	TCAAAGTTT	840
	TGGTTTTACT	CAGTGGTGGG	GTAGACTCAA	CAGTTGTAC	AGCTTTGCTA	AATCGTGCTT	900
	TGAACCAAGA	ACAAGTCATT	GCTGTGCACA	TTGATAATGG	CTTTATGAGA	AAACGAGAAA	960
	GCGAGTCTGT	TGAAGAGGCC	CTCAAAAAGC	TTGGAATTCA	GGTCAAAGTG	ATAAATGCTG	1020
85	CTCATTCTTT	CTACAATGGA	ACAACAACCC	TACCAATATC	AGATGAAGAT	AGAACCCAC	1080
	GGAAAAGAAT	TAGCAAAACG	TTAAATATGA	CCACAAGTCC	TGAAGAGAAA	AGAAAAATCA	1140
	TTGGGATAC	TTTGTGTAAG	ATTGCCAATG	AAGTAATTGG	AGAAATGAAC	TTGAAACAG	1200
	AGGAGGTTTT	CCTTGCCCAA	GGTACTTTAC	GGCCTGATCT	AATTGAAAGT	GCATCCCTTG	1260

TTGCAAGTGG CAAAGCTGAA CTCATCAAAA CCCATCAGAG CTCATCAGAA 1320
 AGTTGAGAGA GGAGGGAAAA GTAATAGAAC CTCTGAAAGA TTTTCATAAA GATGAAGTGA 1380
 GAATTTTGGG CAGAGAACTT GGACTTCCAG AAGAGTTAGT TTCCAGGCAT CCATTTCAG 1440
 5 GTCCTGGCCT GGCAATCAGA GTAATATGTG CTGAAGAACC TTATATTGT AAGGACTTTC 1500
 CTGAAACCAA CAATATTTTG AAAATAGTAG CTGATTTTTC TGCAAGTGT AAAAAGCCAC 1560
 ATACCTATT ACAGAGAGTC AAAGCCTGCA CAACAGAAGA GGATCAGGAG AAGCTGATGC 1620
 AAATTACCAG TCTGCATTCA CTGAATGCCT TCTTGCTGCC AATTAAACT GTAGGTGTGC 1680
 AGGGTGACTG TCGTTCCTAC AGTTACGTGT GTGGAATCTC CAGTAAAGAT GAACCTGACT 1740
 10 GGGAACTACT TATTTTCTG GCTAGGCTTA TACCTCGCAT GTGTCACAAC GTTAACAGAG 1800
 TTGTTTATAT ATTTGGCCCA CCAAGTAAAG AACCTCCTAC AGATGTTACT CCCACTTCT 1860
 TGACAACAGG GGTGCTCAGT ACTTTACGCC AAGCTGATTT TGAGGCCCAT AACATTCTCA 1920
 GGGAGTCTGG GTATGCTGGG AAAATCAGCC AGATGCCGGT GATTTTGACA CCATTACATT 1980
 TTGATCGGGA CCCACTTCAA AAGCAGCCTT CATGCCAGAG ATCTGTGTTT ATTCGAACCT 2040
 15 TTATTACTAG TGACTTCATG ACTGGTATAC CTGCAACACC TGGCAATGAG ATCCCTGTAG 2100
 AGGTGGTATT AAAGATGTG ACTGAGATTA AGAAGATTCC TGGTATTCT CGAATTATGT 2160
 ATGACTTAAC ATCAAAGCCC CCAGGAACCTA CTGAGTGGGA GTAATAAACT TC

Seq ID NO: 365 Protein sequence
Protein Accession #: AAA60331

1 11 21 31 41 51
 MALCNGDSKL ENAGGDLKDG HHHYEGAVVI LDAGAQQYGVV IDRRVRELTV QSEIFPLETP 60
 25 APAIKEQGFRI AIISGGPNIS VYADAPWFD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK 120
 KSVREDGVFN ISVNTCSLFL RGLQKEEVVL LTHGDSVDKV ADGFKVARS GNIVAGIANE 180
 SKKLYGAQFH PEVLGTENGK VILKNFLYDI AGCSGTFTVQ NRELECIREI KERVTGSKVL 240
 VLLSGGVDST VCTALLNRAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
 HSFYNGTTTL PISDEDRTPR KRISKTLNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
 30 EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGVIEP LKDFHKDEVR 420
 ILGRELGLPE ELVSRHPPFG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH 480
 TLLQVRKACT TEEDQEKLMQ ITSLSHSLNLF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 540
 ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSLRLQ ADFAHNILR 600
 ESGYAGKISQ MPVILTPLHF DRDPLQKQPS QRSVVIRTP ITSDFTMTGIP ATPGNEIPVE 660
 35 VVLKMTVEIK KIPGISRMY DLTSKPPGTT EWE

Seq ID NO: 366 DNA sequence
Nucleic Acid Accession #: NM_004219
Coding sequence: 46-654

1 11 21 31 41 51
 GGGGCTCTAG ATGAATGCGG CTGTAAAGAC CTGCAATAAT CCAGAAATGGC TACTCTGATC 60
 45 TATGTTGATA AGGAAAAATGG AGAACCCAGGC ACCCGTGTGG TTGCTAAGGA TGGGCTGAAG 120
 CTGGGGCTCTG GACCTTCAAT CAAAGCCTTA GATGGGAGAT CTCAAGTTTC AACACCCAGT 180
 TTTGGCAAAA CGTTCGATGC CCCACCAGCC TTACTTAAAG CTACTAGAAA GGCTTTGGGA 240
 ACTGTCAACA GAGCTACAGG AAAGTCTGTA AAGACCAAGG GACCCCTCAA ACAAAAACAG 300
 CCAAGCTTTT CTGCCAAAAA GATGACTGAG AAGACTGTTA AAGCAAAAAG CTCTGTTCCT 360
 50 GCCTCAGATG ATGCTATATCC AGAAATAGAA AAATCTTTC CCTTCAATCC TCTAGACTTT 420
 GAGAGTTTGT ACCTGCCCTGA AGAGACCAG ATTGCGCACC TCCCTCTGAG TGGAGTGCTC 480
 CTCATGATCC TTGACGAGGA GAGAGAGCTT GAAAAGCTGT TTCAGCTGGG CCCCCCTTCA 540
 CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCACTCTCC TTCAAGCATT 600
 CTGTGACACC TGGATGTTGA ATTGCCACCT GTTTGCTGTG ACATAGATAT TTAAATTTCT 660
 55 TAGTGCTTCA GAGTTTGTGT GTATTGTAT TAATAAAGCA TTCTTCAACA GAAAAAANA 720
 AAAAAA

Seq ID NO: 367 Protein sequence
Protein Accession #: NP_004210

1 11 21 31 41 51
 MATLIYVDKE NGEPGTRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT 60
 RKALGTVNRA TEKSVKTKGP LKQKQPSFSA KKMTEKTVKA KSSVPSDDA YPEIEKFPPF 120
 65 NPLDFESFDL PEEHQIAHLP LSGVPLMILD EERELEKLQ LGPPSPVKMP SPPWESNLLQ 180
 SPSSILSTLD VELPPVCCDI DI

Seq ID NO: 368 DNA sequence
Nucleic Acid Accession #: NM_000597
Coding sequence: 118-1104

1 11 21 31 41 51
 ATTGGGGGCG AGGGAGGAGG AAGAAGCGGA GGAGGCGGCT CCGCTCGCA GGGCCGTGCA 60
 75 CCTGCCCCGC CGCCGCTCG CTGCTCGCC CGCCGCGCG CGCTGCGGAC CGCCAGCATG 120
 CTGCGGAGAG TGGGCTGCCC CGCGCTGCCG CTGCGCGCG CGCCGCTGCT GCGCTGCTG 180
 CGCTGCTGC TCGTCTACT GGGCGCGAGT GGGCGCGCG CGCGGGCGCG CGCGGAGGTG 240
 CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCTGCGCG CCTGCGGGCC CCGCGCGGT 300
 80 GCGCGCGCG CGCGGTGCG CGCAGTGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC 360
 GTCCGGGAGC CGGGCTGCGG CTGCTGCTCG GTGTGCGCCC GGCTGGAGGG CGAGGCGTGC 420
 GCGCTCTACA CCGCGCGCTG CGGCCAGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG 480
 CTGCCCCCTG AGCGCTGTG CATGGGCGAG GGCACCTGTG AGAAGCGCGG GACGCGCGAG 540
 TATGGCGCCA GCCCGGAGCA GGTTCAGAC AATGGCGATG ACCACTCAGA AGGAGGCGCT 600
 85 GTGGAGAACC ACGTGGACAG CACCATGAAC ATGTTGGGCG GGGGAGGCG TGCTGGCCCG 660
 AAGCCCCCTA AGTCGGGTAT GAAGGAGCTG GCCGTGTTCC GGGAGAAGGT CACTGAGCAG 720
 CACCGGCAGA TGGCAAGGG TGGCAAGCAT CACCTTGGCC TGGAGGAGCC CAAGAAGCTG 780
 CGACCACCCC CTGCCAGGAC TCCCTGCCAA CAGGAAGTGG ACCAGGTCTT GGAGCGGATC 840

TCCACCATGC GCCTTCGGGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
 CCCAAGCTGTG ACAAGCATGG CCTGTACAAC CTCAAACAGT GCAAGATGTC TCTGAACGGG 960
 CAGCGTGGGG AGTGCTGGTG TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
 ACCATCCGGG GGGACCCCGA GTGTCACTCT TTCTACAATG AGCAGCAGGA GGCTTGGCGG 1080
 GTGCACACCC AGCGGATGCA GTAGACCGCA GCCAGCGCGT GCCTGGCGCC CCTGCCCCCC 1140
 GCCCCTCTCC AAACACCGGC AGAAAACGGA GAGTGCCTTG GTGGTGGGTG CTGGAGGATT 1200
 TTCCAGTTCT GACACACGTA TTTATATTG GAAAGAGACC AGCACCGAGC TCGGCACCTC 1260
 CCCGGCCTCT CTCTCCAG CTGCAGATGC CACACCTGCT CCTTCTTGCT TTCCCCGGGG 1320
 GAGGAAGGGG GTTGTGGTCG GGGAGCTGGG GTACAGGTTT GGGGAGGGGG AAGAGAAATT 1380
 TTTATTTTGT AACCCCTGTG TCCCTTTTGC ATAAGATTAA AGGAAGGAAA AGT

Seq ID NO: 369 Protein sequence
 Protein Accession #: NP_000588

1 11 21 31 41 51
 MLPRVGC PAL PLPPPLLLPL LPLLLLLLGA SGGGGGARAE VLFRCPPCTP ERLAACGPPP 60
 VAPPAAVA AV AGGARMPCAE LVREPGCGCC SVCARLEGEA CGVYTPRCQ GLRCYPHPGS 120
 ELPLQALVMG EGTCCKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGGSAG 180
 RKPLKSGMKE LAVFREKYTE QHRQMGKGGK HHLGLEEPPKK LRPPPARTPC QQELDQVLER 240
 ISTMLRPDER GPLLEHLYSLH IPNCDKHGLY NLKQCKRMSLN GQRGECWCVN PNTGKLIQGA 300
 PTIRGDPECH LFYNEQQEAC GVHTQRMQ

Seq ID NO: 370 DNA sequence
 Nucleic Acid Accession #: NM_004264
 Coding sequence: 6-440

1 11 21 31 41 51
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 TTTGTAATGC CATTGGAGTA TTGCAGCAAT GTGGTCCTCC TGCCTCTTTC AATAATATTC 120
 AGACAGCAAT TAACAAAGAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTGT 180
 CAGCACTGAT TGACAGCAACA GCAAAAGACA TTGATGTTTT GATAGATTCC TTACCCAGTG 240
 AAGAATCTAC AGCTGCTTTA CAGGCTGCTA GCTTGATATA GCTAGAAGAA GAAAACCATG 300
 AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
 AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
 AGTCTCTTCC AGACTCATAG CATCAGTGGG TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
 GTGCCATTAA GAATTTCTGCA TCAGACTTAG ATACAAGCCT TACCAACAAT TACAGAAACA 540
 TTAAACACTA TGACACATTA CCTTTTATAG TATTTTAAAT AGTCTTCTAT TTTCACTCTT 600
 GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTTTAACT 660
 GAGTGAATTT ATTAAGGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
 AATTCTGTTA TGACATAATT TATGCTCTCA TTTTGTGTGA TTGGCCAGTA CTTTACAAT 780
 C

Seq ID NO: 371 Protein sequence
 Protein Accession #: NP_004255

1 11 21 31 41 51
 MADRLTQLQD AVNSLADQFC NAIGVLQCCG PPASFNNIQT AINKDQPNP TEEYAQLFAA 60
 LIARTAKDID VLIDSLPSEE STAALQAASL YKLEENHEA ATCVEDVVYR GDMLEKIQS 120
 ALADIAQSQL KTRSGTHSQS LPDS

Seq ID NO: 372 DNA sequence
 Nucleic Acid Accession #: AJ271091
 Coding sequence: 1-1113

1 11 21 31 41 51
 ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTCGA ATTCTTGGGA 480
 TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT 540
 TATGACACAT TCCATACTGT GGTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGA GAAATTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTG TGGAGTGCAA TTGAAATTT CAGGTACTCT 780
 TTCTACATGC TCAGCTGCAT TGACATGGAT TGAAGGTGC TCACATGGCT TCGTTACACT 840
 CTGTGATTTC CTTCTATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAGTTAGAT TTTCTTTTCT TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
 ATAAATTTTC GTCACTTTA TAAACAGCGC AGACTGAAAA TGAGGCGCAGG CGCAGTGGCT 1080
 CATGCCTGTG ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 373 Protein sequence
 Protein Accession #: CAB69070

1 11 21 31 41 51
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
 FLDLVKPEPV YKLQRQVNI TVQKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
 RAKEEERLNK LRLESEGSPE TLTLNLRGYL FMYNLVQFLG FSWIFVNLTV RFCILKESF 180

YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN 240
 KAVVFPFVYL WSAIEIFRYS FYMLTICIDMD WKVLTWLRYT LWIPLYPLGC LAEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA 360
 HACDPSALGG

Seq ID NO: 374 DNA sequence
 Nucleic Acid Accession #: NM_016395
 Coding sequence: 1-1113

1 11 21 31 41 51
 | | | | | |
 ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
 TTCTCCTGGA TCTTTGTCAT CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT 540
 TATGACACAT TCCATCTGT GGTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACCTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
 TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAAGGTG TCACATGGCT TCGTTACACT 840
 CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAGTTAGAT TTTCTTTTTC TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
 ATAAATTTTC GTCACCTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
 CATGCTGTG ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 375 Protein sequence
 Protein Accession #: NP_057479

1 11 21 31 41 51
 | | | | | |
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVVEFHLE 60
 FLDLVKPEPV YKLQQRQVNI TVQKVKVQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
 RAKEERLNK LRLESEGSPE TLTNLRKGYL FMYNLVQPLG FSWIFVNLTV RFCILGKESF 180
 YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN 240
 KAVVFPFVYL WSAIEIFRYS FYMLTICIDMD WKVLTWLRYT LWIPLYPLGC LVEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RRRYGKKRKR 360
 STKKKDLDFG LPV

Seq ID NO: 376 DNA sequence
 Nucleic Acid Accession #: NM_005987
 Coding sequence: 1-270

1 11 21 31 41 51
 | | | | | |
 ATGAATTCCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG 60
 GTGAAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAAC CAAGGAGCCC 120
 TGCCAAACCA AGGTGCCTGA GCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG 180
 ATTCAGAGC CTTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCACCGGT CACTCCAGCA 240
 CCAGCCACAG AGAAGACCAA GCAGAAGTAA

Seq ID NO: 377 Protein sequence
 Protein Accession #: NP_005978

1 11 21 31 41 51
 | | | | | |
 MNSQQKQKPC TPPPQPPQQQ VKQPCPPPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
 IPEPCQPKVP EPCPSTVTPA PAQKTKQK

Seq ID NO: 378 DNA sequence
 Nucleic Acid Accession #: NM_002105
 Coding sequence: 74-505

1 11 21 31 41 51
 | | | | | |
 ACAGCAGTTA CACTGCGGCG GCGCTCTGTT CTAGTGTGTT AGCCGTCGTG CTTACCCGGT 60
 CTACCTCGCT AGCATGTCGG GCCGCGGCAA GACTGGCGGC AAGGCCCGCG CCAAGGCCAA 120
 GTCGCGCTCG TCGCGCGCGC GCCTCCAGTT CCCAGTGGGC CGTGTACACC GGCTGCTGCG 180
 GAAGGGCCAC TACGCGGAGC GCGTTGGCGC CGGCGCGCCA GTGTACCTGG CGGCAGTGCT 240
 GGAGTACCTC ACCGCTGAGA TCCTGGAGCT GCGGGGCAAT GCGGCCCGCG ACAACAAGAA 300
 GACGCGAATC ATCCCCGCC ACCTGCAGCT GGCCATCCGC AAGACGAGG AGCTCAACAA 360
 GCTGCTGGGC GCGGTGACGA TCGCCAGGG AGGCGTCTCT CCCAACATCC AGGCCGTGCT 420
 GCTGCCCAAG AAGACCAGCG CCACCGTGGG GCCGAAGGCG CCTCGGGCG GCAAGAAGGC 480
 CACCCAGGCC TCCAGGAGT ACTAAGAGGG CCCGCGCCGC GCGCGGCCGC CCCAGCTCCC 540
 CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACCGCCC TCATGGAAAG AGCTGAGCCG 600
 CTTCAAGACT CGGGGCAAGC GGGCGCGGCG TCCCTTCCCC TCCCTCCCC TCGCCGCGCT 660
 TCGCGCGCGC GCCTCGAGTC CCCGCCCGCC CCCGCTCCCG TCCCGCACCG CCGCGCGCT 720
 CGGCTCGGG CCGCTCGGTG CCGCGTCCG CCTCCGGTA GGGTTCGGGC CTTCCGGATG 780
 CGGCTTGGGC GCTCTTCGGG GACCTCCGTG GCGCGGAAGA CCCGAGCTG CCGGGGGGAG 840

GCCGGCGGCG CCGCACCTGC CCGCCTCGGC GTTCGTGACT CAGCCGCCCC ATCCCGAGTC 900
 GCTAAGGGGC TGGGGGAGG CCGCAGCACC TTCTGGAAGA CTGGCCCTTC CGCTCTGACG 960
 CAGGGCCGAG GTGGGCGATC CAGGCCGAGA GCCGGCGGCC CTGAAGGTGA GTGAGGCCCT 1020
 CGGCAGCTGC AGCCGGGGTG TCTGGTACCC CCCCAGCGTG GTGCTTAGCC CAGGACTTTC 1080
 5 AGACGGCCGC TGGCCGGGAG GCTTTGGTGG GAGAGACGCG ATCCCGGATT TCGGTCTGGC 1140
 GCCCTTCTG CGGCCGGGAC CAGGCCCTTT CACATCAGCT CTCCCTCCAT CTTTATTTCAT 1200
 AGGTCTGCGC TGGGGCCGGG ACGAAGCACT TGGTAACAGG CACATCTTCC TCCCGAGTGA 1260
 CTGCTCCTA GGAGGACATT TAGGGGAGGG CAGAGGCCCTG CAGTTTGGCT TCACGGCTGG 1320
 10 CTATGTGGAC ACCAAGAGTC GTTTTGCGGA ACGCGACTGG CAGCCAGGCC TGTCCGGGCC 1380
 CCGACGCGC CCAATTTCCT TCCAGCAAA CTCAACTCGG CAATCCAAGC ACCTAGATAC 1440
 CAGCACAAGT CGGTAAATCC CTGTCTGGAC TGAGCCTCCG TTGGCTTCTG AACTGGAATT 1500
 CTGCAGCTAA CCCTTCCACG ACTAGAACCT TAGGCATTGG GGAGTTTATG ATGGACTAAT 1560
 TTTATTAAG GATTGTTTTT TTTTT

Seq ID NO: 379 Protein sequence
 Protein Accession #: NP_002096

1 11 21 31 41 51
 | | | | |
 20 MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGHY AERVGAGAPV YLAADVLEYLT 60
 AEILELAGNA ARDNKKTRII PRHLQLAIRN DEBLNKLGG VTIAQGGVLP NIQAVLLPKK 120
 TSATVGPAP SGGKATQAS QEY

Seq ID NO: 380 DNA sequence
 Nucleic Acid Accession #: AL136942
 Coding sequence: 184-864

1 11 21 31 41 51
 | | | | |
 30 ACGGTCGCG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCC GCGGGCGCAC 60
 GGGCGAGCGG GCGGGGAGCC GAGCGCGCGG AGGAGCGCGC AGCAGCGGCG CGGCGGGCTC 120
 CAGGCGAGGC GGTGAGCGCT CCGTAAACT TGCGCGCGCG CTGCGGCCAC TGCGCCCGGA 180
 GCGATGAAGA TGGTCGCGCC CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC 240
 35 CATGTCCGCA CCGGCACCAT CCGTCTCGGC GTCTGATATC TGATCATCAA TGCTGTGGTA 300
 CTGTTGATTT TATTGAGTGC CTTGGCTGAT CCGGATCAGT ATAACTTTTC AAGTCTTGAA 360
 CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT GCATTGCCAT TCGGATTTCCT 420
 CTTCTCATGA TCCGATATG TGCTATGGCT ACTTACGGAG CGTACAAGCA ACGCGCAGCC 480
 40 TGGATCATCC CATTCTCTG TTACCAGATC TTTGACTTTG CCTGAACAT GTTGGTTGCA 540
 ATCACTGTGC TTATTTATCC AAACCTCATT CAGGAATACA TACGGCACT GCCTCCTAAT 600
 TTTCCCTACA GAGATGATGT CATGTCAGTG AATCCTACCT GTTTGGTCTT TATTATTCTT 660
 CTGTTTATTA GCATTATCTT GACTTTTAAG GGTACTTGA TTAGCTGTGT TTGGAATGTC 720
 TACCGATACA TCAATGATG GAACCTCTCT GATGTCCTGG TTTATGTTAC CAGCAATGAC 780
 ACTACGGTGC TGCTACCCCT GTATGATGAT GCCACTGTGA ATGGTGCTGC CAAGGAGCCA 840
 45 CCGCCACCTT ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGCG AGCAGCTTGA 900
 CTTTGACAGC ATCTGAGCAA TAGTCTCTGT ATTTCACTTT TGCCATGAGC CTCTCTGAGC 960
 TGTGTTGTTG CTGAAATGCT ACTTTTAAAT ATTTAGATGT TAGATTGAAA ACTGTAGTTT 1020
 TCAACATATG CTTTGCTAGA ACACCTGTGAT AGATTAACTG TAGAATCTCT CCTGTACGAT 1080
 50 TGGGGATATA ACGGGCTTCA CTAACCTTCC CTAGGCATTG AAACCTCCCC CAAATCTGAT 1140
 GGACATAGAA GTCTGCTTTT GTACCTGCTG GGGCCCAAGG TTGGGCATT TTTCTCTGCT 1200
 TCCCTCTCTT TTGAAATGT AAAATAAAAC CAAAAATAGA CAACCTTTTC TTCAGCCATT 1260
 CCAGCATAGA GAACAAACCT TTAATGGAAC AGGAATGTCA ATTGTGTAAT CATTGTTCTA 1320
 ATTAGGTAAA TAGAAGTCTT TATGTATGTG TTACAAGAAT TTCCCCCACA ACATCCTTTA 1380
 55 TGAAGTAAAT TCAATGACAG TTTGTGTTTG GTGGTAAAGG ATTTCTCTCA TGGCCTGAAT 1440
 TAAGACCAT AGAAGACACC AGGCGGTGGG AGCAGTGACC ATCTACTGAC TGTTCCTGTG 1500
 GATCTTGTGT CAGGGGACAT GGGGTGACAT GCCTCGTATG TGTAGAGGG TGGAAATGGAT 1560
 GTGTTTGGCG CTGCATGGGA TCTGGTCCCC CTCTCTCTCT GGATTCACAT CCCCACCCAG 1620
 GGGCCGCTTT TACTAAGTGT TCTGCCCTAG ATTGGTTCAA GGAGGTCATC CAACTGACTT 1680
 60 TATCAAGTGG AATTGGGATA TAATTGATAT ACTTCTGCTT AACAACATGG AAAAGGGTTT 1740
 TCTTTTCCCT GCAAGCTACA TCCTACTGCT TTGAACCTCC AAGTATGTCT AGTCACCTTT 1800
 TAAATGTAA ACATTTTCAG AAAAATGAGG ATTGCCTTCC TTGTATGCGC TTTTACCTT 1860
 GACTACCTGA ATTGCAAGGG ATTTTATAT ATTCAATATG TACAAGATCA GCAACTCTCC 1920
 TGTGTTGTTA TTATTGAATG TGCTGTAAAT TAAGTCGTTT GCAATTAAAA CAAGGTTTGC 1980
 CCACATCCAA AAAAAAAAAA AAAAA

Seq ID NO: 381 Protein sequence
 Protein Accession #: CAB66876

1 11 21 31 41 51
 | | | | |
 70 MKMVPWTRF YSNCCCLCCH VRTGILLGV WYLIINAVVL LILLSALADP DQYNFSSSEL 60
 GGDFFEMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAW IIPFFCYQIF DFALNMLVAI 120
 TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN PTCLVLIILL PISIIITFKG YLISCVWNCY 180
 RYINGRNSSD VLVVTSNDT TVLLPPYDDA TVNGAAKEPP PPYVSA

Seq ID NO: 382 DNA sequence
 Nucleic Acid Accession #: NM_002510
 Coding sequence: 92-1774

1 11 21 31 41 51
 | | | | |
 80 CAGATGCCAG AAGAACACTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60
 CCTTGAGTGC CTGCGTCCGT GAGAATTGAG CATGGAATGT CTCTACTATT TCCTGGGATT 120
 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCCCAA CGATTTTCATG ATGTGCTGGG 180
 85 CAATGAAAGA CTTTCTGCTT ACATGAGGGA GCACAATCAA TTAATGGCT GGTCTTCTGA 240
 TGAAATGAC TGGAAATGAA AACTCTACCC AGTGTGGAAG CGGGAGACA TGAGTGGAA 300
 AAACCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTTGACC AGTGACTCAC CAGCCTCTGT 360

	GGGCTCAAAT	ATAACATTTG	CGGTGAACCT	GATATTCCCT	AGATGCCAAA	AGGAAGATGC	420
	CAATGGCAAC	ATAGTCTATG	AGAAGAACTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
	ATATGTTTAC	AACGTGGACG	CATGGTCAGA	GGACAGTGAC	GGGGAAAAATG	GCACCGGCCA	540
5	AAGCCATCAT	AACGTCTTCC	CTGATGGGAA	ACCTTTTCTT	CACCACCCCG	GATGGAGAAG	600
	ATGGAATTTT	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCAGAAAT	TGGGACGATG	660
	TTCACTGAGA	GTTTCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCCCTCAAC	TCATGGAAGT	720
	GACTGTCTAC	AGAAGACATG	GACGGGCATA	TGTTCCCATC	GCACAAGTGA	AAGATGTGTA	780
	CGTGGTAACA	GATCAGATTG	CTGTGTTTGT	GACTATGTTT	CAGAAGAAGC	ATCGAAATTC	840
10	ATCCGACGAA	ACCTTCTCTA	AAGATCTCCC	CATTATGTTT	GATGTCCTGA	TTCATGATCC	900
	TAGCCACTTC	CTCAATTTAT	CTACCATTA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960
	CCTGTTTGT	TCCACCAATC	ATACTGTGAA	TCACACGTAT	GTGCTCAATG	GAACCTTCAG	1020
	CCTTAACCTC	ACTGTGAAAG	CTGCAGCACC	AGGACCTTGT	CCGCCACCGC	CACCACCACC	1080
15	CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAAACCCC	TGGAGCTGAG	1140
	TAGGATTCCT	AACGTGAAAT	GCCAGATTAA	CAGATATGGC	CACCTTCAAG	CCACCATCAC	1200
	AAATGTAGAG	GGAAATCTTAG	AGGTTAACAT	CATCCAGATG	ACAGACGTCC	TGATGCCGGT	1260
	GCCATGGCCT	GAAGCTCTCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCAITCCCAC	1320
	GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGAGAT	ACCCAGAAAC	CAGCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
20	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCTT	1500
	GATTTCGTGT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAAAC	GTGCCCTGAT	1560
	CTCCGTTGGC	TGCTTGCCCA	TATTTGTGAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTGAGAAGCA	AAGGCCTGAG	1680
	TGTCCTTTCT	AACCGTGCAC	AAGCCGTGTT	CTTCCCGGGA	AACCAAGAAA	AGGATCCGCT	1740
25	ACTCAAAAC	CAAGAATTTA	AAGGAGTTTC	TTAAATTTTC	ACCTTGTTC	TGAAGCTCAC	1800
	TTTTCACTGC	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTT	TTCCTAAAGA	1860
	TTATTGTTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGT	TAAATGTCAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACCTATA	AAGTCTTAGG	2040
30	TAACTAGTAG	GATAGTAAGC	CTGTGCTCCG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
	AGCCTAACCC	AGGTTAACTG	CAAGAAGAGG	CGGGATACCT	TCAGCTTCC	ATGTAACCTG	2160
	ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
	TTCAATACAC	ACTCATGAGC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
35	TGACAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCAT	2400
	GGACATTTAG	TTAGTGCCTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460
	ATTTCCAAAT	TTTTGTATAG	TCGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGGTC	CCTGTTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTCAAC	TCTGTTTGTA	2580
40	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCCTTC	CTGAAAAATA	2640
	AAGTGTGGGA	AGAGACAAAA	AAAAAATA				

Seq ID NO: 383 Protein sequence
Protein Accession #: NP_002501

45	1	11	21	31	41	51	
	MECLYYFLGF	LLLAARLPD	AAKRFHDLV	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
	VWKRGRMRWK	NSWKGGRVQA	VLTSDSPALV	GSNITFAVNL	IFPRCQKEDA	NGNIVYEKNC	120
	RNEAGLSADP	YVYNWTAWSE	DSGNGTGTG	SHNVFPDQK	PPPHHPGWR	WNFIYVFTL	180
50	QYFQKLGR	SVRVSVNTAN	VTGPPQLMEV	TVYRRHGRAY	VPIAQVKD	VVDQIPV	240
	TMFQKNDN	SDFTFLKDL	IMFDVLHDP	SHFLNYSTIN	YKWSFGDNTG	LFVSTNHTVN	300
	HTYVLNGTFS	LNLTVKAAAP	GPCPPPPPPP	RPSKPTPSLG	PAGDNPLELS	RIPDENCQIN	360
	RYGHFQATIT	IVEGILEVNI	IQMTDVLMPV	PWPESSLDIF	VVTCQGSIPT	EVCTIISDPT	420
	CEITQNTVCS	PVDVDEMCLL	TVRRTFNGSG	TYCVNLTLGD	DTSLALSTSL	ISVPRDRPAS	480
55	PLRMANSALI	SVGCLAIFVT	VISLLVYKXH	KEYNPIENSP	GNVVRSKGLS	VFLNRAKAVF	540
	FPGNQEKDPL	LKNQEPKGV					

Seq ID NO: 384 DNA sequence
Nucleic Acid Accession #: NM_001134
Coding sequence: 48-1877

60	1	11	21	31	41	51	
	TCCATATTGT	GCTTCCACCA	CTGCCAATAA	CAAAATAACT	AGCAACCATG	AAGTGGGTGG	60
	AATCAATTTT	TTTAATTTTC	CTACTAAATT	TTACTGAATC	CAGAACACTG	CATAGAAATG	120
65	AATATGGAAT	AGCTTCCATA	TTGGATTCTT	ACCAATGTAC	TGCAGAGATA	AGTTTAGCTG	180
	ACCTGGCTAC	CATATTTTTC	GCCGAGTTTG	TTCAGAAGC	CACCTACAAG	GAAGTAAGCA	240
	AAATGGTGAA	AGATGCATTG	ACTGCAATTG	AGAAACCCAC	TGGAGATGAA	CAGTCTTCAG	300
	GGTGTTTAGA	AAACCGCTA	CCTGCTTTTC	TGGAAGAACT	TTGCCATGAG	AAAGAAATTT	360
70	TGGAGAAGTA	CGGACATTCA	GACTGCTGCA	GCCAAAGTGA	AGAGGGAAGA	CATAACTGTT	420
	TTCTTGACCA	CAAAAAGCCC	ACTCCAGCAT	CGATCCCACT	TTTCCAAGTT	CCAGAACCTG	480
	TCACAAGCTG	TGAAGCATAT	GAAGAAGACA	GGGAGACATT	CATGAACAAA	TTCATTTATG	540
	AGATAGCAAG	AAGGCATCCC	TTCTGTATG	CACCTACAAT	TCTTCTTTGG	GCTGCTCGCT	600
	ATGACAAAAT	AATTCATCT	TGCTGCAAG	CTGAAAATGC	AGTTGAATGC	TTCCAAACAA	660
75	AGGCAGCAAC	AGTTTACAAA	GAATTAAAG	AAAGCAGCTT	GTTAAATCAA	CATGCATGTG	720
	CAGTAATGAA	AAATTTTGGG	ACCCGAACTT	TCCAAGCCAT	AACTGTTACT	AAACTGAGTC	780
	AGAAGTTTAC	CAAGTTTAAT	TTTACTGAAA	TCCAGAAACT	AGTCTGGGAT	GTGGCCCATG	840
	TACATGAGCA	CTGTGTCAGA	GGAGATGTGC	TGGATTGTCT	GCAGGATGGG	GAAAAATCA	900
	TGTCCTACAT	ATGTTCTCAA	CAAGACACTC	TGTCAAACAA	AATAACAGAA	TGCTGCAAAC	960
80	TGACCAAGCT	GGAACTGGGT	CAATGTATAA	TTCATGCAGA	AAATGATGAA	AAACCTGAAG	1020
	GTCTATCTCC	AAATCTAAAC	AGGTTTITAG	GAGATAGAGA	TTTAAACCAA	TTTCTTCAG	1080
	GGGAAAAAAA	TATCTTCTTG	GCAAGTTTTC	TTCATGAATA	TTCAAGAAGA	CATCTTCAGC	1140
	TTGCTGTCTC	AGTAATTTCTA	AGAGTTGCTA	AAGGATACCA	GGAGTTATTG	GAGAAGTGTT	1200
	TCCAGACTGA	AAACCTCTT	GAATGCCAAG	ATAAAGGAGA	AGAAGAATTA	CAGAAATACA	1260
85	TCCAGGAGAG	CCAAGCATTC	GCAAGCGSAA	GCTGCGGCCT	CTTCCAGAAA	CTAGGAGAAT	1320
	ATTACTTACA	AAATGCGTTT	CTGTTGCTT	ACACAAAGAA	AGCCCCCAG	CTGACCTCGT	1380
	CGGAGCTGAT	GGCCATCACC	AGAAAAATGG	CAGCCACAGC	AGCCACTTGT	TGCCAACTCA	1440
	GTGAGGACAA	ACTATTGGCC	TGTGGCGAGG	GAGCGGCTGA	CATTATTATC	GGACACTTAT	1500

GTATCAGACA TGAAATGACT CCAGTAAACC CTGGTGTGG CCAGTGTGTC ACTTCTTCAT 1560
 ATGCCAACAG GAGGCCATGC TTCAGCAGCT TGGTGGTGGG TGAACATAT GTCCCTCCTG 1620
 CATTCTCTGA TGACAAGTTC ATTTTCCATA AGGATCTGTG CCAAGCTCAG GGTGTAGCGC 1680
 TGCAAAACGAT GAAGCAAGAG TTTCTCATTA ACCTTGTGAA GCAAAAGCCA CAAATAACAG 1740
 AGGAACAAC TGAAGCTGTC ATTGCAGATT TCTCAGGCCT GTTGGAGAAA TGCTGCCAAG 1800
 GCCAGGAACA GGAAGTCTGC TTTGCTGAAG AGGACAAAA ACTGATTTC AAAACTCGTG 1860
 CTGCTTTGGG AGTTTAAAT ACTTCAGGGG AAGAGAAGAC AAAACGAGTC TTTATTTCGG 1920
 TGTGAACTTT TCTCTTAAAT TTTAACTGAT TTAACACTTT TTGTGAATTA ATGAAATGAT 1980
 AAAGACTTTT ATGTGAGATT TCCTTATCAC AGAAATAAAA TATCTCCAAA TG

Seq ID NO: 385 Protein sequence
 Protein Accession #: NP_001125

1 11 21 31 41 51
 MKWVESIFLI FLNFTESRT LHRNEYGIAS ILDSYQCTAE ISLADLATIF PAQFVQEATY 60
 KEVSKMVKDA LTAIEKPTGD EQSSGCLLENQ LPAFLEELCH EKEILEKYGH SDCCSQSEEG 120
 RHNCFLAHKK PTPASIPLEFQ VPEPVTSCBA YEEDRETFMN KFIYBIARRH PFLYAPTILL 180
 WAARYDKIIP SCCKAENAVE CFQTKAATVT KELRESSLLN QHACAVMKNP GTRTFQAITV 240
 TKLSQKPTKV NFTEIQKLVL DVAHVHEHCC RGDVLDCLQD GEKIMSYICS QQDTLSNKIT 300
 ECKLITTLER QQCIIHAEND EKPEGLSPNL NRPLGDRDFN QFSSGEGNIF LASFVHEYSR 360
 RHPQLAVSVI LRVAQGYQEL LEKCFQTEPN LECQDKGEE LQKYIQESQA LAKRSCGLFQ 420
 KLGEYYLQNA FLVAYTKKAP QLTSSSELMAI TRKMAATAAT CCQLSEDKLL ACGEGAADII 480
 IGHLCIRHEM FTVNPGVGQC CTSSYANRRP CFSSLVVDET YVPPAFSDDK FIFHKDLCOA 540
 QGVALQTMKQ EFLINLVKQK PQITEEQLEA VIADFSGLLE KCCQGGQEV CPABEGQKLI 600
 SKTRALGV

Seq ID NO: 386 DNA sequence
 Nucleic Acid Accession #: NM_002205.1
 Coding sequence: 1..3149

1 11 21 31 41 51
 ATGGGGGAGCC GGACGCCAGA GTCCCTCTC CACGCCGTGC AGCTGCGCTG GGGCCCCCGG 60
 CGCCGACCCC GCTGCTGTG GCTGCTGTG CCGCCGCCACC CAGGGTCGGG 120
 GGCTTCAACT TAGACGCGGA GGCCCGACCA GTACTCTCGG GGCCCGCGG CTCTCTCTTC 180
 GGATTCTCAG TGGAGTTTAA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCAAGGCTA ATACAGGCA GCCAGGAGTG CTGACGGGTG GTGCTGTCTA CTCTGTCTCT 300
 TGGGGTGCCA GCCCACACA GTGCACCCCC ATTGAATTG ACAGCAAAGG CTCTCGGCTC 360
 CTGGAGTCTC CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCCCTGTCAG 420
 TGGTTCGGGG CAACAGTTTG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CTCTCCACA 540
 GATAACTTCA CCCGAATTCT GGAGTATGCA CCTGCGCGCT CAGATTTTCA CTGGGCAGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCAGATTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGTGGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAGAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCAGCCA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGGGTGAA 840
 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAATT CTCAGGGGAA 960
 CAGATGGCTC CTACTTTTGG CTATGTCAGT GCCGCCACAG ACCTCAATGG GGACGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGTCTC ATGGATCGGA CCCTGACGG GCGGCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACC 1140
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 CAGGTTCTGC AGCCCTCTGT GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCTGATC TGATTGTGGG GTCCCTTTGGT 1440
 GTGGACAAGG CTGTGGTATA CAGGGGCGCG CCCATCGTGT CCGCTAGTGC CTCCCTCACC 1500
 ATCTTCCCCG TATCTTCCAA CCCAGAGGAG CGAGAGTGCA GCTTAGAGGG GAACCTGTG 1560
 GCCTGCATCA ACCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620
 GGTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTTCCCTG GTTCCCTTCA GGCACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800
 CTCTCGCGCA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGACAGC 1860
 CACGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGTIT 1980
 GGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC 2040
 CAGAAATGTG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
 TTTGCCGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGGACAC TAAGAAAACC 2280
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT 2340
 TCCTTTCGGC TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAAGCCT 2400
 GAGGCAGTGC TATCCCTAGT AAGCGACTGG CATCCCGAG ACCAGCTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCAATGCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
 AGCCAGGGTG TGCTGGAAC TCACTGTCCC CAGGCTCTGG AAGGTGAGCA GCTCCTATAT 2580
 GTGACAGAG TACCGTGTGA CAACCTGACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640
 GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAC GGGAACTCC AAGCCGAGC 2700
 TCTGCTTCTC CGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTIT CAGGCTGCGC 2760
 TGTGAGCTCG GGGCTGGCTA CCAACAAGAG AGCCAAAGTC TGCAAGTGCA TTTCCGAGTC 2820
 TGGGCCAAGA CTTTCTTGA GCGGGAGCAC CAGCCATTTA GCCTGCAAGT TGAGGCTGTG 2880
 TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCTGGC AGCTGCCCCA AAAAGAGCGT 2940
 CAGGTGGCCA CAGCTGTGCA ATGACCAAG GCAAGAAGCA GCTATGGCGT CCACTGTGG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCTAG GTCTACTCAT CTACATCTCT 3060
 TACAAGCTTG GATTCTTCAA ACGTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120
 CTCAGCCTC CAGCCACCTC TGATGCTGTA

Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

5	1	11	21	31	41	51	
	MGSRTPEspl	HAVQLRWGPR	RRPPLPLLLL	LLLPppPRVG	GFNLDAEAPA	VLSGPPGSFF	60
	GFSVEFYRPG	TDGVSVLVGA	PKANTSQPGV	LQGGAVVLCp	WGASPTQCTP	IEFDskGSRL	120
	LESSLSSESG	EEpVEYKSLQ	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTcYLST	180
10	DNFTRILEYA	PCRSDFSWAA	GQGYCQGGFS	AEFTKTGRVV	LGGPGSYFWQ	GQILSATQEQ	240
	IAESYYPEYL	INLVQGGQLQT	RQASSIYDDS	YLGYSVAVGE	PSGDDTEdFV	AGVPKGNLTy	300
	GYVTILNGSD	IRSLYNFSGE	QMAsYFGYAV	AATDVNGDGL	DDLVLVAPLL	MDRTPDGRPQ	360
	EVGRVYVVLQ	HPAGIEPTPT	LTLTGHDEFG	RFGSSLTPLG	DLDDQDGYNDV	AIGAPFGGET	420
	QQGVVVFVFP	GPGLGSKSPS	QVLQPLWAAS	HTPDFFGSAL	RGRDLdGNG	YFDLIVGSFG	480
15	VDKAVVYRGR	PIVSASASLT	IFPAMFNPEE	RSCSLEGNPV	ACINLSFCLN	ASGKHVADSI	540
	GFTVELQLDW	QKQKGGVRRR	LFLASRQATL	TQTLIIQNGA	REDCREMKIY	LRNESEFRDK	600
	LSPIHIALNF	SLDPQAPVDS	HGLRPALHYQ	SKSRIEDKAQ	ILLDCGEDNI	CVPDLQLEVP	660
	GEQNHVYLGd	KDLNLTTFHA	QNVGEGGAYE	AELRVTAPPE	AEYSGLVRRH	GNFSSLSdCY	720
	FAVNQSRLLV	CDLGNPMKAG	ASLWGLRFT	VPHLRDTKKT	IQDFQILSK	NLNNSQSDVV	780
20	SFRLSVEAQA	QVTLNGVSKP	EAVLFPVSDW	HPRDQPQKEE	DLGPAVHHVY	ELINQGPSSI	840
	SQGVLELSCP	QALGGQQLLY	VTRVTGLNCT	TNHPINPKGL	ELDPEGSLHH	QQKREAPSRs	900
	SASSGFQILK	CPEAECFRLR	CELGPLHQQE	SQSLQLHFRV	WAKTFLQREH	QPFSLQCEAV	960
	YKALKMPYRI	LPRQLPQKER	QVATAVQWTK	AEGSYGVPLW	IIILAILPGL	LLGLLIYIL	1020
25	YKLGFFKRSL	PYGTAMEKAQ	LKPPTSdA				

Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

30	1	11	21	31	41	51	
	AAAGAAGGTA	AGGGCAGTGA	GAATGATGCA	TCTTGcATTc	CTTGTGCTGT	TGTGTCTGCC	60
	AGTCTGCTCT	GCCTATCCTC	TGAGTGGGGC	AGCAAAAGAG	GAGGACTCCA	ACAAGGATCT	120
	TGCCCAGCAA	TACCTAGAAA	AGTACTACAA	CCTCGAAAAG	GATGTGAAAC	AGTTTAGAAG	180
35	AAAGGACAGT	AATCTCATTG	TTAAAAAATG	CCAAGGAATG	CAGAAGTTCC	TGGGTtGGA	240
	GGTGACAGGG	AAGCTAGACA	CTGACACTCT	GGAGGTGATG	CGCAAGCCCA	GGTGTGGAGT	300
	TCCTGACGTT	GGTCACTTCA	GCTCCTTTCC	TGGCATGCCG	AAGTGGAGGA	AAACCCACCT	360
	TACATACAGG	ATTGTGAATT	ATACACCAGA	TTTGCCAAGA	GATGCTGTGG	ATTCTGCCAT	420
	TGAGAAAGCT	CTGAAAGTCT	GGGAAGAGGT	GACTCCACTC	ACATTCTCCA	GGCTGTATGA	480
40	AGGAGAGGCT	GATATAATGA	TCTCTTTGCG	AGTTAAAGAA	CATGGAGACT	TTTACTCTTT	540
	TGATGGCCCA	GGACACAGTT	TGGCTCATGC	CTACCCACCT	GGACCTGGGC	TTTATGGAGA	600
	TATTCACTTT	GATGATGATG	AAAAATGGAC	AGAAGATGCA	TCAGGCACCA	ATTTATTCTT	660
	CGTTGCTGCT	CATGAACCTG	GCCACTCCCT	GGGGCTCTTT	CACTCAGCCA	ACACTGAAGC	720
	TTTGATGTAC	CCACTCTTCA	ACTCATTACG	AGAGCTCGCC	CAGTTCGGCC	TTTCGCAAGA	780
45	TGATGTGAAT	GGCATTCACT	CTCTCTACGG	ACCTCCCCCT	GCCTCTACTG	AGGAACCCCT	840
	GGTGGCCACA	AAATCTGTTC	CTTCGGGATC	TGAGATGCCA	GCCAAGTGTG	ATCCTGCTTT	900
	GCCTCTCGAT	GCCATGCTCT	CTCTGAGGGG	AGAATATCTG	TTCTTTAAAG	ACAGATATTT	960
	TTGGCGAAGA	TCCCACTGGA	ACCCTGAACC	TGAATTTTCAT	TTGATTCTTG	CATTTTGCCG	1020
	CTCTCTTCCA	TCATATTTCG	ATGCTGCATA	TGAAGTTAAC	AGCAGGGACA	CCGTTTTTAT	1080
50	TTTTAAAGGA	AGATGATTTT	GGGCGATCAG	AGGAAATGAG	GTACAAGCAG	GTTATCCAAG	1140
	AGGCATCCAT	ACCCTGGGTT	TTCTCTCAAC	CATAAGGAAA	ATTGATGCAG	CTGTTCTCTG	1200
	CAAGGAAAAA	AAGAAACAT	ACTTCTTTGC	AGCGGACAAA	TACTGGAGAT	TTGATGAAAA	1260
	TAGCAGTCC	ATGGAGCAAG	GCTTCCCTAG	ACTAATAGCT	GATGACTTTC	CAGGAGTTGA	1320
	GCCTAAGGTT	GATGCTGTAT	TACAGGCATT	TGGATTTTTC	TACTTCTTCA	GTGGATCATC	1380
55	ACAGTTTGAG	TTTGACCCCA	ATGCCAGGAT	GGTGACACAC	ATATTAAAGA	GTAACAGCTG	1440
	GTACATTGCT	TAGCGGAGAT	AGGGGGAAGA	CAGATATGGG	TGTTTTTAAT	AAATCTAATA	1500
	ATTATTATC	TAATGTATTA	TGAGCCAAAA	TGGTTAATTT	TTCTGCTATG	TTCTGTGACT	1560
	GAAGAAGATG	AGCCTTGcAG	ATATCTGCAT	GTGTcATGAA	GAATGTTTCT	GGAATTCCTC	1620
	ACTTGCTTTT	GAATTGCACT	GAACAGAATT	AAGAAATACT	CATGTGCAAT	AGGTGAGAGA	1680
60	ATGTATTTTC	ATAGATGTGT	TATTACTTCC	TCAATAAAAA	GTTTTATTTT	GGGCTGTGTC	1740
	CTT						

Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

65	1	11	21	31	41	51	
	MHLAFLVLLC	LPVCSAYPLS	GAKEEDSNK	DLAQQYLEKY	YNLEKDVQKF	RRKDSNLIVK	60
	KIQGMQKFLG	LEVtGKLDTd	TLEVMRKPRC	GVPDVGHFSS	FPGMpKWRKT	HLTYRIVNYT	120
70	PDLPRDAVDS	AIEKALKVWE	EVTPLTFsRL	YEGEADIMIS	FAVKEHGDFY	SFDGPghSLA	180
	HAYPPPGGLY	GDIHFDDDEK	WTEdASGTNL	FLVAaHELGH	SLGLFHSANT	EALMYPLYNs	240
	PTELAQFRLS	QDDVNGIQSL	YGPpPASTEE	PLVPTKsVPS	GSEMPAKCDP	ALSFDaISTL	300
	RGEYLFFKDR	YFWRRSHWNP	EPEFHLISAF	WPSLPSYLDa	AYEVNSRDTV	FIFKGRNEFWA	360
	IRGNEVQAGY	PRGHTLGF	PTIRKIDAaV	SDKEKKKTYF	FAADKYWRFD	ENSQSMEQGF	420
75	PRLIADDFPG	VEPKVDAVLQ	AFGFFYFFSG	SSQFEFDpNA	RMVTHILKSN	SWLHC	

Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

80	1	11	21	31	41	51	
	ATGCACAGCT	TTCTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGgAAAAA	120
85	TACTACAACC	TGAAGAAATG	TGGGAGGCAA	GTTGAAaAGC	GGAGAAATAG	TGGCCcAGTG	180
	GTTGAAAAAT	TGAAGCAAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACcAGAT	240
	GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCTGTATGT	GGCTCAGTTT	300

GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
 TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACAC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCACTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAGAAAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTT 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAAGT 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGAGGATAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
 GGAATTGGCC ACAAGTTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTCTTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 391 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLRQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDEP ERWTNNFREY NLHRVAAHEL GHSGLGLSHST DIGALMYPSTY 240
 TFSGDVQLAQ DDIDIGIQAII GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMEFFKDR 300
 FYMRTNPFYP EVELNFIISVF WPQLPNGLEA AYEFAADRDEV RFFKGKNKYWA VQGQNVHLGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRV DEYKRSMDPG YPKMIAHDFF 420
 GIGHKVDVAV MKDGGFFYPFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 392 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

1 11 21 31 41 51
 ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTTGGTGT ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAGAAA 120
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAGC GGAGAAATAG TGGCCAGTG 180
 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
 GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
 TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACAC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCACTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAGAAAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTT 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAAGT 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGAGGATAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
 GGAATTGGCC ACAAGTTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTCTTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 393 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLRQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDEP ERWTNNFREY NLHRVAAHAL GHSGLGLSHST DIGALMYPSTY 240
 TFSGDVQLAQ DDIDIGIQAII GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMEFFKDR 300
 FYMRTNPFYP EVELNFIISVF WPQLPNGLEA AYEFAADRDEV RFFKGKNKYWA VQGQNVHLGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRV DEYKRSMDPG YPKMIAHDFF 420
 GIGHKVDVAV MKDGGFFYPFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 394 DNA sequence
 Nucleic Acid Accession #: NM_014331.2
 Coding sequence: 1..1506

1 11 21 31 41 51
 | | | | |

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	AACGGGAGGC	TGCCTTCCT	GGGCAACAAG	GAGCCACCTG	GGCAGGAGAA	AGTGCAGCTG	120
	AAGAGGAAAG	TCACCTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATGGAGCA	180
5	GGAAATCTCA	TCTCTCTAA	GGGCGTGTCT	CAGAACACGG	GCAGCGTGGG	CATGTCTCTG	240
	ACCATCTGGA	CGGTGTGGG	GGTCTGTCA	CTATTGGAG	CTTTGTCTTA	TGCTGAATTG	300
	GGAAACAATA	TAAAGAAATC	TGGAGGTGAT	TACACATATA	TTTTGGAAAT	CTTTGGTCCA	360
	TTACCAGCTT	TTGTACAGAT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTGG	ACGCTACATT	CTGGAAACAT	TTTTTATTC	ATGTGAAATC	480
10	CCTGAACCTG	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTTAAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACTTTTG	CAAGCTCACA	600
	GCAATTCTGA	TAATTATAGT	CCCTGGAGTT	ATGCAGCTAA	TTAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTTCAGG	AAGAGATTCA	AGTATTACGC	GGTTGCCACT	GGCTTTTAT	720
	TATGGAATGT	ATGCATATGC	TGGCTGGTTT	TACCTCAACT	TTGTTACTGA	AGAAGTAGAA	780
15	AACCTGAAA	AAACCAITTC	CTTGTCAATA	TGTATATCCA	TGGCCATTGT	CACCATGGCC	840
	TATGTGCTGA	CAATGTGGC	CTACTTTACG	ACCATTATATG	CTGAGGAGCT	GCTGCTTTCA	900
	AATGCAGTGG	CAGTGACCTT	TTCTGAGCGG	CTACTGGGAA	ATTTCTCATT	AGCAGTTCCG	960
	ATCTTTGTTG	CCCTCTCTCG	CTTTGGCTCC	ATGAACGGTG	GTGTGTTTGC	TGCTCCAGG	1020
	TTATTTCTATG	TTGCGTCTCG	AGAGGGTCAC	CTTCCAGAAA	TCCTCTCCAT	GATTCTATGC	1080
20	CGCAAGCACA	CTCCTCTACC	AGCTGTATT	GTTTTGACCC	CTTTGACAAT	GATAATGCTC	1140
	TTCTCTGGAG	ACCTCGACAT	TCTTTGAAT	TTCTCTAGTT	TTGCCAGGTG	GCTTTTATT	1200
	GGGCTGGCAG	TTGCTGGGCT	GATTTATCTT	CGATACAAAT	GCCAGATAT	GCATCGTCTC	1260
	TTCAAGGTGC	CAGTGTTCAT	CCCAGCTTTG	TTTTCTCTCA	CATGCCTCTT	CATGGTTGCC	1320
	CTTTCCCTCT	ATTCGGACCC	GATTAGTACA	GGGATTGGCT	TGCTCATCAC	TCGACTGGA	1380
25	GTCCCTGCGT	ATTATCTCTT	TATTATATGG	GACAAGAAAC	CCAGGTGGTT	TAGAATAATG	1440
	TCAGAGAAAA	TAACCAAGAA	ATTACAAATA	ATACTGGAAG	TTGTACCAGA	AGAAGATAAG	1500
	TTATGAACCTA	ATGACCTTGA	GATCTTGGCA	ATCTGCCCAA	GGGGAGACAC	AAAAAGGGA	1560
	TTTTTACTTC	ATTTTCTGAA	AGTCTAGAGA	ATTACAACCT	TGGTGATAAA	CAAAAGGAGT	1620
	CAGTTATTTT	TATTCATATA	TTTTCAGATA	TTTCAAGTAA	TTTCTAAGAA	ATTTAGTTAT	1680
30	AACTCTATGT	AGTTATAGAA	AGTGAATATG	CAGTTATTTCT	ATGAGTCGCA	CAATTCCTGA	1740
	GTCTCTGATA	CCTACCTATT	GGGGTTAGGA	GAAAAGACTA	GACAATTACT	ATGTGGTCAT	1800
	TCTCTACAAC	ATATGTTAGC	ACGGCAAGA	ACCTTCAAAT	TGAAGACTGA	GATTTTCTG	1860
	TATATATGGG	TTTTGTAAAG	ATGGTTTAC	ACACTACAGA	TGCTTACT	GTGAAAAGTG	1920
	TTTTCAATTC	TGAAAAAAG	CATACATCAT	GATTATGGCA	AAGAGGAGAG	AAAGAAATTT	1980
35	ATTTTACATT	GACATTGCAT	TGCTTCCCT	TAGATACCAA	TTTAGATAAC	AAACACTCAT	2040
	GCTTTAATGG	ATTATACCCA	GAGCACTTG	AACAAGGTC	AGTGGGATT	GTGAATAACA	2100
	TTAAAGAAGA	GTTTCTAGGG	GCTACTGTTT	ATGAGACACA	TCCAGGAGTT	ATGTTTAAGT	2160
	AAAAATCCTT	GAGAATTTAT	TATGTCAGAT	GTTTTTCAT	TCATTATCAG	GAAGTTTATG	2220
40	TTATCTGTCA	TTTTTTT	TCACATCAGT	TTGATCAGGA	AAGTGATAAA	CACATCTTAG	2280
	AGCAAGAGTT	AGTTTGTGAT	TAAATCTCA	TTAGAACAAC	CACCTGTTTC	ACTAATAACT	2340
	TACCCTGAT	GAGCTATCT	AAACATATGC	ATTTTAAGCC	TTCAAATTAC	ATTATCAACA	2400
	TGAGAGAAAT	AACCAACAAT	GAAGATGTT	AAAATAATAG	TCCCATATCT	GTAATCATAT	2460
	CTACATGCAA	TGTTAGTAAT	TCTGAAGTTT	TTTAAATTTA	TGGCTATTTT	TACACGATGA	2520
	TGAATTTTGA	CAGTTTGTG	ATTTTCTTTA	TACATTTTAT	ATTTCTCTGT	TAAATATCT	2580
45	CTTCAGATGA	AACTGTCCAG	ATTAATTAGG	AAAAGGCATA	TATTAACATA	AAAATTGCAA	2640
	AAGAAATGTC	GCTGTAATA	AGATTTACAA	CTGATGTTTC	TAGAAAATTT	CCACTTCTAT	2700
	ATCTAGGCTT	TGTAGTAAT	TTCCACACCT	TAATTATCAT	TCAACTTGCA	AAAGAGACAA	2760
	CTGATAAGAA	GAAATTTGAA	ATGAGAACT	TGGGATAAGT	GTTTGTGTTT	AGAAGATGTT	2820
	GTTTTGCCAG	TATTAGAAAA	TACTGTGAGC	CGGGCATGGT	GGCTTACATC	TGTAATCCCA	2880
50	GCACCTTGGG	AGGCTGAGGG	GGTGGATCAC	CTGAGGTCGG	GAGTCTAGTA	CCAGCTGAC	2940
	CAACATGGAG	AAACCCATC	TCTACTAAAA	ATACAAAT	AGCTGGGCAT	GGTGGCACAT	3000
	GCTGGTAATC	TCAGCTATTG	AGGAGGCTGA	GGCAGGAGAA	TTGCTTGAAC	CCGGGAGGCG	3060
	GAGGTTGCAG	TGAGCCAAAG	TTGCACCACT	GTACTCCAGC	CTGGGTGACA	AAGTCAGACT	3120
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Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

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	GIFISPKVL	QNTGSVMSL	TIWTVCGVLS	LFGALSYAEL	GTTIKSSGGH	YTYILEVFGP	120
	LPAPVRVWVE	LLIIRPATA	VISLAFGRYI	LEPFIQCEI	PELAIKLITA	VGITVVMVLN	180
	SMSVSWSARI	QIFLTFCKLT	AILIIIVPGV	MQLIKGQTQN	FKDAFSGRDS	SITRLPLAFY	240
65	YGMAYAGWPF	YLNFTVEEVE	NPEKTIPLAI	CISMAITIGV	YVLTNVAYFT	TINAEELLS	300
	NAVAVTFSEF	LLGNFSLAVP	IFVALSCFGS	MNGGVFAVSR	LPYVASREGH	LPEILSMIHV	360
	RKHTPLPAVI	VLHPLTMIML	FSGDLDSLNL	FLSFARWLFI	GLAVAGLIYL	RYKCPDMHRP	420
	FKVPLFIPAL	FSFTCLFMVA	LSLYSDPFST	GIGFVITLTG	VPAYYLFIIW	DKKPRWFRIM	480
	SEKITRTLQI	ILEVVPBEDK	L				

Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

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75	GCCGCCAGCG	GCTTTCTCGG	ACGCTTGCC	CAGCGGGCCG	CCCGACCCCC	TGCACCATGG	60
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80	GCGATGTGTC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
	ACGGACCTCG	CCGGCCCTTA	CTTCTCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCCT	GTAAGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCCT	TAACTAAGT	TCCATGACAT	420
85	GTGAAAAATT	CTTTTCCGGT	GGGTGTCAAC	GGAACCGGAT	TGAGAACAGG	TTTCCAGATG	480
	AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAAATTC	ATCATTTTGC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCAAATGTA	CTCGCTATTA	TTTTAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACTTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660

AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGA AAAAGAA AAAGAAGATG CCAAAGCTTC 720
 GCTTTGCCAG TAGAATCCGG AAAATTCGGA AGAAGCAATT TTAACATTC TTAATATGTC 780
 ATCTTGTTTG TCTTTATGGC TTATTTGCCT TTATGGTTGT ATCTGAAGAA TAATATGACA 840
 GCATGAGGAA ACAAATCATT GGTGATTTAT TCACCAGTTT TTATTAATAC AAGTCACTTT 900
 5 TTCAAAAATT TGGATTTTTT TATATATAAC TAGCTGCTAT TCAAAATGTA GTCTACCATT 960
 TTTAATTTAT GGTTCACACTG TTTGTGAGAC GAATTCCTGC AATGCATAAG ATATAAAAGC 1020
 AAATATGACT CACTCATTTT TGGGGTCTG ATTCTGATT TCAGAAGAGG ATCATAACTG 1080
 AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG 1140
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Seq ID NO: 397 Protein sequence
 Protein Accession #: NP_006519

1 11 21 31 41 51
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 CRQFLYGGCE GNANFPYWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
 TCEKFFSGGC HNRNIENRFP DEATCMGFCA PKKIPSF CYS PKDEGLCSAN VTRYFNP RY 180
 20 RTCDAPTYTG CGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASRIRKI RKKQF

Seq ID NO: 398 DNA sequence
 Nucleic Acid Accession #: NM_001508.1
 Coding sequence: 1..1361

25 1 11 21 31 41 51
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 30 TTCTGTATGG GCTTCTGGG GAACAGCGTC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
 TTGGTGTTC TCATCGGCAT GCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 ACGTCCAGCT ACACCTCTGC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCAGGTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC 420
 35 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTGCTCTGG 480
 GTCACTCTCG CCTGTGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 540
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCAG CCACCACGAG 600
 CAGCCCGAGA CCTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACGCTGTT 660
 CAGTCCAGCA TCTTCGGCGC CTTCTGGTGC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGGCGGGGGC 780
 ACGCGGCTCT CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
 ACCATCATCT TCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG 900
 ATTCGAGGGA TCATGCTGTC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG 960
 45 GCGTACATGA TCCTCTCTCC CTTCTCGGAG ACGTTTTTCT ACCTCAGTTC GGTCACTAAC 1020
 CCGCTCTCTG ACACGGTGTG CTGCGAGCAG TTTGGGCGGG TGTTCTGTGA GGTGCTGTGC 1080
 TGCGCGCTGT CGCTGAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
 ACCACGACA GCGCCGCTT TGTGCAGCGC CCGTTGCTCT TCGGCTCCCG GCGCCAGTCC 1200
 TCTGCAAGGA GAACGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
 50 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC 1320
 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 399 Protein sequence
 Protein Accession #: NP_001499.1

55 1 11 21 31 41 51
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 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLCKL HTFLFEACSY 120
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
 60 VNPSPHRLT CNRSSTRHHE QPETSNSMIC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
 MCWNNMQVLM KSKQGLSAGG TRPPQLRKSE SEESRTARRQ TIIPLRLIVV TLAVCWMPNQ 300
 IRRIMAAKPK KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STPQSEAEPO 420
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Seq ID NO: 400 DNA sequence
 Nucleic Acid Accession #: NM_006475.1
 Coding sequence: 28..2538

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 75 AAAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
 AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
 TGCCCGACAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
 ACAACGAGC GCTATTCTGA CGCTCAAAA CTGAGGAGG AGATCGAGGG AAAGGGATCC 420
 TTCATTACT TTGCACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCGTAGA 480
 80 GGTTTGGAGA GCAACGTGAA TGTGTAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
 AAGAGATGTG TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT 600
 TTGGGGCTTT TCATTAACCA TTATCTTAAT GGGGTTGTCA CTGTTAATTG TGCTCGAATC 660
 ATCCATGGGA ACCGATTTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA 720
 85 CCAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
 GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACTC 840
 TTTGCTCCCA CCAATGAGCG TTTTGAGAAA CTTCCACGAG GTGTCCTAGA AAGGTTCTAG 900
 GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
 TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

	GGATGTGACG	GTGACAGTAT	AACAGTAAAT	GGAATCAAAA	TGGTGAACAA	AAAGGATATT	1080
	GTGACAAATA	ATGGTGTGAT	CCATTTGATT	GATCAGGTCC	TAATTCCTGA	TTCTGCCAAA	1140
	CAAGTTATTG	AGCTGGGTGG	AAAACAGCAA	ACCACCTTCA	CGGATCTTGT	GGCCCAATTA	1200
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	GCATTTCTG	ATGATACTCT	CAGCATGTTT	CAGCGCTCC	TTAAATTAAT	TCTGCAGAAAT	1320
	CACATATTGA	AAGTAAAGT	TGGCCTTAAT	GAGCTTTACA	ACGGGCAAAT	ACTGGAAACC	1380
	ATCGGAGGCA	AACAGCTCAG	AGTCTTCGTA	TATCGTACAG	CTGTCTGCAT	TGAAATTTCA	1440
	TGCATGGAGA	AAGGGAGTAA	GCAAGGGAGA	AACGGTGGGA	TTACATATAT	CCGCGAGATC	1500
10	ATCAAGCCAG	CAGAGAAATC	CCTCCATGAA	AAGTTAAAC	AAGATAAGCG	CTTTAGCACC	1560
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	CTGATACGGG	ACAAAAATGC	TCTTCAAAAC	ATCATTCTTT	ATCACCTGAC	ACCAGGAGTT	1740
	TTCATTGGAA	AAGGATTGTA	ACCTGGTGT	ACTAACATTT	TAAAGACCAC	ACAAGGAAGC	1800
15	AAAACTCTTC	TGAAGAAGT	AAATGATACA	CTTCTGGTGA	ATGAATTGAA	ATCAAAAGAA	1860
	TCTGACATCA	TGACAACAAA	TGGTGTAAAT	CATGTTGTAG	ATAAATCTCT	CTATCCAGCA	1920
	GACACACCTG	TGTGAAATGA	TCAACTGCTG	GAAATACTTA	ATAAATTAAT	CAAAATACATC	1980
	CAAAATTAAGT	TTGTTCTGGG	TAGCACCTTC	AAAGAAATCC	CCGTGACTGT	CTATACAAC	2040
	AAAAATATAA	CCAAAGTTGT	GGAACCAAAA	ATTAAAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100
20	ATTATCAAAA	CTGAAGGACC	CACACTAACA	AAAGTCAAAA	TTGAAGGTGA	ACCTGAATTC	2160
	AGACTGATTA	TGAAGGTGGA	AACAATAACT	GAAGTGATCC	ATGGAGAGCC	AATTATTAAA	2220
	AAATACACCA	AAATCATTGA	TGGAGTGCCT	GTGAAATAA	CTGAAAAAGA	GACACGAGAA	2280
	GAACGAATCA	TTACAGGTCC	TGAAATAAAA	TACACTAGGA	TTTCTACTGG	AGGTGGAGAA	2340
	ACAGAAGAAA	CTCTGAAGAA	ATTGTTACAA	GAAGAGGTCA	CCAAGGTGAC	CAAAATTCATT	2400
25	GAAGGTGGTG	ATGGTCATTT	ATTGTAAGAT	GAAGAAATTA	AAAGACTGCT	TCAGGGAGAC	2460
	ACACCGGTGA	GGAAAGTGA	AGCCAAACAA	AAAGTTCAAG	GTCTTAGAAG	ACGATTAAAG	2520
	GAAGGTGCTG	CTCAGTGAAG	ATCCAAAAAC	CAGAAAAAAA	TGTTTATACA	ACCTTAAGTC	2580
	AATAACCTGA	CCTTAGAAAA	TTGTGAGAGC	CAAGTTGACT	TCAGGAACCTG	AAACATCAGC	2640
	ACAAAGAAGC	AATCATCAAA	TAATTTCTGAA	CACAAATTTA	ATATTTTCTT	TCTGAATGA	2700
30	GAAACATGAG	GGAAATGTGG	GAGTTAGCCT	CCTGTGGTAA	AGGAATTGAA	GAAAAATATA	2760
	CACCTTACAC	CCTTTTTCAT	CTTGACATTA	AAAGTTCTGG	CTAACTTTGG	AATCCATTAG	2820
	AGAAAAATCC	TGTGACAGC	ATTCTATTACA	ATTCAAATCG	AAGAGTTGTG	AACTGTTATC	2880
	CCATTGAAAA	GACCGAGCCT	TGTATGTATG	TTATGGATAC	ATAAATATGA	CGCAAGCCAT	2940
	TATCTCTCCA	TGGGAAGCTA	AGTTATAAAA	ATAGGTGCTT	GGTGTACAAA	ACTTTTATA	3000
35	TCAAAAGGCT	TGTGACATTT	CTATATGAGT	GGGTTTACTG	GTAAATATATG	TTATTTTATA	3060
	CAACTAATTT	TGTACTCTCA	GAATGTTTGT	CATATGCTTC	TTGCAATGCA	TATTTTATA	3120
	TCTCAAACGT	TTCAATAAAA	CCATTTTTC	GATATAAAGA	GAATTACTTC	AAATTGAGTA	3180
	ATTCAAGAAA	ACTCAAGATT	TAAGTTAAAA	AGTGGTTTGG	ACTTGGGAA		

Seq ID NO: 401 Protein sequence
Protein Accession #: NP_006466.1

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	KLREELEGKG	SFTTFAPSNE	AWNDLSDIR	RGLESNNVVE	LLNALHSHMI	NKRLMTKDLK	180
	NGMIIPSMYN	NLGLFMINYP	NGVVTNVCAR	IIHGNQIATN	GVVHVDRVL	TQIGTSIQDF	240
	IEAEDDLSSF	RAAAITSDEL	EALGRDGHFT	LFAPTNEAFE	KLPRGVLERF	MGDKVASEAL	300
50	MKYHILNTLQ	CSEIMGGAV	FETLEGNITIE	IGCDGDSITV	NGIKMVNKKD	IVTNNGVIHL	360
	IDQVLIPDSA	QVETFDLVAQ	QTTFTDLVAQ	LGLSALRPD	GEYTLAPVN	NAPSDDTLSM	420
	VQRLKLILQ	NHILKVKVGL	NELYNGQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKGSKQG	480
	RNGAIIHRE	IIKPAEKLH	EKLKQDKRFS	TFLSLLEAAD	LKELLTQPGD	WTLFVPTNDA	540
	FKGMTSEEKE	LIIRDKNTPG	NIIILYHLTPG	VFIGKGFEPG	VTNILKTQGG	SKIFLKEVND	600
55	TLLVNELKSK	ESDINTNGV	IHVVDKLLYP	ADTPVGNQDL	LEILNKLIKY	IQIKFVRGST	660
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	TEVIHGEPII	KKYTKIIDGV	PVEITEKETR	EERIITGPEI	KYTRISTGGG	ETEETLKKLL	780
	QEEVTKVTKF	IEGGDGHLE	DEBIKRLQGG	DTPVRKLQAN	KKVQGSRRRL	REGRSQ	

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Coding sequence: 40..417

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	AAGGGTCGCT	GTTCTCTGAT	CAGCACCAC	CAAGGGACTA	TCCACCTACA	ATCCTTGAAA	180
	GACCTTAAAC	AATTTGCCCC	AAGCCCTTCC	TGCCAGAAAA	TTGAAATCAT	TGCTACACTG	240
70	AAGAAATGGAG	TTCAACATG	TCTAAACCCA	GATTCAGCAG	ATGTGAAGGA	ACTGATTAAA	300
	AAGTGGGAGA	AACAGGTGAG	CCAAAAGAAA	AAGCAAAAGA	ATGGGAAAAA	ACATCAAAAA	360
	AAGAAAGTTC	TGAAAGTTTG	AAAATCTCAA	CGTCTCTGTC	AAAAGAAAGC	TACATAAGAG	420
	ACCACTTCAC	CAATAAGTAT	TCTGTGTTAA	AAATGTTCTA	TTTAAATTAT	ACCGCTATCA	480
	TTCCAAAGGA	GGATGGCATA	TAATACAAAG	GCTTATTAAT	TTGACTAGAA	AATTTAAAC	540
75	ATTACTCTGA	AATGTAACT	AAAGTTAGAA	AGTTGATTTT	AAGAATCCAA	ACGTTAAGAA	600
	TTGTTAAAGG	CTATGATTGT	CTTTGTTCTT	CTACCACCCA	CCAGTTGAAT	TTTATCATGC	660
	TTAAGGCCAT	GATTTTAGCA	ATACCCATGT	CTACACAGAT	GTTCACCCAA	CCACATCCCA	720
	CTCACAACAG	CTGCCTGGAA	GAGCAGCCCT	AGGCTTCCAC	GTACTGCAGC	CTCCAGAGAG	780
	TATCTGAGGC	ACATGTCAGC	AAGTCTTAAG	CCTGTTAGCA	TGCTGGTGAG	CCAAGCAGTT	840
80	TGAAATTGAG	CTGACCTTCA	CCAAGCTGCT	GTGGCCATCA	ACCTCTGTAT	TTGAATCAGC	900
	CTACAGGCCT	CACACACAT	GTGCTGAGA	GATTCATGCT	GATTGTTATT	GGGTATCACC	960
	ACTGGAGATC	ACCAGTGTGT	GGCTTTTACA	GCTTCTTCTC	TGGCTTTTGA	AGCCATGTGA	1020
	TTCCATCTTG	CCCGCTCAGG	CTGACCACTT	TATTTCTTTT	TGTTCCCTTT	TGCTTCATTC	1080
	AAGTCAGCTG	TCTGCTAAT	TACCAATG	CAGTGCCTTT	CTTCTCTCCA	GTGACCTGTT	1140
85	CATATGCTCT	GATTTATCTG	AGTCAACTCC	TTTCTCATCT	TGTCCCAAC	ACCCACAGCA	1200
	AGTGCTTTCT	TCTCCCAATT	CATCTCACT	CAGTCCAGCT	TAGTTCAAGT	CCTGCCTCTT	1260
	AAATAAACCT	TTTGGACAC	ACAATATATC	TTAAACTCC	TGTTTCACTT	GGTTCAGTAC	1320
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AAAATCATAT AATCTTACAA TGAAGAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
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GGAGGTTCTG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
CTTCCCAAAT TTGAATTCCT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
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Seq ID NO: 403 Protein sequence
Protein Accession #: NP_002407

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Seq ID NO: 404 DNA sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

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AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCGGGGCGCC CGCCGCGGG 120
GACGGGCGTC TCGGCTGGC GCGACTAGCG CTGCTACTCC TGGGCTGGGT CTCCTCGTCT 180
TCTCCCACTC CTCTGGCATC CTCTTCTTCC TCCTCGGCGC CGTTCCTGGC TTCCGCGGTG 240
TCCGCCAGCG CCGCGCTGCC GGACCACTGC CCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300
CGCACAGTCA AGTGCGTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCCTAC 360
GTGCGCAACC TCTTCTTAC CGGCAACAG CTGGCCGTGC TCCTTCCCGG CGCCTTCGCC 420
CGCCGCGCGC GCGTGGCGGA GCTGGCGCG CTCAACCTCA CGCGCAGCG CCTGGACGAG 480
GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
CCACTGGCGC ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC 600
AGTCCCTTGG TGGAACTGAT CCTGAACAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
CTGCCAGGCC TCAGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
TCCTTCCGCA ACCTGACACA TCTAGAAAGC CTCCACCTGG AGGACAATGC CCTCAAGGTC 900
CTTCACAATG GCACCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCTCTGGAC 960
AACAACTCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
CAAACTCTTT ATGTCTTCTT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
AGGGATCACA TGAAGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAAAC 1320
AACTCAGTT TAACTCTGTA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACCTG 1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
TAGATACAAC GGACTTTGAC TAAAGCAGT GAAGGGGATT TGCTTCTTGG TTATGTAAAG 1500
TTTCTCGGTG GTTCTGTGTA ATGTAAGAC ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
TTCTTTTCTT TGAACCTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
ACAGATAGCA TTCACAAAAA GCTGCCTCAA CTTTTTCGAG AAAAAACTT TATTCATAAA 1740
TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAT AATGTCATCC TATAAACTGC 1800
CTGCAGAGCT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
AGAGCATGCT TACATTTTAC TGTCTGCAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAAATGT ACTGATTTTT 1980
TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
ATCTTAAAA GAA

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Seq ID NO: 405 Protein sequence
Protein Accession #: NP_006661

75
80
85

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1 11 21 31 41 51
MPGGCSRGP AGDGRRLRL LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPPLPD 60
QCPALCECSE AARTVKCNR NLTEVPTDLP AYVRNLFTG NQLAVLPAGA FARRPPLAEL 120
AALNLSGSLR DEVRAFAFH LPSLRQLDLS HNPLADLSPF AFGSNASVS APSPLVELIL 180
NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPDVL AQLPSLRHLD 240
LSNNLSVSLT YVSFNLTHL ESHLEDNAL KVLHNGTLAE LQGLPHIRVP LDNNPWVDC 300
HMDMVTWLK ETEVVQGDOR LTCAYPEKMR NRVLLELSNA DLDCDPIPLP SLQTSYVFLG 360
IVLALIGAIF LLVLYLNRKG IKKWMHNRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

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Seq ID NO: 406 DNA sequence
Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

	1	11	21	31	41	51	
5	ATGCCTGGGG	GGTGTCTCCG	GGGCCCCGCC	GCCGGGGACG	GGCGTCTGCG	GCTGGCGCGA	60
	CTAGCGCTGG	TACTCTCTGG	CTGGGTCTCC	TCGTCTTCTC	CCACCTCTCT	GGCATCTCTC	120
	TTCTCTCTCT	CGGCGCCGTT	CCTGGCTTCC	GCCGTGTCCG	CCCAGCCCCC	GCTGCCGGAC	180
	CAGTGCCCCG	CGCTGTGCGA	GTGCTCCGAG	GCAGCGCGCA	CAGTCAAGTG	CGTTAACCGC	240
	AATCTGACCG	AGGTGCCAC	GGACTGCCCC	GCCTACGTGC	GCAACCTCTT	CCTTACCGGC	300
10	AACCAGCTGG	CCAGCAACCA	CTTCTTTTAC	CTGCCGCGGG	ATGTGCTGGC	CCAAGTGGCC	360
	AGCCTCAGGC	ACCTGGACTT	AAGTAATAAT	TCGTGTGTGA	GCCTGACCTA	CGTGTCTTTC	420
	CGCAACCTGA	CACATCTAGA	AAGCTCCAC	CTGGAGGACA	ATGCCCTCAA	GGTCTCTTAC	480
	AATGGCACCC	TGGCTGAGTT	GCAAGGTCTA	CCCCACATTA	GGGTTTTCCT	GGACAACAAT	540
	CCCTGGGTCT	GCGACTGCGA	CATGGCAGAC	ATGGTGACCT	GGCTCAAGGA	AACAGAGGTA	600
15	GTGCAAGGCA	AAGACCGGCT	CACCTGTGCA	TATCCGGA	AAATGAGGAA	TCGGGTCTCT	660
	TTGGAAGTCA	ACAGTGCTGA	CCTGGACTGT	GACCCGATTG	TTCCCCCATC	CCTGCAAAAC	720
	TCCTATGTCT	TCCTGGGTAT	TGTTTATAGC	CTGATAGGCG	CTATTTTCTT	CCTGGTTTTC	780
	TATTTGAACC	GCAAGGGGAT	AAAAAAGTGG	ATGCATAACA	TCAGAGATGC	CTGCAGGGAT	840
20	CACATGGAAG	GGTATCATT	CAGATATGAA	ATCAATGCGG	ACCCCAGATT	AACAAACCTC	900
	AGTTCTAACT	CGGATGTCTT	CGAGTGA				

Seq ID NO: 407 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
25	MPGGCSRGP	AGDRLRLAR	LALVLLGWVS	SSSPTSSASS	FSSSAPFLAS	AVSAQPPLPD	60
	QCPALCECSE	AARTVKCVNR	NLTVEPTDLP	AYVRNLFITG	NQLASNHFLY	LPRDVLQALP	120
	SLRHLDLN	SLVSLTYVSF	RNLTHLESLH	LEDNALKVLH	NGTLAEQLGL	PHIRVFLDNN	180
30	PWVCDCHMAD	MVTWLKETEV	VQKDRILTCA	YPERMNRNVL	LELNSADLDC	DPILPPLSLQ	240
	SYVFLGIVLA	LIGAIFLLVL	YLNRRGIKKW	MHNIRDACRD	HMEGYHYRYE	INADPRLTNL	300
	SSNSDVLE						

Seq ID NO: 408 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

	1	11	21	31	41	51	
40	CAGCACCCAG	CTCCCCGCCA	CCGCCATGGT	CCCCGACACC	GCCTGCGTTC	TTCTGCTCAC	60
	CCTGGCTGCC	CTCGCGCGCT	CCGACAGGGG	CCAGAGCCCG	TTGGGCTCAG	ACCTGGGCCCC	120
	GCAGATGCTT	CGGGAAGTGC	AGGAAACCAA	CGCGGCGCTG	CAGGACGTGC	GGGACTGGCT	180
	GCGGCAGCAG	GTCAGGGAGA	TCACGTTCTT	GAAAAACACG	GTGATGGAGT	GTGACGCGTG	240
	CGGGATGCAG	CAGTCAGTAC	GCACCGGCTT	ACCCAGCGTG	CGGCCCTGCG	TCCACTGCGC	300
45	GCCCGGCTTC	TGCTTCCCGG	GCGTGGCCTG	CATCCAGACG	GAGAGCGGCG	GCCGCTGCGG	360
	CCCTTGCCCC	GCGGGCTTCA	CGGGCAACGG	CTCGCACTGC	ACCGAGCTCA	ACGAGTGCAA	420
	CGCCACCCCC	TGCTTCCCGG	GAGTCCGCTG	TATCAACACC	AGCCCGGGGT	TCCGCTGCGA	480
	GGCTTGCCCG	CCGGGTACAC	GCGGCCCCAC	CCACCAGGGC	GTGGGGCTGG	CTTTCGCCAA	540
	GGCCAAACAG	CAGGTTTGCA	CGGACATCAA	CGAGTGTGAG	ACCGGGCAAC	ATAACTGCGT	600
50	CCCCAACTCC	GTGTGCATCA	ACACCCGGGG	CTCCTTCCAG	TGCGGCCCGT	GCCAGCCCGG	660
	CTTCGTGGGC	GACCAGGCGT	CCGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCCGAOCG	720
	CTCGCCACAG	GAGTGCCACG	AGCATGCAGA	CTGGCTCCTA	GAGCGCGATG	GCTCGGGGTC	780
	GTGCGTGTGT	GCGGTGGGCT	GGGCGGGCAA	CGGGATCCTC	TGTGGTGGCG	ACACTGACCT	840
	AGACGGCTTC	CCGGACGAGA	AGCTGCGCTG	CCCGGAGCCG	CAGTGCCGTA	AGGACAACATG	900
55	CGTGACTGTG	CCCCACTCAG	GGCAGGAGGA	TGTGGACCGC	GATGGCATCG	GAGACGCTTG	960
	CGATCCGGAT	GCCGACCGGG	ACGGGTGCC	CAATGAAAAG	GACAACTGCC	CGCTGGTGGG	1020
	GAACCCAGAC	CAGCGCAACA	CGGACGAGGA	CAAGTGGGGC	GATGCGTGCG	ACAACCTGCC	1080
	GTCCACAGAG	AACGACGACC	AAAAGGACAC	AGACCAGGAC	GGCCGGGGCG	ATGCGTGCGA	1140
	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAG	AACTGCCCTA	GGGTACCCAA	1200
60	CTCAGACCAG	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTGTCCCCA	1260
	GAAGAGCAAC	CCGGATCAGG	CGGATGTGGA	CCACGACTTT	GTGGGAGATG	CTTGTGACAG	1320
	CGATCAAGAC	CAGGATGGAG	ACGGACATCA	GGACTCTCGG	GACAACTGTC	CCACGGTGCC	1380
	TAAAGTGACC	CAGGAGGACT	CAGACCACGA	TGGCCAGGGT	GATGCTGCGG	ACGACGACGA	1440
	CGACAAATGAC	GGAGTCCCTG	ACAGTCCGGA	CAACTGCCGC	CTGGTGCTTA	ACCCCGGCCA	1500
65	GGAGGACGCG	GACAGGGGAC	GCGTGGGCGA	CGTGTGCCAG	GACGACTTTG	ATGCAGACAA	1560
	GGTGTAGAC	AAGATCGACG	TGTGTCCGGA	GAACGCTGAA	GTCACGCTCA	CCGACTTCAG	1620
	GGCCTTCCAG	ACAGTCTGTC	TGGACCCGGA	GGGTGACGCG	CAGATTGACC	CCAACCTGGT	1680
	GGTGCTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAATGAAC	AGCGACCCAG	GCCTGGCTGT	1740
	GGGTTACACT	GCCTTCAATG	GCGTGGACTT	CGAGGGCACG	TTCCATGTGA	ACACGGTCAC	1800
70	GGATGACGAC	TATGCGGGCT	TCATCTTTGG	CTACCAGGAC	AGCTCCAGCT	TCTACGTGGT	1860
	CATGTGGAAG	CAGATGGAGC	AAACGTATTG	GCAGGCCAAG	CCCTTCCGTG	CTGTGGCCGA	1920
	GCCTGGCATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
	AAACGTGGGT	TGGAAGGACA	AGAAGTCTTA	TCGTTGGTTC	CTGCAGCAAC	GGCCCCAAGT	2100
75	GGGCTACATC	AGGGTGCATG	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
	CTTGGACACA	ACCATGCGGG	GTGGCCGCTT	GGGGGTCTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CATCTGGGCC	AACCTGCGTT	ACCGCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
	TCAGCTGCGG	CAAGCCTAGG	GACCAGGGTG	AGGACCCGCC	GGATGACAGC	CACCCCTACC	2340
80	GCGGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGGTGGC	CGTCCTGAGG	GGGAAGTGAG	2400
	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGCAGGG			

Seq ID NO: 409 Protein sequence
Protein Accession #: NP_000086.1

	1	11	21	31	41	51	
85	MVPDTACVLL	LTLAALGASG	QGQSPLGSDL	GPQMLRELQE	TNAALQDVDR	WLRQQVREIT	60

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FLKNTVMBCD ACGMQQSVRT GLPSVRPLH CAPGFCPPGV ACIQTESGGR CGPCPAGPTG 120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INECTGQHN CVPNVSVICNT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240
ADCVLERDGS RSCVCRVGA GNGLLCGRDT DLGFPDEKL RCPEPQCRKD NCVTVPNSSQ 300
EDVDRDGIAD ACDPDADGDG VPNEKDNCLP VRNPDQRNTD EDKWDACDN CRSQKNDQDK 360
DTDDQDGRDA CDDIDIGDRI RNQADNCPRV PNSDQKSDG DGIGDADNC POKSNPDQAD 420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPS 480
RDNCRLVPNP QGEDADRQDV GDVQDDFDA DKVVDKIDVC PENAETVLT D FRAFTVVL 540
PEGDAQIDFN WVVLNQGREI VQTMSNDPGL AVGYTAFNGV DFEFTFHVNT VTDDDYAGFI 600
FGYQDSSSFY VVMWQMEQT YWQANPFRV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
RLGVPCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

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Seq ID NO: 410 DNA sequence

Nucleic Acid Accession #: NM_001565.1

Coding sequence: 67..363

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1      11      21      31      41      51
|      |      |      |      |      |
20 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
AGCACCATTGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC 120
ATTCAAGGAG TACTCTCTTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CCTGTTAATC CAAGGTCTTT AGAAAAAATT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
CGTGTGAGA TCATTGTCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
25 TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
TAAAACCGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CTGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
GTTACACTAA AAGGTGACCA ATGATGTCAT CCAAATCAGC TGCTACTACT CCTGTAGGAA 540
GGTTAATGTT CATCATCTCA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
30 GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTCTGACC CTGCTTCAA TATTTCCCTC 660
ACCTTTCCCA TCTTCCAAGG TACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTC 720
TCAGAACTCT AAATAACTAA AAGGTATGCA ATCAAACTCG CTTTTTAAAG AATGCTCTTT 780
ACTTCATGGA CTTCCTCTGC CATCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
35 CATAAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
CTTATTTAAT GAAAGACTGT ACAAGATATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
TTTCAGTGA CATGGAATTA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGS 1080
TTTCAATAA AAAATGAGGT ACTCTCTGG AAATATTAAG

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Seq ID NO: 411 Protein sequence

Protein Accession #: NP_001556.1

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1      11      21      31      41      51
|      |      |      |      |      |
45 MNQTAILICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60
EIIATMKKKG EKRCNLPESK AIKNLLKAVS KEMSKRSP

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Seq ID NO: 412 DNA sequence

Nucleic Acid Accession #: XM_057014

Coding sequence: 143..874

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1      11      21      31      41      51
|      |      |      |      |      |
55 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG 120
CGCTGCCCGG CAGCGCGGAG CCATGCGACC CCAAGGCCCC GCGGCTCCCG CGCAGCGGCT 180
CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
60 CATTCCGGGT ACACCTGGGA TCCAGGTCG GGTAGGATTC AAAGGAGAAA AGGGGGAATG 420
TCTGAGGGAA AGCTTTGAGG AGTCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
ATTGAATTAT GGCATAGATC TTGGGAAAT TGGCGAGTGT ACATTTACAA AGATGCGTTC 540
AAATAGTGCT CTAAGAGTTT TGTTCACTGG CTCACTTCGG CTAATAATGCA GAAATGCATG 600
CTGTCAGCGT TGGTATTTC CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTA 660
65 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720
CACTTCTTCT GTGGAAGGAC TTTGTGAAG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
70 TTTTITATT ATGCCTTGA ATGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
CATCTGAATG AAAAGCAAAG CTAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
TTTAAATCTA GCATTATTC TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTITAGT 1080
TGGTTAGAA ACTTCTTCTA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
GGTCTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200
75 TGTACAATTT GTAAATGTTT AGAATTTTTT TTATATCTGT TAAATAAATA TTATTTCCAA 1260
CAACCTTAAA AAAAAAAAAA AAAA

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Seq ID NO: 413 Protein sequence

Protein Accession #: XP_057014

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1      11      21      31      41      51
|      |      |      |      |      |
80 MRPGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA 60
GVPGRDGSPG ANGIPGTGPI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACQWRWYFT FNGAECGSL PLEAIYLDQ 180
85 GSPENMNSTN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
LPK

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5	1	11	21	31	41	51	
	CTCGTGCCGA	ATTCGGCAGC	AGACCGCGTG	TTCGCGCCTG	GTAGAGATT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAC	CAAACTCTGC	CGCGTGGCCG	GGCCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCTG	ACCTTTTGCCC	180
10	TCTCTGTAC	AAATCCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTTGAAGGGT	360
	TCAGAAAATT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
	ACCACGACCA	TCACCTCAGC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
15	AGCATCACTC	AGACCCAGAG	CATCACTCTG	ACCATGATCA	TCACCTCCAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAG	CGAAAGGCTC	TTTGCCGAGA	CCATGACTCA	GATAGTTTCA	600
	GTAAGATCC	TAGAAACAGC	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCAACTGTG	TACAACACTG	720
	TCTCTGAAGG	AACTCACTTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
20	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTCACATC	AAAGAGCCCG	GTGAGCCGGC	840
	TGGCTGGTAG	GAAACAAAT	GAATCTGTGA	GTGAGCCCGG	AAAAGGCTTT	ATGTATTCCA	900
	GAAACACAAA	TGAAATCCTT	CAGGAGTGTT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
	GCATGGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
	TCAACCAAT	TGATGCTAGA	TCTTGTCTGA	TTCATACAAG	TGAAAAGAAG	GCTGAAATCC	1080
25	CTCCAAAGAC	CTATTCTATA	CAATAGCCTT	GGGTTGGTGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCTT	GTCTCTGCTG	GGGGTTATCT	TAGTGCCTCT	CATGAATCGG	GTGTTTTTCA	1200
	AATTTCTCTT	GAGTTTCTCT	GTGGCACTGG	CCGTGGGGAC	TTTGAGTGGT	GATGCTTTT	1260
	TCACCTTCTT	TCCACACTTT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
	CAATGGAAAT	GAAAAGAGGA	CCACTTTTCA	GTCATCTGTC	TTCTCAAAAC	ATAGAAGAAA	1380
30	GTGCTTATTT	TGATTTCCAG	TGGAAGGGTC	TAACAGCTCT	AGGAGGCCCTG	TATTTTCATG	1440
	TTCTTGTGGA	CATGTCTCTT	ACATTGATCA	AACAATTAA	AGATAAGAAG	AAAAAGAATC	1500
	AGAAGAAACC	TGAAAATGAT	GATGATGTGG	AGATTAAGAA	GCAGTTGTCC	AAGTATGAAT	1560
	CTCAACTTTC	AACAAATGAG	GAGAAAGTAG	ATACAGATGA	TCGAACGTGA	GGCTATTTAC	1620
	GAGCAGACTC	CAAGAGGCC	TCCCACTTTG	ATTCTCAGCA	GCCTGCAGTC	TGGAAGAAG	1680
35	AAGAGGTGAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCCACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
	CTCACAGTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTGCCCACTT	1920
	TGGCCTGGAT	GGTGATAATG	GGTGATGGCC	TGCACAATTT	CAGCGATGGC	CTAGCAATTG	1980
40	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTGTCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CTTTTATAAT	GCTATTGTCA	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
	GAATTTTCAT	TGGTCATTAT	GCTGAAATG	TTTCTATGTG	GATATTGGA	CTTACTGCTG	2220
	GCTTATTCAT	GTATGTTGCT	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
45	GTGACCATGG	ATGTAGCCGC	TGGGGGTATT	TCTTTTACA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTGGAAAT	TATGTTACTT	ATTTCCATAT	TTGAACATAA	AATCGTGTTT	CGTATAAATT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
	TTGTATTGAA	TATGTCTGTC	TGTTACAAAG	TCAGTTAAAG	GTACGTTTAA	ATATTAAAGT	2580
50	TATTCTATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCAAC	GGTATTACCA	GTTTATTATG	2640
	TAAACAAGAG	ATTTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAAATGT	CTTTAATGCT	2700
	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAATCTGCTG	2760
	TGTTTAGGAA	TAAGAATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTTA	2820
	AGCAAGAGAA	TAAAGGAGAA	AAGAGAAGAA	TCTGAGAATT	GGGGAGGCAT	AGATTCTTAT	2880
55	AAAAATCACA	AAATTGTTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAA	TATAAAAGG	2940
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Seq ID NO: 415 Protein sequence
Protein Accession #: XP_084007

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	EHHSDDHDS	HHNHAASGKN	KRKALCPDHD	SDSSGKDPNN	SQKGGAHRPE	HASGRNNVKD	180
75	SVSASEVTST	VYNTVSEGT	FLETIETPRP	GKLPFKDVSS	STPPSVTSKS	RVSRLAGRKT	240
	NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMIQIV	PLNATEFNVL	CPAIINQIDA	300
	RSCLHTSEK	KAIEPPKTY	LQIAWVGFI	ASISIFLSL	LGIVILPLMN	RVFFKFLLSF	360
	LVALAVGTL	GDAPFLHLPH	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIEESAYFDS	420
	TKWGLTALGG	LYFMFLVEHV	LTLIKQFKDK	KKKNQKKPEN	DDDVEIKKQL	SKYESQLSTN	480
	EKVDTDDRT	EGYLRADSQE	PSHFDSQQA	VLEEEVEMIA	HAHPQEVYNE	YVPRGCKNKC	540
80	HSHFHDTLGQ	SDDLHHDHHD	YHHILHHHHH	QNHHPHSHSQ	RYSRRELKDA	GVATLAWMVI	600
	MGDGLHNFSD	GLATGAAPTE	GLSSGLSTSV	AVFCHELPHE	LGDFAVLLKA	GMTVQAVLY	660
	NALSAMLAYL	GMATGIFTGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720
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Seq ID NO: 416 DNA sequence
Nucleic Acid Accession #: NM_015419.1
Coding sequence: 1..8487

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	AATTTGGGGT	TTAATAGCAT	ACAGGCCCTG	TCAGAAACCT	CATTTCAGAG	ACTGACCAAG	240
	TTGGAGCTAC	TTATGATTCA	CGGCAATGAG	ATCCCAAGCA	TCCCGATGG	AGCTTTAAGA	300
10	GACCTCAGCT	CTCTTCAGGT	TTTCAAGTTC	AGCTACAACA	AGCTGAGAGT	GATCACAAGGA	360
	CACAGCCCTC	AGGGTCTCTC	TAACTTAATG	AGGCTGCACA	TTGACCACAA	CAAGATCGAG	420
	TTTATCCACC	CTCAAGCTTT	CAACGGCTTA	ACGTCTCTGA	GGCTACTCCA	TTTGGAAAGGA	480
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Seq ID NO: 417 Protein sequence
 Protein Accession #: NP_056234.1

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	PQLGVTRRPQ	IPTSPAPVMR	ERKVIPOGYN	RIHSHSTFHL	DFGPPAPPLL	HTPQTGSPS	1800
	TNLQNIPIVMS	STQSSISFIT	SSVQSSGSFH	QSSSKFPAGG	PPASKFWSLG	EKPQILTKSP	1860
	QTVSVTAETD	TVFPCEATGK	PKPVTWTKV	STGALMTPT	RIQRFEVLKN	GTLVIRKVVQ	1920
30	QDRGQYMCFA	SNLHGLDRMV	VLLSVTVQOP	QILASHYQDV	TVYLGDTIAM	ECLAKGTAP	1980
	QISWIFPDRR	VWQTVSPVES	RITLHENRTL	SIKEASPSDR	GVYKCVASNA	AGADSLAIRL	2040
	HVAALPPVTH	QKLENIISLP	PGLSIHICT	AKAAPLPSVR	WVLGDGTQIR	PSQFLHGNLF	2100
	VFPNGTLYIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSFRRDVRV	2160
	GGTLKLDCA	SGDPWPRIW	RLPSKRMIDA	LFSFDSRIKV	FANGTLVVK	VTDKDAGDYL	2220
35	CVARNKVQDD	YVVLKVDVVM	KPAKIEHKEE	NDHKVYFGGD	LKVDVCATGL	PNPEISWSLP	2280
	DGSLVNSFMQ	SDDSGGRTRK	YVVFNNGLTY	FNEVGMREEG	DYTCFAENQV	GKDEMVRVRK	2340
	VVTAPATIRN	KTYLAVQVPY	GDVVTVACEA	KGEPMKVTW	LSPTNKVIPT	SSEKYQIYQD	2400
	GTLILQKAQR	SDSNGYTCLV	RNSAGEDRKT	VWILHVNQPP	KINGNPNPIT	TVREIAAGGS	2460
	RKLIDCKAEG	ITPRVLWAF	PEGVVLPAFY	YGNRITVHGN	GSLDIRSLRK	SDSVQLVCM	2520
40	RNEGGEARLI	VQLTVLEPME	KPIFHDPISE	KITAMAGHTI	SLNCSAAGTP	TPSLVWVLPN	2580
	GTDLQSGQQL	QRFYHKADGM	LHISGLSSVD	AGAYRCVARN	AAGHTERLVS	LKVGLKPEAN	2640
	KQYHNLVSI	NGETLKLPCY	PPGAGQGRFS	WTLFNGMHLE	GPQTLGRVSL	LDNGILTvre	2700
	ASVFDRTGYV	CRMETEYGPS	VTSIPVIVIA	YPPRITSEPT	PVIYTRPGNT	VKLNCMAMGI	2760
	PKADITWELP	DKSHLKAGVQ	ARLYGNRFLH	PQGLTITQHA	TQRDAGFYKC	MAKNILGSDS	2820
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Seq ID NO: 418 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..5001

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	ACCTCTCAAG	AGGACGAATT	GGATGTACCT	GACGACATCA	GCGTCCGGGT	TATGTCTACT	120
55	CAGTCTGTGC	TTGTGTCCTG	GGTGGATCCT	GTTCTGGAAA	AACAGAAGAA	AGTTGTGTGCA	180
	TCAAGACAGT	ACACCGTGGC	CTATCGAGAG	AAGGGGGAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGCGGTG	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATTT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAATGGA	GTACGTCAGT	CTTCCAAAGA	360
	ACACCAAGAT	CTGCCCCATC	CACAGCTCCT	GAAAACTTGA	ACGCTGCGCC	AGTCAATGGC	420
60	AAACCTACAG	TTGTGCTGAC	ATCTTGGGAT	GCGCTACCGA	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGTCTGC	TGGACACAGG	ACTGTTTTCA	GTTTCTCCTC	TCCAACCATC	TGCCAAATCA	540
	TTTCAGAATA	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTGAGGACA	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAACGCTATC	660
	TTTTCAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
	TCGCTATGCC	AACAGAAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
65	ATCGATATCC	AAACCAACA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
	CCATGTTTTC	TTTTCTACTT	CCTCACATTT	ATGCTGGATA	TTGGCGGCTT	TTCTTTCATT	900
	ATGTGCTATG	AAGACCCANN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACCTGAG	1020
70	CCTTCTCTAC	CTTCTCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGCGC	CCCGAAACCC	CCAGCTTCGC	GCCAAGAAGG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTCCCGGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAAG	ACGGAACCTG	AGGCGGCCAA	GTAAGACACG	CCACTCGGTG	1320
75	GTGTCTCCCG	CGAGGACTGC	AGTAGGGGCC	CGGATGCCAG	CGCTGCCCGC	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCGGCC	CAGGGGCGCC	CCCCTCGGCT	1440
	TCGGCTCTCT	CTGCCACCA	CGGCTCCACC	CAGGGCACCT	CTCATCGTCC	TTCCCTGCCT	1500
	GCCAGCTTGA	ATGACACGA	CTTGGTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCGCCTT	CGCCACGCCC	CGGCCAGCCC	TGTCCCCCAG	CGCCAGTCC	1620
	CGGTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCACCCCG	CGCCAAAGCC	AGCCTCGCCG	1680
80	GCGCGGAGGA	CCCCGATTTC	GAGGCGCGCA	GAGGAAGATT	CCAGTGCCTC	AGCCCCACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTCGGCTGC	TGCCCCACCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAAGGG	CGGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	GCGCATCAC	GGTCCACCAT	GTCTCTCTCC	GTCTCTCTCT	ATCTCTCGTC	CAGGACGCG	1920
	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGCGCA	TAGGGAAGAC	1980
85	GGCGGAAGGC	AGGCGGAGGC	CACGGCCACG	ACGCTGCGGG	CCCGGCTCTG	CTCTGGACAC	2040
	TTCAATTGCG	TCAGACAAA	ACCTTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTGACG	2100
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	GCCCCACCCCA	GGGTTCCCTC	TCACTCTGAT	TCCCACCCCTA	AGCTTAGCTC	AGGTATCCAT	2220
	GGAGACGAGG	AGGATGAGAA	GCCGCTTCCT	GCCACCGTTG	TCAATGACCA	CGTGCTTCC	2280
	TCCTCCAGGC	AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA	GGAGAAGCCC	GCAGAGAGGG	2340
5	GCCAGCCTGC	ATCGGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
	CATCCTCAGG	GCAAGTACTC	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTCA	ACAGAGCACA	2460
	GACGCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CGGCCACGGG	2520
	TCCCTCTGCT	GTCTCTCCGC	AGCAGCGTCA	CAGCAGCATC	CCAGTGTTC	CAGAAGGATG	2580
	ACACCCGGCC	GGGCCCCAGA	ACAGCAGCCC	CCTCCTCCCG	TCGCCACGTC	CCAGCACCAC	2640
10	CCGGGACCCC	AGAGCAGAGA	CGCGGGTGGG	TCACCTTCCC	AGCCCAGGCT	CTCACTGACC	2700
	CAGGCGGGG	GGCCCGGCC	CACGTGCGAG	GGCCGCTCCC	ACTCCTCCTC	GGACCCCTAC	2760
	ACGGCGAGCT	CCAGAGGGAT	GCTCCCCACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCCAG	2820
	GGCAGCTACG	ACGACGACAG	CACAGAAGTC	GAGGCCCAGG	ATGTGCGGGC	CCCCCGGCAC	2880
	GCCGCGGGG	CCAAGGAGGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
15	ACAGGCGCAG	GGGCGAGTGG	CGACCACAGG	TCCCAGGCGG	GACATGCGGC	CTCCCCCGCC	3000
	AGGCCCGAGC	GACCCGCGGG	CCCCCAGTCC	CGCGCCCGGG	TCCCCAGCAG	GGCAGCGCCG	3060
	GGGAAGTCGG	AGCCTCTTTC	TGACGGGCC	CTGTCTCCA	AGTCCCAGCA	GTGCGTCTCA	3120
	GCCGAGGACG	AGGAGGAGGA	GGACGCGGGG	TTTTTTAAAG	GCGGAAAGA	AGACCTTCTG	3180
	TCCTCTCTG	TGCCAAAGTG	GCCCTCTTCC	TCCACTCCCA	GGGGCGGCAA	AGACGCCGAT	3240
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	CTGGCTCTG	TGAAGCGACC	TCTCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCCTCCAC	3360
	GTCCCTTCCC	GACGCGCGG	TCGCGAGGCT	GCCACCGTGA	GCCCCGTGCG	GGGACCCAC	3420
	CCCTGGCGCG	GGTACACCAC	GCGCGCCCV	CCTGGCCAAT	TCTCCACCAC	CCCGATGCTG	3480
	TCCTTGGGCC	AGAGGATGAT	GCATGCCAGA	TTCCGTAACC	CTCTCTCCCG	ACAGCCTGCC	3540
	AGACCTCTT	ACAGACAAGG	TTATAATGGC	AGACCAATG	TAGAAGGGAA	AGTCTCTCCT	3600
25	GGTAGTAATG	GAAACCGAAG	TGACAGAGA	ATTATCAATG	GCCCTCAAG	AACAAAGTGG	3660
	GTTGTGGACC	TTGATCGTGG	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
	CATGGAATTC	CTCTTCGATG	TAAACTAGGA	GGAGATGGTC	GAACCATTTG	AGATCTGGAA	3780
	GGGACCCGCG	TGCTGAGTCC	TCGCGGCTC	CCACTCTTG	GGCAGGGGCG	ACATGGCACA	3840
30	CCTCTGGCCA	ATGCCCAAGA	TAAGCCAATT	TTGAGTCTTG	GAGGAAAGCC	GCTGGTGGGC	3900
	TTGGAGGTCA	TCAAAAAAAC	CACCCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
	ACGACGCCCC	TGCCTACCAC	TACAACCCCG	AGGCCACCA	CTGCCACCAC	CATGCAGCCC	4020
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35	GACGATGATG	GCAACCTGAT	AATGAGTCC	AATGGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260
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	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCA	CCACCACTGA	GCCTTCGACC	4380
	ACTGCTACCA	CACCGAGGGT	GATCCCAGAG	GAAGGCGCCA	TCAGTTCTCT	TCCTGAAGAA	4440
40	GAATTTGATC	TGGCTGGAAG	GAAACGATTT	GTTGCTCCTT	ACGTGACGTA	CCTAAATAAA	4500
	GACCCATCAG	CCCCGTGCTC	TCTGACTGAT	GCACTGGATC	ACTTCCAAGT	GGACAGCCTG	4560
	GATGAAATCA	TCCCAATAGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCCGC	4620
	AACATCACCG	TGGTGGCGGT	GGAAGGTTGC	CACCTATTG	TCATTGTGGA	TTGGGACAAA	4680
	GCCACCCAG	GAGATTGGT	CACAGGTTAT	TTGGTTTACA	GTGCATCCTA	TGAAGATTTC	4740
45	ATCAGGAACA	AGTTTTCAC	TCAAGCTTCA	TCAGTAACTC	ACTTGCCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCATT	TGTCACCGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCC	4920
	CCAGGCGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAAACA	TGATCCGAGC	TACACGGACT	4980
	GCCATGGACG	GCAATATGTG	AAGCGCACGT	GGTATCGAAA	GTTCGTGGGA	GTTGTTCTTT	5040
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	TTGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAAGGC	TACTATCGCC	5220
	AGTATCGTCA	GGAGCCTGTC	AGGTTTGGGA	ACATCGGCTT	CGGAACCCCC	TACTACTATG	5280
	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAGTG	GTAATCACAG	GACCGTCATG	5340
55	CTGCAAGCTT	GCCCTGCCCA	GCCCCACCAA	CTAAGTGGCA	CTAGGGGCTG	TGAGCAAAGA	5400
	CAGCCAGCAT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCACAGAT	GGACACTGGC	5460
	CATTCTGGTC	ATCTCAGTAT	GGAACCTCAGT	CCCACCTTCT	GGCCTGGACA	ATGAACAGGA	5520
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	CCAGAGACAT	CAGAAACAG	CAACTGATTC	AGTGTGATTT	CCCAGACTTT	TTAGGCATGA	5640
60	AATTCGGACA	CTTCAGTATT	TCCAGGAATA	GCATATGCAC	GCTGTCTTGT	CTTCATGGAA	5700
	TGCTACATGC	TTTCTGTTTT	TCTCATTITG	GATTTCTCCA	AAACTAACTG	AATTTAAGCT	5760
	TCAGGTCCCT	TGTATGACAG	TAGAAAGGAA	TTATTAATAA	CACCACCAA	GAAATAAAT	5820
	ATATCTACT	TGAAATTTAC	TCTATGGACT	TACCCACTGC	TAGAATAAAT	GTATCAAATC	5880
	TTATTTGTA	ATTCTCAATT	TTGATATATA	TATGTATATA	TGCATATACA	TATCCACACT	5940
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Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

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75	TPESAPTTAP	ENLNVWPVNG	KPTVVAASWD	ALPETEGKVK	VCLLDLTGLFS	VSSFPQSAKS	180
	FQNTFFHFTFR	LSNMLEQSPS	PILETLLELPW	WMVCSLGNAI	FSKSGPQTGE	AWDLTPKPSL	240
	SLCQCECSCT	QKDFSCLAYL	IDIQTKQVKN	DPQLEGSVFG	PCFLPYFLTF	MLDIGGPFIF	300
	MCYEDPVSSL	TGNSLKSVA	SKADVQNTTE	DNGKPEKPEP	SSPSPRAPAS	SQHPSVPASP	360
	QGRNAKDLLE	DLKNKILANG	GAPRKPQLRA	KKAEEELDLS	TEITGEEELG	SREDSPPMSPS	420
80	DTQDQKRTL	PFSRHGHSV	APGRTAVRAR	MPALPRREGV	DKPGPSLATQ	PRPGAPPSAS	480
	ASPAHHASTQ	LTARAPASGH	SLNDNDLVDS	DEDERAVGSL	HPKGAFAPQR	PALSPSRQSP	540
	SSVLDRDSSV	HPGAKPASPA	RRTPHSGAAE	EDSSASAPPS	RLSPPHGGSS	RLLPQPHLS	600
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	GRQAEATAQT	LRARAPASGH	HLRHKPFPA	NGRSPSRFSI	GRGPRLQPPS	SPQSTVPSRA	720
85	HPRVPSHSDS	HPKLSSGIHG	DEDEKPLPA	TVVNDHVPSS	SRQPISRGWE	DLRRSPQRGA	780
	SLHRKEPIQE	NPKSTGADTH	PQGYSSLAS	KAQDVQQSTD	ADTEGHSPKA	QPGSTDRHAS	840
	PARPPAARSQ	QHPSPVRMT	PGRAPQPPP	PPVATSQHHP	GPQSPRDAGRS	PSQPRLSLTQ	900
	AGRPRPTSQG	RSHSSDPYPT	ASSRGMPLTA	LQNQDEDAQG	SYDDSDTEVE	AQDVRAPAHA	960

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 SLAKEEREPA IALAPRGGSL APVKRPLPPP PGSSPRASHV PSRPPPSAA TVSPVAGTHP 1140
 WPRYTTRAPP GHFSTTMLS LRQRMHARF RNPLSRQPAR PSYRQGYNGR PNVEGKVLPG 1200
 5 SNGKPNQRI INGPQGTQWV VDLDRGLVLN AEGRYLQDSH GNPLRIKLGG DGRITVDLEG 1260
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Seq ID NO: 420 DNA sequence
 Nucleic Acid Accession #: NM_022743
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Seq ID NO: 421 Protein sequence
 Protein Accession #: NP_073580

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 50 MRCSQCRVAK YCSAKQKKA WPDHKRECK LKSKPRYP PDSVRLGRV FKLMDGAPSE 60
 SEKLYSPYDL ESNINKLTED KKEGLRQLVM TFQHFMRBEE QDASQLPPAF DLFEAPAKVI 120
 CNSFTICNAE MQEVGVGLYP SISLNNHSCD PNCISIVFNGP HLLLRVRDI EVGEELTICY 180
 55 LDMLMTSEER RKQLRDCYCF ECDRCRCQTO DKDADMLTGD EQVWKEVQES LKKIEELKAH 240
 WKWEQVLAMC QALISSNSER LPDINIYQLK VLDCAMDACI NLGLLEALF YGTRTMEPYR 300
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Seq ID NO: 422 DNA sequence
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 Coding sequence: 238..648

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 5 CTAGAAGAGT AGGGAATAA ATGCTTGTTA CAATTGACC TAATATGTGC ATGTAAAT 1620
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 TATCTGTGTG TGCAATGTTA GTGATGTTTT AAAATGTGAT GAAAAATATA TGTTTTAAAG 1740
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 TTTTGTGAT GAAAGGGGAT TTTTGAAGA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860
 10 TGTGTTTTT TACCAATGAC TTCAGTTTCT GTTTTATAGCT AGAACTTAA AAACAAAAAT 1920
 AATAATAAG AAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATTC CTGTTTTTGG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACCAGAA 2040
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 ATTTTATACC CACAAGAGAG GTATGTCAT CATCTTACTT CCCAGGACAT CCACCTGAG 2160
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 15 TTAATAATTT TCTTTGCTTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
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 AGGCATTTCA TAAATGCACA ACGCCCAAG GAAATAAAT CCTATCTAAT CCTACTCTCC 2520
 20 ACTACACAGA GTCATCATC ATTAGTATT TGGCATATTA TTCTCCAGGT GTTGTCTTAT 2580
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 TGCCTCTCTT TGCTTGGCCC TTTATTGAGA TAAGTTTTC TGTCAGAAA GCAGAAACCA 2700
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 25 TATTGGATAC TTAGTGTGTT TCTTCACTGA CAATACCTC TAAACATCTC ACCGGAATTC

Seq ID NO: 423 Protein sequence
 Protein Accession #: NP_003005.1

1 11 21 31 41 51
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 YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPCKSV CQRARDDECP LMKMYNHSWP 120
 ESLACDELVP YDRGVCSIFE AIVTDLPELV KWIDITPDMM VQERPLDVDC KRLSPDRCKC 180
 35 KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVDV KEIFKSSSPI PRQVPLITN 240
 SSRQCPHILP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300
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Seq ID NO: 424 DNA sequence
 Nucleic Acid Accession #: BC010423
 Coding sequence: 248..1780

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 CRAGTGCGAG AGGCAAGAAC TCTGCAGCTT CCTGCCTTCT GGGTCAGTTC CTATTCAAG 180
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 50 GCTGTACTAG CTGGCATCAT TTACAGGCCG GTGCCCGCGG GGTGAGCTGG AGACCTCAGA 360
 CGTGGTAAC TGTGTGTGCG GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC 420
 CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGTGGGAC GCGGGCGAAG GCGCCAGGA 480
 ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC CCGGCTTACG AGGGCCCGCT 540
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 55 GCGCGCGCTG CGGCTCCGAG TGCTGGTGCC TCCCTGCCCC TCACTGAATC CTGGTCCAGC 720
 ACTAGAAGAG GGCCAGGGCT TGACCTGGC AGCCTCCTGC ACAGCTGAGG GCAGCCAGC 780
 CCCAGCGGTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCCAGCCGTT CCTTCAAGCA 840
 CTCCCGCTCT GCTGCGCTCA CCTCAGAGTT CCATTTGGTG CCTAGCCGCA GCATGAATGG 900
 60 GCAGCCACTG ACTTGTGTGG TGTCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA 960
 CATCCTCCAC GTGTCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT 1020
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 65 CAATGAGTTC TTCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA 1260
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 85 GAGGCTTGAA CTGTTACAGA AGCCCTCTGC CCTCTGGTGG CCTCTGGGCC TGCTGCATGT 2460
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Seq ID NO: 425 Protein sequence

Protein Accession #: AAH10423

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DEGEYECRV	TFPAGSPQAR	LRLRVLPPL	PSLNPFGPALE	EGQGLTLAAS	CTAEGSPAPS	180
VTWDTVEKGT	TSSRSFKHSR	SAAVTSEPHL	VPSRSMNGQP	LTCVVSHPL	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGRGGAMLKC	LSEGGPPPSY	NWTRLGDLPL	SGVRVDGDTL	300
GFPPPLTEHS	GIYVCHVSNE	FSSRDSQVTV	DVLDPQEDSG	KQVDLVASV	VVVGVIALL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDSLKN	SSCSVMSSEF	BGRSYSTLTT	VREIETQTEL	LSPGSGRAEE	EEDQDEGIQ	480
AMNHPVQENG	TLRAKPTGNG	IYINGRGHLV				

Seq ID NO: 426 DNA sequence

Nucleic Acid Accession #: NM_003474.2

Coding sequence: 37..3036

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CTTTTAAATA	AATGAAAGGC	TAGAAGAGCT	CAGCGGCGGC	GCGGGCCGTG	CGCGAGGCT	180
CCGGAGCTGA	CTGCGCAGG	CAGGAAATCC	CTCCGGTGGC	GACGCCCGGC	CCCGCTCGGC	240
GCCCCGCTGG	GATGGTGCAG	CGCTCGCCGC	CGGGCCCGAG	AGCTGCTGCA	CTGAAGGCCG	300
GCGACGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
GCCGGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
GCTGATGAAG	TTGTCACTGC	CTCTGTTGCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
TTGCACTCCA	AGAACTCATC	AGAAGTGCTG	AATATTCGAC	TACAACGGGA	AAGCAAAGAA	540
CTGATCATAA	ATCTGGAAG	AAATGAAGGT	CTCATTGCCA	GCACTTTCAC	GGAAACCCAC	600
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TGTGGATCAC	ATCAACAACAC	ACCAAACCTC	GCTGCAAGAA	ATGTGTTTCC	ACCAACCTCT	900
CAGACATGGG	CAAGAAGGCA	TAAAAGAGAG	ACCTCAAGG	CAACTAAGTA	TGTGAGCTG	960
GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
CAGCGATTAA	TAGACATTCG	TAATCAAGTT	GACAAGTTTT	ACAGACCACT	GAACATTTCG	1080
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CCATTACCA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAA	1200
TCCCATGACA	ATGGCGACAG	TGTCACTGGG	GTTTATTTC	AAGGGACCA	CATCGGCATG	1260
GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCATTC	1320
GACAAATCCC	TTGGTGCAGC	CGTGACCTTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
AATCATGACA	CAGTCGACAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTCG	1440
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AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
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AGCCCTCACT	GCCAGCCCAA	CGTGTACCTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
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CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980
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GTTTCCATAG	AAACAAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
CACGTGTACT	TGGGCGATGA	CATGCCGGAC	CCAGGGCTTG	TGCTTGCAGG	CACAAAGTGT	2220
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GGCCCATCC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATTCGTGT	GACCATCTCT	2460
TGTCTTCTTG	CTGCCGGATT	TGTGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGTGT	2520
TTTACAAATA	AGAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
CGTGGCTTCC	AACCTGTCCA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCT	GATGAGGAAG	2640
CCGCCAGATT	CCTACCCACT	GAAGGACAAT	CCAGGAGAT	TGCTGCAGTG	TCAGAATGTT	2700
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CTTCTCCCC	TCCACCGGGC	CCCACGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
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CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
GTGCCAGAT	CCAGCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTCAACAG	3060
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GCTGTGCTGT	GCTATGGTGC	TCTGTCTACT	TGCACAGGTA	CTTGTAATTT	ATTAATTTAT	3240
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CCATGGCAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACTTGAAAT	ATCCTGCTTG	3360
ATGGGATTCT	GGACAGGATG	TGTTTGCTTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
CCAATACACC	CCAGCTGTGC	TTATGCTACC	AGATGCAGCT	CAAGAGATCC	CAAGTAGAAT	3480
CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
TGTGTTTGGC	TTTCAAGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCAGGG	3600
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AGGAATCTTA	AGGTGTAGCC	ACACCAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAAGT	3720
TGACCTGAG	CTGACAGGCC	GTGAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
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	CTGCAACCG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
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5	TGAACCATTA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGGG	4140
	TATAGTTCAT	GTCTGCTATC	ATTATTGCTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCTTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTTCT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAAATGTG	ATAAGGAAAT	4320
10	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTGAA	4380
	CTCTTCACTC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGAAT	4440
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	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCTTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	FYRPLNIRIV	GCCITCCAGA	AAACAAACT	GCATTTCACT	TTCCCGGTGT	4680
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20	AGATGCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCTC	CCAATTATAA	GAGGATATGA	5040
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Seq ID NO: 427 Protein sequence
Protein Accession #: NP_003465

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30	YHGHVRGYS	SAVSLSTCSG	LRGLIVFENE	SYVLEPMKSA	TNRYKLFPK	KLKSVRGSCG	180
	SHINTPNLAA	KNVFPSPST	WARRHKRETL	KATKYVELVI	VADNREFQRQ	GKDLKVKQR	240
	LIBIANHVDK	FYRPLNIRIV	LVGVEVWDM	DKCSVSQDPF	TSLEHEFLWR	KMKLLPRKSH	300
	DNAQLVSGVY	FQGTITGMAP	IMSMCTADQS	GGIVMDHSDN	PLGAAVTLAH	ELGHNFGMNH	360
	DTLDRGCSQ	MAVEGGGCM	NASTGYPPFM	VFSSCSRKDL	ETSLEKMGV	CLFNLPEVRE	420
35	SFGGQKQGNR	FVEEGECCD	GEPEECMNR	CNATTCTLKP	DAVCAHGLCC	EDCQLKPAGT	480
	ACRDSNSNCD	LPEFCTGASP	HCPANVYLHD	GHSCQDVG	CYNGICQTHE	QQCVTLWPG	540
	AKPAPGICFE	RVNSAGDPYG	NCGVKSSSF	AKCEMRDAK	GKIQCGGAS	RPVIGTNAV	600
	IETNIPLQQG	GRILCRGTHV	YLGDDMPDPG	LVLAGTKCAD	GKICLNRCQ	NISVFGVHEC	660
40	AMQCHGRGVC	NNRKNCHCEA	HWAPPFCDF	GFGGSTDGSP	IROADNQLT	IGILVTILCL	720
	LAAGFVVYLK	RKTLIRLLFT	NKKTITIEKL	CVRPSRPPRG	FQPCQAHLG	LGKGLMRKPP	780
	DSYFPKDNPR	RLLCQCNVDI	SRPLNGLNVP	QPQSTQRVLP	PLHRAPRAPS	VPARPLPAKP	840
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	RSHTAYIK						

Seq ID NO: 428 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 135..1043

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	TAATACCAAG	AACCATGTGT	GCCGAGCGGC	TGGGCCAGTT	CATGACCCGT	GCTTTGGTGT	180
55	TGGCCACCTT	TGACCCGCGC	CGGGGACCGC	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240
	ACAGGAGCTC	CCAGCAGAAA	GGCCGCCTGT	CCCTGCAGAA	TACAGCGGAG	ATCCAGCACT	300
	GTTTGGTCAA	CGCTGCGCAT	GTGGGGTGTG	GCGTGTTTGA	ATGTTTCGAG	AACTACTCTT	360
	GTGAGATTGG	GGGCTTACAT	GGGATTGCA	TGACTTTTCT	GCACAACGCT	GGAAAAATTG	420
	ATGCCCAAGG	CAAGTCATTC	ATCAAAGACG	CCTTGAAATG	TAAGGCCAC	GCTCTGCGGC	480
60	ACAGGTTCCG	CTGCATAAGC	CGGAAGTGCC	CGGCCATCAG	GGAAATGGTG	TCCAGTTG	540
	AGCGGGAATG	CTACCTCAAG	CACGACCTGT	GCGCGGTG	CCAGGAGAAC	ACCCGGGTGA	600
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70	GTCCATTTCT	TTATCTATGG	ACATTCCAAA	ACATTACCA	TTAGAGAGGG	GGGATGTAC	1140
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75	GCAGGGCCCC	CAGAGCTGGG	CACACAGTGC	GGTGCTGGGC	CTCGCCCGCA	AGCTTCTGGT	1440
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	CTCTTGGCGA	GGGTGGAGGG	AGGAGTGTCA	TTTCTATGTG	TAATTTCTGA	GCCATTGTAC	1680
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80	ACTGCTTCAA	ATCTCGATT	CACCTTTTTT	ATTTATCCAG	TTATATCTAC	ATATCTGTCA	1800
	TCTAAATAAA	TGGCTTTCAA	ACAAAGCAAC	TGGGTCAATTA	AAACCAGCTC	AAAGGGGGTT	1860
	TAAAAAATAA	AAACACAGCC	CATCCTTTGA	GGCTGATTTT	TCTTTTTTTT	AAGTTCTATT	1920
	TAAAAAGCTA	TCAAACAGCG	ACATAGCCAT	ACATCTGACT	GCCTGACATG	GACTCCTGCC	1980
	CACCTGGGGG	AAACCTTATA	CCCAGAGGAA	AATACACACC	TGGGGAGTAC	ATTTGACAAA	2040
85	TTTCCCTTAG	GATTTCGTTA	TCTCACCTTG	ACCCTCAGCC	AAGATTGGTA	AAGCTGCGTC	2100
	CTGGCGATTG	CAGGAGACCC	AGCTGGAAC	CTGGCTTCTC	CATGTGAGGG	GATGGGAAAG	2160
	GAAAGAAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	AAATGCTGAC	CTTTTACATA	2220

AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAG 2280
 TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340
 GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC

5 Seq ID NO: 429 Protein sequence
 Protein Accession #: NP_003705

10 1 11 21 31 41 51
 MCAERLQQFM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRLSLQNT AEIQHCLVNA 60
 GDVGGCVFEC FENNSCIEIRG LHGICMTFLH NAGKFDAQGK SFIKDALCKK AHALRHRFGC 120
 ISRKCPAIRE MVSQIQRECY LKHDLCAAQ ENTRVIVEMI HFQDLLLHEP YVDLVNLLLT 180
 CGEEVKRAIT HSVQVQCQN WSLCSILSF CTSAIQKPPPT APPERQPOVD RTKLSRAHHG 240
 EAGHHLPEPS SRETGRGAKG ERGSKSHPNH HARGRVGGLG AQQPSGSSEW EDEQSEYSDI 300
 RR

Seq ID NO: 430 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

20 1 11 21 31 41 51
 AAGCCCAGCA GCCCCGGGGC GGATGGCTCC GGCCGCTCGG CTCGCGAGCG CGGCCGCGCG 60
 CGCCCTCCTG CCCCAGATGC TGCTGCTGCT GCTCCAGCCG CCGCGCTGCG TGGCCCGGGC 120
 25 TCTGCCGCGG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
 AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCC GGCCCTGCCAG 240
 CAGCCTCAGG CCTCCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300
 CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
 GATCCTTCGG TCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
 30 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCCGTGC 480
 TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC 540
 TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC 660
 35 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
 GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT 780
 TCACACCTTA TATGGCCAGC CCTGGCCAC TGTCACTTCC AGGACCCAG CCCTGGGCCC 840
 CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC 900
 CTGTAGAGGC CTCTTTGAGC CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960
 40 GGGCTTTGTG TGGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTTGGCCTC 1020
 TCGCCACTGG CAGGGACTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080
 CATTTGGTTC TTCCAAGATG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTCTGG 1140
 CCCCACACCC CTCACCGAGC TGGGCTGGT GAGGTTCCTG GTCCATGCTG CCTTGGTCTG 1200
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACCC 1260
 45 CAGCACCCGG CGTGTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320
 CTCTGAGATC GACGTGCTCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGGCGGCGCG 1380
 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGTCTCTGT 1440
 GGGTCTGTAC TTCTTTGAGC GTGCCGAGCC TGCCCAACTT TTCTCTGAGC CATGGCTTGG 1500
 ATGCCCTCAG GGGTGTGAC CCCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560
 50 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGTCTCTGTC AGGGGGATGG 1620
 GGTGGGGTAC AACCAAGATG ACAACTGCCG GGAGGGCCAC GCGAGTCTGT GTACCTCTGC 1680
 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740
 GGGACCCGCT ATGCAAGTCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800
 GTAGACCAT GGCAGGACTG GGGGAACCTG AGTGTCTTGG CTGTATCCCT GTTGTGAGGT 1860
 55 TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920
 TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980
 ATCTGTCTGC CTCTGGCTG ACAATCTGTC AAATCTGTTC TCCAGAATCC AGGCCAAAAA 2040
 GTTCACAGTC AAATGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
 CAACATACCT CAATCTGTGC CCAGGCCGGA TCCTCTGTAA GCCCTTTTCG CAGCACTGCT 2160
 60 ATCTTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
 TTTTAAACT GAGGATTGTC ATTAACACA GTTGTTTTCT

Seq ID NO: 431 Protein sequence
 Protein Accession #: NP_005931

65 1 11 21 31 41 51
 MAPAAWLRS AARALLPPLM LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA 60
 PAPATQEAPR PASSLRPPRC GVPDPDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ 120
 70 LVQEQVQRTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DPGGILAHA 180
 FFPKTHREGD VHFYDETWT IGDDQGTDL QVAAHEFGHV LGLQHTTAAL ALMSAFYTFR 240
 YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA 360
 QYVWYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFPRGRDYWR FHPSTRRVDS 420
 75 PVPRATDWR GVPSEIDAP QDADGYAYFL RGRLYWKFDL VKVKALEGF PRLVGPDPFGC 480
 AEPANTFL

Seq ID NO: 432 DNA sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

80 1 11 21 31 41 51
 ACCGGGCACC GGACGGCTCG GGTACTTTTC TTCTTAATTA GGTATGCCC GTGTGAGCCA 60
 GGAAGGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGTGC CTACTATCTC TTCCGTGGTG 120
 85 CATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGC 180
 AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCGC CTGTGTGTA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTGTC ACCAGATGCA 300

	GATGCTGTTG	CTGCACAGAT	CCTGTCACCTG	CTGCCATTGA	AGTTTTTTTC	AATCATCGTC	360
	ATTGGGATCA	TTGCATTGAT	ATTAGCACTG	GCCATTGGTC	TGGGCATCCA	CTTCGACTGC	420
	TCAGGGAAGT	ACAGATGTGC	CTCATCTTTT	AAGTGTATCG	AGCTGATAGC	TCGATGTGAC	480
5	GGAGTCTCGG	ATTGCAAAAG	CGGGGAGGAC	GAGTACCGCT	GTGTCCGGGT	GGGTGGTCAG	540
	AATGCCGTGC	TCCAGGTGTT	CACAGCTGCT	TCGTGGAAGA	CCATGTGCTC	CGATGACTGG	600
	AAGGGTCACT	AGCAAAATGT	TGCCTGTGCC	CAACTGGGTT	TCCCAAGCTA	TGTGAGTTCA	660
	GATAACCTCA	GAGTGAGCTC	GCTGGAGGGG	CAGTTCCGGG	AGGAGTTTGT	GTCCATCGAT	720
	CACCTCTTGC	CAGATGACAA	GGTGACTGCA	TTACACCACT	CAGTATATGT	GAGGGAGGGA	780
10	TGTGCCTCTG	GCCACGTGGT	TACCTTGCA	TGCACAGCCT	GTGGTCATAG	AAGGGGCTAC	840
	AGCTCACGCA	TGCTGGGTGG	AAACATGTCC	TTGCTCTGCG	AGTGGCCCTG	GCAGGCCAGC	900
	CTTCAGTTCC	AGGGGTACCA	CCTGTGCGGG	GGCTCTGTCA	TCACGCCCTT	GTGGATCATC	960
	ACTGCTGCAC	ACTGTGTTTA	TGACTTGTAC	CTCCCCAAGT	CATGGACCAT	CCAGGTGGGT	1020
	CTAGTTTCCC	TGTTGGACAA	TCCAGCCCCA	TCCCACTTGG	TGGAGAAGAT	TGTTCTACCA	1080
15	AGCAAGTACA	AGCCAAAGAG	GCTGGGCAAT	GACATCGCCC	TTATGAAGCT	GGCCGGGCCA	1140
	CTCACGTTCA	ATGAAATGAT	CCAGCCTGTG	TGCCTGCCCA	ACTCTGAAGA	GAACCTCCCC	1200
	GATGGAAAAG	TGTGCTGGAC	GTGAGGATGG	GGGGCCACAG	AGGATGGAGG	TGACGCCTCC	1260
	CCTGTCTTGA	ACCAGCGGCG	CGTCCCTTTG	ATTTCCAACA	AGATCTGCAA	CCACAGGGAC	1320
	GTGTACGGTG	GCATCATCTC	CCCCCTCCATG	CTCTGCGCGG	GCTACCTGAC	GGGTGGCGTG	1380
20	GACAGCTGCC	AGGGGGACAG	CGGGGGGCC	CTGGTGTGTC	AAGAGAGGAG	GCTGTGGAAG	1440
	TTAGTGGGAG	CGACCACTTT	TGGCATCGGC	TGCGCAGAGG	TGAACAAGCC	TGGGGTGTAC	1500
	ACCCGTGTCA	CCTCCTTCTC	GGACTGGATC	CACGAGCAGA	TGGAGAGAGA	CCTAAAAACC	1560
	TGAAGAGGAA	DGWKGHYANV	AGCCACCTGA	GTTCTTGAGG	TGATGAAGAC	AGCCCCGATC	1620
	TCCCCCTGGAC	TCCCGTGTAG	GAACCTGCAC	ACGAGCAGAC	ACCCTTGGAG	CTCTGAGTTC	1680
25	CGGCACCACT	AGCAGGCCCG	AAAGAGGCAC	CCTTCCATCT	GATTCCAGCA	CAACCTTCAA	1740
	GCTGCTTTTT	TGTTTGTGTT	TTTTTGAGGT	GGAGTCTGCG	TCTGTTGCC	AGGCTGGAGT	1800
	GCAGTGGCGA	AATCCCTGCT	CACTGCAGCC	TCCGCTTCCC	TGGTTCAGC	GATTCTCTTG	1860
	CCTCAGCTTC	CCAGTAGCTC	GGGACCAAG	GTGCCGCCCA	CCACACCCAA	CTAATTTTTG	1920
30	TATTTTATGT	AGAGACAGGG	TTTACCATG	TTGCCAGGC	TGCTCTCAA	CCCTGACCT	1980
	CAAATGATGT	GCCTGCTTCA	GCCTCCACA	GTGCTGGGAT	TACAGGCATG	GGCCACCACG	2040
	CCTAGCCTCA	CGCTCCTTTC	TGATCTTCA	TAAGAACAAA	AGAAGCAGCA	ACTTGCAAGG	2100
	GGGGCCTTTC	GCAGTGTGCC	ATCTGGTTT	CTCTCCAGGG	GTCTTGCAA	ATTCTTGAGC	2160
	AGATAAGCAG	TTATGTGACC	TCACGTGCAA	AGCCACCAAC	AGCCACTCAG	AAAAGACGCA	2220
	CCAGCCCAAG	AGTGACAGAA	TGCAGTCACT	GCACGTTTTC	ATCTCTAGGG	ACCAGAACCA	2280
35	AAACCCACCT	TGTACTTCCC	AAGACTTATT	TTACATGTG	GGGAGGTTAA	TCTAGGAATG	2340
	ACTCGTTTAA	GGCCTATTTT	CATGATTCT	TTGTAGCATT	TGGTGCTTGA	CGTATTATTG	2400
	TCCTTTGATT	CCAAATAATA	TGTTTCCTTC	CCTCAAAAAA	AAAAAATAAA	AAAAAATAAA	2460
	AAAAA						

Seq ID NO: 433 Protein sequence
Protein Accession #: NP_076927

	1	11	21	31	41	51	
45	MGENDPPAVE	APFSFRSLFG	LDDLKISPVA	PDADAVAAQI	LSLLPLKFFP	IIVIGIIALI	60
	LALAILGLIH	FDCSKYKRCR	SSFKICIELIA	RCDGVSDCKD	GEDEYRCVRV	GGQNAVILQVF	120
	TAASWKMTCS	DWKGHYANV	ACAQLGFPSY	VSSDNLRVSS	LEGQFREEFV	SIDHLLPDDK	180
	VTALHHSVYV	REGCAGSHVV	TLQCTACGHR	RGYSSRIVGG	NMSLLSQWPW	QASLQFGQYH	240
	LCGGSVITPL	WIITAAHCYV	DLYLPSKWTI	QVGLVSLLDN	PAPSHLVEKI	VYHSKYKPKR	300
50	LGNIDIALMKL	AGPLTFNEMI	QPVCLPNSSE	NFPDGKVCWT	SGWGATEDGG	DASPLVNHAA	360
	VPLISNKICN	HRDVYGGIIS	PSMLCAGYLT	GGVSDSCQDS	GGPLVCQERR	LWLVLGATSF	420
	GIGCAEVNKP	GVYTRVTSFL	DWIHEQMERD	LKT			

Seq ID NO: 434 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

	1	11	21	31	41	51	
60	CACCTTCTGC	ACTGCTCATC	TGGGCAGAGG	AAGCTTCAGA	AAGCTGCCAA	GGCACCATCT	60
	CCAGGAACCT	CCAGCAGCGA	GAATCCATCT	GAGAATATGC	TGCCACAAAT	ACCCTTTTTC	120
	CTGCTAGTAT	CCTTGAACCT	GGTTCATGGA	GTGTTTACG	CTGAACGATA	CCAAATGCC	180
	ACAGGCATAA	AAGGCCCACT	ACCCAACACC	AAGACACAGT	TCTTCATTCC	CTACACCATA	240
	AAGAGTAAAG	GTATAGCAGT	AAGAGGAGAG	CAAGGTACTC	CTGGTCCACC	AGGCCCTGCT	300
65	GGACCTCGAG	GGCACCCAGG	TCCTTCTGGA	CCACCAGGAA	AACCAGGCTA	CGGAAGTCTC	360
	GGACTCCAAG	GAGAGCCAGG	GTTGCCAGGA	CCACCGGGAC	CATCAGCTGT	AGGGAAACCA	420
	GGTGTGCCAG	GACTCCCAGG	AAAACCAGGA	GAGAGAGGAC	CATATGGACC	AAAAGGAGAT	480
	GTTGGACCA	GTGGCTTACC	AGGACCCCGG	GGCCACCCAG	GACCACTGG	AATCCCTGGA	540
	CCGGCTGGAA	TTTCTGTGCC	AGGAAAACCT	GGACAACAGG	GACCCACAGG	AGCCCCAGGA	600
70	CCCAGGGGCT	TTCTGGGAGA	AAAGGGTGCA	CCAGGAGTCC	CTGGTATGAA	TGGACAGAAA	660
	GGGGAATAG	GATATGGTGC	TCCTGGTCTG	CCAGGTGAGA	GGGTCTTCC	AGGCCCTCAG	720
	GGTCCACAG	GACCATCTGG	CCCTCCTGGA	GTGGGAAAAA	GAGGTGAAAA	TGGGGTTCCA	780
	GGACAGCCAG	GCATCAAAGT	TGATAGAGGT	TTTCCGGGAG	AAATGGGACC	AATTGGCCCA	840
75	CCAGGTCCCC	AAGGCCCTCC	TGGGGAACGA	GGGCCAGAA	GCATTGGAAA	GCCAGGAGCT	900
	GCTGGAGCCC	CAGGCCAGCC	AGGGATTCCA	GGAACAAAAG	GTCTCCCTGG	GGCTCCAGGA	960
	ATAGCTGGGC	CCCCAGGGCC	TCCTGGCTTT	GGGAAACCAG	GCTTGCCAGG	CCTGAAGGGA	1020
	GAAAGAGGAC	CTGCTGGCCT	TCTGGGGGT	CCAGGTGCCA	AAGGGGAACA	AGGGCCAGCA	1080
	GGTCTTCTGT	GGAAGCCAGG	TCTGACTGGA	CCCCCTGGGA	ATATGGGACC	CCAAGGACCA	1140
	AAAGGCATCC	CGGGTAGCCA	TGGTCTCCCA	GGCCCTAAAG	GTGAGACAGG	GCCAGCTGGG	1200
80	CCTGCAGGAT	ACCCTGGGCC	TAAGGGTGAA	AGGGGTTCCC	CTGGGTGAGA	TGGAAAAACA	1260
	GGGTACCCAG	GAAAACCAGG	TCTCGATGGT	CCTAAGGGTA	ACCCAGGGTT	ACCAGGTCCA	1320
	AAAGGTGATC	CTGGAGTTGG	AGGACCTCCT	GGTCTCCAG	GGCCTGTGGG	CCCAGCAGGA	1380
	GCAAGGGGAA	TCGCCCGGCA	CAATGGAGAG	GCTGGCCCAA	GAGGTGCCCC	TGGAAATACA	1440
	GGTACTAGAG	GCCCTATTGG	GCCACCAGGC	ATTCCAGGAT	TCCTGGGTC	TAAAGGGGAT	1500
85	CCAGGAAGTC	CGGTCTCTCC	TGGCCAGGCT	GGCATAGCAA	CTAAGGGCCT	CAATGGACCC	1560
	ACCCGGCCAC	CAGGGCCCTC	AGTCCCAAGA	GGCCACTCTG	GAGAGCCTGG	TCTTCCAGGG	1620
	CCCCCTGGGC	CTCCAGGCCC	ACCAGGTCAA	GCAGTCAATG	CTGAGGGTTT	TATAAAGGCA	1680
	GGCCAAAGGC	CCAGTCTTTC	TGGGACCCCT	CTTGTAGTGT	CCAACAGGGG	GGTAACAGGA	1740

5 ATGCCCTGTT CTGCTTTTAC TGTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAACTCCC 1800
 ATACCATTG ATAAAATTTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC 1860
 TTTACTTGT AGATACCAAG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
 CATGTTTGGG TAGGCTGTGA TAAGAATGGC ACCCCTGTAA TGTACACCTA TGATGAATAC 1980
 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAAATGAC 2040
 CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAATATGGC TATACTCTCT TGAGTATGTC 2100
 CACTCTCTTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCAC AGAGCTAATC 2160
 TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220
 AGGTAGGCTG AAAAGAAATG AATTTTATT TTCTGAAATA CAGATTGTAG CTATCAGACC 2280
 10 AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
 AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTTCT CCAATATTAA AAAATATCAC 2400
 CAAAGAAATC CTGCTATGTT AAAAAACAAC AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460
 TAAAAAATA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTTGATTGA GAAACTCGGC 2520
 ATTTCTTTTT TAAAAAGCC TGTCTCTAAC TATGAATATG AGAACTCTA GGAACATACC 2580
 15 AGGAGGTATC ATATACTTT GTAGAACTTA AATACTTGAA TATTCAAATT TAAAGACAC 2640
 TGTATCCCTT AAAATATTTC TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTCAT 2700
 CAATATCTAT TCAATATATC AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAGC 2760
 CCCAAATAT TGAAGTTCAT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTCAAAA 2820
 CTTTTCTATG ATTGCAGAGA AGCTTTTTAT ATACCCAGCA TAACTTGGAA ACAGGTATCT 2880
 20 GACCTATTCT TATTAGTTA ACACAAGTGT GATTAAATTG ATTTCTTAA TTCCTTATTG 2940
 AATCTTATGT GATATGATT TCTGGATTGA CAGAACATTA GCACATGTAC CTTGTGCCCTC 3000
 CCATTCAAGT GAAGTTATAA TTACACTGA GGGTTTCAA ATTGACTAG AAGTGGAGAT 3060
 ATATTATTTA TTTATGCAC TACTGTATT TTTATATTGC TGTTTAAAC TTTTAAGCTG 3120
 25 TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTACGAC ACAATAAAAT 3180
 AACATCAATA GATTTTATG CTGAATTAAT TTGAAAGCAG CAATTGTCTG TTCTCAACCA 3240
 TTCTTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG

Seq ID NO: 435 Protein sequence
Protein Accession #: NP_000484.2

30 1 11 21 31 41 51
 | | | | |
 MLPQIPFLLL VSLNLVHGVF YAERYQMPGT IKGPLPNTKT QFFIPYTIKS KGIIVRGEQG 60
 TPGPFGPAGP RHHPGSPGPP GKPGYSPGL QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120
 35 GPYGPKGDVG PAGLPGRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GFPGEKGAPG 180
 VPGMNGQKGE MGVGAPGRGP ERGLPGPQGP TGPSGPPGVG XRGENGVPQG PGIKGDRGFP 240
 GEMGPPIPPG PQGPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPFGK 300
 PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMGPQGPKG IPGSHGLPGP 360
 40 KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLGDGPK GNPGLPGPKG DPGVGGPPGL 420
 PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RGPFGPPGIP GFPGSKGDPG SPFGPPGAGI 480
 ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
 SANQGVGTMP VSAFTVILSK AYPAGTPIP FDKILYNRQO HYDPRTGIFT CQIPGIYFYS 600
 YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQAGSSA IIDLTENDQV WLQLPNAESN 660
 GLYSSEYVHS SFGGFLVAPM

Seq ID NO: 436 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

50 1 11 21 31 41 51
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 ATGTGGGGCG CTCGCCGCTC GTCCGTCTCC TCATCCTGGA ACGCCGCTTC GCTCCTGCAG 60
 CTGCTGCTGG CTGCGCTGCT GCGCGCGGG GCGAGGGCCA GCGGCGAGTA CTGCCACGGC 120
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 180
 55 GGGCAGCGCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 240
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 300
 CGGGCGGACA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTACGTGCC GTTCCTCATT 360
 GTTGGCTCCG TGTTTGTGCG CTTTATCATC TTGGGGTCCC TGGTGGCAGC CTGTTGCTGC 420
 AGATGTCTCC GGCCTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
 60 ATGGAGACCA TCCCATGAT CCCCAGTGCC AGCACCTCCC GGGGGTCTC CTCACGCCAG 540
 TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAACTCAG GGGCCCGGGC GCCCCCAACA 600
 AGGTACAGCA CCAACTGTTG CTTGCCGGA GGGACCATGA ACAACGTGTA TGTCAACATG 660
 CCCACGAATT TCTCTGTGCT GAACTGTGAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
 65 CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
 GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CTTGGCTACA GGCAGATTCA GTCCCCCTTC 840
 CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 437 Protein sequence
Protein Accession #: XP_062811

70 1 11 21 31 41 51
 | | | | |
 MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
 GDATICGSGC ALRYCCSSAE ARLDQGGCDN DRQQAGGEPG RADKDGPDGS AVPIYVPLFI 120
 75 VGSVFAPII LGSIVAACCC RCLRPKQDPQ QSRAPGNGRL METIPMIPSA STSRGSSSRQ 180
 SSTAASSSSS ANSGARAPPT RSQTNCLLPE GTMNVVYVM PTNFSVLNCO QATQIVPHQG 240
 QYLHPYVGY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 438 DNA sequence
Nucleic Acid Accession #: NM_004004.1
Coding sequence: 1..681

80 1 11 21 31 41 51
 | | | | |
 85 ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACTC CACCAGCATT 60
 GGAAAGATCT GGCTCACCGT CCTCTTATT TTTGCGATTA TGATCCTCGT TGTGGCTGCA 120
 AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180

AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCCA TCCGGCTATG GGCCCTGCAG 240
 CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACCTGGCCTA CCGGAGACAT 300
 GAGAAGAAGA GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTAAAGGA CATCGAGGAG 360
 ATCAAAACCC AGAAGGTCCG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
 TTCTTCCGGG TCATCTTCGA AGCCGCTTTC ATGTACGTCT TCTATGTCAT GTACGACGGC 480
 TTCTCCATGC AGCGGCTGTG GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
 TTTGTGTCCC GGCCACGGGA GAAGACTGTC TTCACAGTGT TCATGATGTC AGTGTCTGGA 600
 ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTTCG TAATTAGATA TTGTTCTGGG 660
 AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 439 Protein sequence
 Protein Accession #: NP_003995.1

1 11 21 31 41 51
 | | | | |
 MDWGTLTQTL GGVNKHSTSI GKIWLTVLFI PRIMILVVAA KEVWGDEQAD FVCNTLQPGC 60
 KNVCYDHYFP ISHRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEPKDIEE 120
 IKTKQVRIEG SLWWTYTSSI PFRVIFEAAF MYVFVVMYDG FSMQRLVKCN AWPCTNTVDC 180
 FVSRPTEKTV FTFVMIASVG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 440 DNA sequence
 Nucleic Acid Accession #: XM_061091.1
 Coding sequence: 1..2481

1 11 21 31 41 51
 | | | | |
 ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTGGGC TTCTCCAAGA GCCGCCCGGG 60
 CACCGAGCGC TGGTCGCGCG TCTCTTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG 120
 CCGGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
 CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTTA 240
 GTTGGGAAGC CTCCTTTTGA GGCACACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
 ATTTTCAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTCTGTTA 360
 GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
 GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
 TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
 AGAATCAAGA GGATGTTTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
 CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
 GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
 GGTGTCACTG TGTGTGCTGT GGGGGTCAGG TTTCACAGGT GGGAGGAGCT GCATGCACTG 780
 GCCAGCGAGC CTAGAGGCCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
 GGCTCTTTCA GCACCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
 CCGGAGCTTG TCTTCATGGA CGCGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
 CAGCCCTGCG AGAATGGAGG CAGATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCTCT 1020
 TGCCCGCTGG CTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
 GTCCAGCTCC TCTTCTGCT GGCAGCTCTT GCGGGCACCA CTCTGGACGG CTCTCTGCGG 1140
 GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
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 GATGTGCTCG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCTG 1320
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 CAGGACCGGC CACGTAGAGT GGTGGTTTTG CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
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 GCGGTGCGGC CAGAGCTGCA GAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
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 GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
 GAGGTGAACC CTGACGTGAC ACAGGTGCGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
 GCCTTCGGGC TGGACACCAA ACCCAACCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
 CCCTACCTAG TTGGGGTGGG TCCAGCGGC ACCGCCCTGC TGACATCTA TGACAAAGTG 1920
 ATGACCGTCC AGAGGGGTGC CCGGCCTGGT GTCCCAAAAG CTGTGGTGGT GCTCACAGGC 1980
 GGGAGAGGCG CAGAGGATGC AGCCGTTCCT GCCCAGAAAG TGAGGAACAA TGGCATCTCT 2040
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 GTCTGTGCCC CAGGTCTCTTA G

Seq ID NO: 441 Protein sequence
 Protein Accession #: XP_061091.1

1 11 21 31 41 51
 | | | | |
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 QMHGKVDLW SLGLVCEYFL VGKPPFEANE VHVSKETIGK ISAASKMMWC SAAVDIMFL 120
 DGSNSVKGKS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQOEKVA 180
 RIKRMVFKGK RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTTFVAVGVR FPRWEELHAL ASEPRGQHLV LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 VDPLFLDSS AGTFLDGLFL AKVFKRFVR AVLSSEDSRAR VGVATYSREL LVAVPVGEYQ 420
 DVPDLVWGLD GIPFRGGPTL TGSALRQAAE RFGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEBIT GSPKHMVYVS DPQDLFNQIP ELQGLKCSRQ 540
 RFGCRTQALD LVFMLDTSAS VGPFNAQMQ SFVRSALQF EVNPDVTQVG LVVYGSQVQT 600
 AFGLDTKPRF AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAVP AQKLRRNGIS VLVVGVGPVL SEGLRLRAGP RDSLHVAAY ADLRVHQDVL 720

IEWLCCGEARQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSSCVVCVSQ 780
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Seq ID NO: 442 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

10 1 11 21 31 41 51
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AGCGTCGGGA AAGGGAGCTT TGAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
CTGGACATCA GCCCGAGAGG GGTGAGAGTG GGAGCATTCC AGTTCACTTC CACTCCTCAT 300
15 CTGGAATTCC CTTGGATTTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
ATGCTTTTCA AAGGAGGGCG CACGGAGACG GAACCTGTCT TGAATACCT TCTGCACAGA 420
GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCAGATGCC TCATCATCGT CACTGATGGG 480
AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACGTGT 540
TTTGTCTGTG GGGTCAGGTT TCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
20 AGAGGGCAGC ACGTCTCTGT GGTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTGG CTGGCAATGC CCCATGCTGG 780
AGAGGATCCG GCGGACGCTT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCTGTGAC 900
25 TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAAGTGC 960
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CGGGCCAAAG TCTTCTGTAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
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30 CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCGTGG TGCCCCACC 1260
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35 TCGGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
TCAGTAGGGC CCGAGAAATT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
ACTGCCCTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
40 GCCCCTTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
GTGATGACCG TCCAGAGGGT TGCCCGGCTT GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920
GGCGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC 1980
TCTGTCTTGG TCGTGGGCGT GGGGCTGTCT CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
45 CCCCGGATT CCTGTATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100
CTCATTTAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
TGCATGAATG AGGGCAGCTG CGTCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT 2220
GGCTGGGAGG GCCCCACTG CGAGAACCGT GAGTGGAGCT CTGTCTCTGT ATGTGTGAGC 2280
CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGCAGCAGC 2340
50 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCATG AAATGGTGCC TACCTTCTGG 2400
AATGTCTGTG CCCCAGGTCC TTAG

Seq ID NO: 443 Protein sequence

Protein Accession #: Eos sequence

55 1 11 21 31 41 51
MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVKGGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
60 MVFKGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSGGDVALPS KQLKERVTV 180
FAVGVRPPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVFKRFP RAVLSDSRA RVGVATYSRE LLVAVPVGEY QDVDPVLVSL DGIPFRGGPT 420
65 LTGSALRQAA ERFGSATRT QDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVGS 480
EAVRAELEBI TGSPKHMVY SDPQDLFNQI PELQKLCRS QRPGRCTQAL DLVFMLD TSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDVTVQ GLVVYGSQVQ TAFGLDKPT RAAMLRAISQ 600
APYLGVGSGA GTALLHIYDK VMTVQRGARF GVPKAVVVL T GGRGAEDAAV PAQKLRRNGI 660
SVLVVGVGVP LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCEAK QPVNLCKPSP 720
70 CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSSCVVCVS QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

Seq ID NO: 444 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 89..2356

75 1 11 21 31 41 51
GCCCCCTGGC CCGAGCCGCG CCCGGGCTCT TGAGTAGAGC CGCCCCGGCA CCGAGCGCTG 60
80 GTCCCGCTC TCCTTCCGTT ATATCAACAT GCCCCTTTC CTGTTGCTGG AAGCCGCTCT 120
TGTTTTCTCT TTTTCCAGAG TGCCCCATC TCTCCTCTC CAGGAAGTCC ATGTAAGCAA 180
AGAAACCATC GGAAGATTT CAGCTGCCAG CAAAATGATG TGGTGCTCGG CTGCAGTGGA 240
CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA 300
GCACTTTGCC ATCAGAGTCT GTGACGGTCT GGACATCAGC CCGAGAGGGG TCAGAGTGGG 360
85 AGCATTCAG TTCAAGTTCCA CTCTCATCT GGAATCCCC TTGGATTCAT TTTCAACCCA 420
ACAGGAAGTG AAGGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA 480
ACTTGCTCTG AAATACCTTC TGACAGAGG GTTGCTTGA GGCAGAAATG CTCTGTGCC 540
CCAGATCCTC ATCATCGTCA CTGATGGGAA GTCCAGGGG GATGTGGCAC TGCCATCCAA 600

	GCAGCTGAAG	GAAAGGGGTG	TCAGTGTGTT	TGCTGTGGGG	GTCAGGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TCGGCCATCT	GCTCCAGCGC	780
5	CACGCCAGAC	TGCAGGGTGC	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTGCGT	GGAATGCCCC	CATGCTGGAG	AGGATCGCGG	CGGACCCCTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCAGAAGGA	CTGGAAGGCT	ACCAGTGCCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
10	CTGTGCCCTG	AAGCTGAGCC	TGGAATGCAG	GGTCCGACCTC	CTCTTCCTGC	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGACG	GCTTCCTGCG	GGCCAAAGTC	TTCTGTAAGC	GGTTTGTGCG	1200
	GGCCGTGCTG	CGGAGGAGCT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGTGGCG	GTCCTGTGG	GGGAGTACCA	GGATGTGCCT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCCC	TTCCGTGGTG	GCCCCACCTT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCGA	1380
	GCTGGGCTTC	GGGAGCGCCA	CAGGACACGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
15	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGGTCAACG	CAAGGGCGCG	1500
	AGAGCTGTCT	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGAGGCCCA	AAGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTTC	ACCAATCCC	1620
	TGAGCTGCAG	GGGAAGCTGT	GCAGCCGGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
	CCTCGTCTTC	ATGTTGGACA	CCTCTGCCTC	AGTAGGGCCC	GAGAATTTTG	CTCAGATGCA	1740
20	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
	CCTGGTGGTG	TATGGCAGCC	AGGTGCAGAC	TGCCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TAGCCAGGCG	CCCCTACCTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGGCTCGG	1980
25	TGTCCCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTCC	2040
	TGCCCAGAAG	CTGAGGAACA	ATGGCATCTC	TGTCTTGGTC	GTGGGCGTGG	GGCCTGTCTT	2100
	AAGTGAGGGT	TGCGGAGGCT	TTCAGGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCACC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	CGCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GGCAGCTGG	TCCTGCAGAA	2280
	TGGGAGCTAC	CGCTGGCACT	GTCCGGATGG	CTGGGAGGGG	CCCACTGCG	AGAACCGATT	2340
30	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
	AGCAACTACA	GAGAAGGCGT	GGGCACTGAA	ATGGTGCCTA	CCTTCTGGAA	TGTCTGTGCC	2460
	CCAGGTCCTT	AGAATGTCTG	CTTCCGCGCG	TGGCCAGGAC	CACTATTCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTACCCAC	2580
	AAACGATGTT	GTGAAAAAGT	TTTGTATGTT	AAGTAAATAC	CCACTTTCTG	TACCTGCTGT	2640
35	GCCTTGTGTA	GAGTATGTGA	TTCGCCACCT	TTCCTTGAG	GATAAACAG	GGGTCTTGAA	2700
	GACTTAAATT	TAGCGGCGCT	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCAGCA	GAGGCCCTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 445 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
45	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
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	MVPKGGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFPRW	EBLHALASEP	RQGHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
	SQPCQNGTGC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
50	RAKVFVRKFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPLDVWSL	DGIPFRGGPT	420
	LTGSALRQAA	ERGFSGSATRT	QDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEEI	TGSPKHVMYV	SDPQDLFNQI	PELQKLCISR	QRPGRCTQAL	DLVFMLD TSA	540
	SVGPENFAQM	QSFVRSALQ	FEVNPDTVQV	GLVVYGSQVQ	TAFLDLDKPT	RAAMLRAISQ	600
55	APYLGGVGS	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAV	PAQKLRRNGI	660
	SVLVVGVGPV	LSEGLRRLAG	PRDSLHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
	CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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	CCGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCGAGAA	AGATCTCAGA	180
	GTAAAGAAGA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAAC	GAGGCTGCAG	300
70	TCAGTTCCGG	AAGGCTGTAG	GACCCGCAGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCTCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAGC	AGAGTCCCCG	420
	CAGCCCTCAG	AGAAATCTGT	GACTGATTCC	AACTCCGATT	CAGAAGATGA	AAGTGGAAATG	480
	AATTTTTTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAACTC	540
	ATGTCTGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCC	CCCAGGCTCC	600
75	GACTCACAA	CAAGAGAGCT	GCGAAGCGGT	ACATTCCCGG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCAGAA	GCGCTCGCTC	CAGATCATCC	840
	GTGACCCCTC	CGCATATAAT	TCGCCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTTGGAGAAC	900
80	GCTCTGAGCA	ATTCTCGAGA	GAAGATATAT	AACCGTTCAC	TGGGCTCTAC	TTGTCTATCA	960
	TGCCGTGAGA	GAAACTTTGA	TACCAAAACA	AACTGCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	TCTGTGGCCC	CTGCCCTTGA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTGGGA	TGCCCCGCTT	TGTCGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGACGCGAG	ATGGAGAGCT	TGCGACTGGG	GTCCTTGTGT	ATTAGCCAA	ATATCATGGC	1200
85	TTTGGGAATG	TGCATGCCTA	CTTGAAAAGC	CTGAAACAGG	AATTTGAAAT	GCAAGCATAA	1260
	TATCTGGAAA	ATTTGCTGCC	TGCCTTTTAC	TTCTCAAATC	TTTCTGTGAA	AAGTTTCCAA	1320
	TTTTTTCATC	GAAACCTGAG	TAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

TACACTTTGC CCTCCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCC 1500
 TCTATTTCCA ATGCTCCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560
 TATGAAAGCA TATTTTATTT ACTTGGTGTT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
 GAAACACAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
 CTTGTTTACA CAAAAACGAG TATGATTTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
 TCAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860
 CTCTAATTT CTCTGCCCG AAGGGTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
 AAGGTTGGTG GGCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
 ATGAGTAAGC TGATTGTAA TTTTCAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAAGT 2040
 TTATTTTCAGT TCACATTGAA GGTATTGCAA ATAAATCTCT GGACAAATTT GTATGGAAAC 2100
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 CTGTGTCAGT ATTCCCCCTC CTCTTGCCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
 AAGTGTGTTG ATGTCCAATT TACTTGCCATA TGTAAACCAT TGCCTGTCCA TTCAATGTTT 2400
 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTATCT GTAATGCTTT 2460
 TATACAAAAG TTTATTTTAA TAATAAAATG TTTGTTCTAA AAAAAAAAAA

Seq ID NO: 447 Protein sequence
 Protein Accession #: NP_114148.1

1 11 21 31 41 51
 MDARRVPQKD LRVKKNLKKP RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
 RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNDSSEDES GMNFLEKRAL 120
 NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRPR RRTFPGVASR RNPERRARPL 180
 TRSRRI LGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR 240
 PVEEITEEEL ENVCNSRREK IYNRLSGSTC HQCRQKTDIT KTCNRPDCW GVRGQFCGPC 300
 LRNRGEEVR DALLDPNWHC PPCRGICNCS PCRQRDGRCA TGVLVYLAKY HGFGNVHAYL 360
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Seq ID NO: 448 DNA sequence
 Nucleic Acid Accession #: NM_019894
 Coding sequence: 1..1314

1 11 21 31 41 51
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 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
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 GGGAACTGGT TCTCTGCTGT TTTGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
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 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
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 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
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 GCCACCCAC CTTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
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 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCCG GCACCCAGAG AGTATACACC 1260
 AAGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 449 Protein sequence
 Protein Accession #: NP_063947.1

1 11 21 31 41 51
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 GNWFSACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV 240
 LTAHCFRKH TDVFNWVRA GSDKLSFPFS LAVAKIIIE FNPMPKND IALMKLQFPL 300
 TFSGTVRPIC LPFDEELTP ATPLWIIWGW FTQKNGGKMS DILLQASVQV IDSTRCNADD 360
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Seq ID NO: 450 DNA sequence
 Nucleic Acid Accession #: XM_051860.2
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1 11 21 31 41 51
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	GCGGAGGTTG	GGCTTCTGAG	CCGGAACATC	ATAGTGATGG	GGGAGATGGA	GGACAAATGC	480
	TACCCCTACA	GAACACCAT	CTGCAATTTT	TTTGACTTCG	ATACCTTTGG	GGGCCACATC	540
5	AAGTTTGCTC	TGGGATTAA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTCACTA	CCCGATTAC	TTCCACCTGG	CCGGTGATGT	AGACGAAAGG	660
	GGAGGTTATG	ACCCACCCAC	ATACATCAGG	GACCTCTCCA	TCCATCATAC	ATTCTCTCGC	720
	TGCGTCACAG	TCCATGGCTC	CAATGGCTTG	TTGATCAAGG	ACGTTGTGGG	CTATAACTCT	780
	TTGGGCCACT	GCTTCTTCAC	GGAAGATGGG	CCGGAGGAAC	GCAACACTTT	TGACCACTGT	840
10	CTTGGCTCC	TTGTCAAGTC	TGGAACCTCT	CTCCCTCGG	ACCGTGACAG	CAAGATGTGC	900
	AAGATGATCA	CAGGAGACTC	CTACCCAGGG	TACATCCCA	AGCCCAAGCA	AGACTGCAAT	960
	GCTGTGTCCA	CCTTCTGGAT	GGCCAATCCC	AACAACAACC	TCATCAACTG	TGCCGCTGCA	1020
	GGATCTGAGG	AAACTGGATT	TTGGTTTATT	TTTACCACG	TACCAACGGG	CCCCCTCCGT	1080
	GGAAATGACT	CCCCAGTTA	TTCAGAGCAC	ATTCCACTGG	GAAAAATCTA	TAACAACCGA	1140
15	GCACATTCCA	ACTACCGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCTGCCAAGG	ACAAGCGGGC	GTTCCTCTCA	ATCATCTCTG	CCAGATACAG	CCCTCACCAG	1260
	GACGCCGACC	CGCTGAAGCC	CCGGAGGCCG	GCCATCATCA	GACACTTCAT	TGCCTACAG	1320
	AACCAGGACC	ACGGGGCCTG	GCTGCGCGGC	GGGGATGTGT	GGCTGGACAG	CTGCCGTTT	1380
	GCTGACAATG	GCATTGGCCT	GACCTTGGCC	AGTGGTGGAA	CCTTCCCGTA	TGACGACGGC	1440
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	ATGATGGACA	ATAGGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCTTCCCT	1560
	ATAGGCCAGA	ATTTTCCAAT	TAGAGGAAAT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACCT	TCCGAAAGTT	TGTGGCCCTG	GAGGGCCGGC	ACACCAGCGC	CCTGGCCTTC	1680
	CGCTGGAATA	ATGCTTGGCA	GAGCTGCCCC	CATAACAACG	TGACCGGCAT	TGCCTTTGAG	1740
25	GACGTTCCGA	TTACTTCCAG	AGTGTCTTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTC	CATGACGTCG	ACGGCTCCGT	GTCGAGTAC	1860
	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGGTCC	GGCACCAGCA	CTGCATCAAT	1920
	GTTCGCGACT	GGAGAGGGGC	CATTTGCAGT	GGGTGCTATG	CACAGATGTA	CATTCAAGCC	1980
	TACAAGACCA	GTAACCTGCG	AATGAAGATC	ATCAAGAATG	ACTTCCCCAG	CCACCTCTTC	2040
30	TACCTGGAGG	GGGCGCTCAC	CAGGAGCACC	CATTACCAAC	AATACCAACC	TCTTGTCACT	2100
	CTGCAGAAAG	GCTACACCAT	CACTGGGAC	CAGACGGCCC	CCGCGAACT	CGCATCTGG	2160
	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGTACCCC	GCGAGGCACC	2220
	ACATTTCTCCA	TCTCTCTGGA	TTCTTCAAT	CGCCTGCTGA	AGCAAAACGTC	CAAGACGGCC	2280
	GTCTTCTGTA	GGACCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTTGG	CAGGAGCCAC	2340
35	TACTACTGGG	ACGAGGACTC	AGGGCTGTGT	TTCTGAAGC	TGAAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
	CCAAAGAACG	CAGGCGCTAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
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40	CATTCTTTGG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAAACGAC	2640
	TTGCTTTACA	TTGAAGTGGA	TGGGAAGAA	TACCCAGATT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACCTCCATT	2760
	CTGCAAGGCA	TACCATGGCA	GCTTTTCAAC	TATGTGGCGA	CCATCCCTGA	CAATTCCATA	2820
	GTGCTTATGG	CATCAAGAGG	AAGATACGTC	TCCAGAGGCC	CATGGACCAG	AGTGTGGAA	2880
	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAAGAGCAAA	TGGCATTGCT	TGGCTTCAAA	2940
45	GGCAGCTTCC	GGCCATCTGG	GCTGTCACTG	GACACTGAGG	ATCACAAGC	CAAAATCTTC	3000
	CAAGTTGTGC	CCATCCCTGT	GGTGAAGAA	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
	GCCACCTCGT	GGTAGACTAT	GACGGTGACT	CTTGGCAGCA	GACCAGTGGG	GGATGGCTGG	3120
	GTCCCCAGC	CCCTGCCAGC	AGCTGCCCTG	GAAGGCCGTG	TTTCAGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TCAGAGACCC	TGGTGCTGCC	ACCTGCCCTT	ACTCAAGTGT	CTACCTGGAG	3240
50	CCCTCGGGG	GGTGCTGGCC	AATGCTGGAA	ACATTCACTT	TCCTGCAGCC	TCTTGGGTGC	3300
	TTCTCTCCTA	TCTGTGGGCT	TTTCTGGGCT	GTCTGGGGAC	CATATCAGGA	GACCTGGGTT	3360
	GTGCTGACAG	CAAAGATCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAAGTCTGA	3420
	GGGCTGGTCA	TTACAGATGC	CCCATGGTCT	TCAGCAGACA	AGTGAGGGTG	GTAAGTGTAG	3480
	GAGAAGAGCG	CTTGGCCTTA	AGGAAATCTT	TACTCTGTGA	AGCAAGAGCC	AACCTCACAG	3540
55	GATTAGGAGC	TGGGTTAGAA	CTGGCTATCC	TTGGGGAAGA	GGCAAGCCCT	GCCTCTGGCC	3600
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	AGGCCCTTTT	AGTTCTGAGC	TTCCAGAAAT	CTGCTGCATT	TCACATGGTA	CCTGGAACCC	3720
	AACAGTTCAT	GGATATCCAC	TGATATCCAT	GATGCTGGGT	GCCCCAGCGC	ACACGGGATG	3780
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	ATGATGGAGA	AGTGTGGTCA	GAGGGGAGCA	ATGGGCTTTG	CTGCTTATGA	GCACAGAGGA	4140
65	ATTCACTCCC	CAGGCAGCCC	TGCTCTGAC	TCCAAGAGGG	TGAAGTCCAC	AGAAGTGAGC	4200
	TTCTGCTCTA	GGGCTCTGAT	TGCTCTTCAT	CCAGGGAAC	GAGCACAGGG	GGCCTCCAGG	4260
	AGACCTTAGA	TGTGCTGCTA	CTCCCTCGGC	CTGGGATTTT	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA	TTTTAACAGA	TGGGGAAAGT	GAGCCCCCAA	GATGGGAAAG	4380
70	AACCAACAG	CTAAGGGAGG	GCCTGGGGAG	CCCCACCCTA	GCCCTTGTGT	CCACACCACA	4440
	TTGCTCAAC	AACCGGCCCC	AGAGTGCCCA	GGCACTCCTG	AGGTAGCTTC	TGGAATGGG	4500
	GACAAGTCCC	CTCGAAGGAA	AGGAAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
	CCCTCTGCT	CCGAGCGCAC	ACAAACCCGC	CCTCCCTTGT	GTGTGGCGG	TCCCTGTGGC	4620
	CTTCACTTGT	TTCACTACCT	GTCAGCCCG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCCAT	4680
	TGGTGCTACC	TGGCTCTCCT	GTCTCTGAG	CTCTACAGGT	GAGGCCAGC	AGAGGGAGTA	4740
75	GGGCTCGCCA	TGTTTCTGGT	GAGCCAAATT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTC	AGCTGCTGCT	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
	ATAGAGAGCC	CAAAGAGCTC	CTGTAAAGAG	GAGAACTCTA	TCTGTGGTTT	ATAATCTTGC	4920
	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACACT	ATTATATCCC	TTTCTCGCCC	4980
	CAACCACAAA	CTCTTTCCTT	CAAAGAGGGC	CTGCCTGGCT	CCCTCCACCC	AACTGCACCC	5040
80	ATGAGACTCG	GTCCAAGAGT	CCATTCCCA	GGTGGGAGCC	AACTGTCAAG	GAGGTCTTTC	5100
	CACCAACACA	TCTTTACAGT	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTGATGGAG	5220
	AGGAGAGTTA	AAATGACCTC	ATGTCTTCTT	TGTCCACGGT	TTTGTGAGT	TTTCACTCTT	5280
	CTAATGCAAG	GGTCTCACAC	TGTGAACAC	TTAGGATGTG	ATCACTTCA	GGTGGCCAGG	5340
85	AATGTTGAAT	GTCTTTGGCT	CAGTTCAATT	AAAAAAGATA	TCTATTGTA	AGTTCTCAGA	5400
	GTGTTACATA	TGTTTACAG	TACAGGATCT	GTACATAAAA	GTTTCTTTC	TAAACCATTC	5460
	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
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Seq ID NO: 451 Protein sequence
 Protein Accession #: XP_051860.2

1 11 21 31 41 51
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Seq ID NO: 452 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 261..2861

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Seq ID NO: 453 Protein sequence
 Protein Accession #: Eos sequence

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 SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTUVKGNPSS SVEDHIEYHG HRGSAARVF 300
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 KDVVGYNSLG HCFPTEDGPE ERNTFDHCLG LLVKSGLTLP SDRDSKMKCM ITEDSYPGYI 660
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Seq ID NO: 454 DNA sequence
 Nucleic Acid Accession #: NM_013282.2
 Coding sequence: 85..2466

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Seq ID NO: 455 Protein sequence
Protein Accession #: NP_037414.2

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PADEDMWDET ELGLYKVNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTRPALEE 180
DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMNLNPNP NPKERGFWD 240
AEISRKRETR TARELYANVN LGDDSLNDCR IIFVDEVFKI ERPGEGSPMV DNPMMRKSGP 300
SCKHKDDVN RLCRCVACHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSEDEWYC 360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTEEC TIVPSNHYGT 420
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Seq ID NO: 456 DNA sequence
Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

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Seq ID NO: 457 Protein sequence
Protein Accession #: NP_001191.1

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Seq ID NO: 463 Protein sequence
 Protein Accession #: Eos sequence

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Seq ID NO: 465 Protein sequence
 Protein Accession #: BAB21525.1

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Seq ID NO: 466 DNA sequence
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	GCCCCCTCAG	AGGCATCCGT	CCCTCAAGAA	GAAGCTGCGG	GCACGGAGCC	AGCTCTCTGA	180
15	GTTCCTGGAAA	TCCCATAAAT	TGGACATGAT	CCAGTTCACC	GAGTCCTGCT	CAATGGACCA	240
	GAGTGCCAAG	GAACCCCTCA	TCAACTACTT	GGATATGGAA	TACTTCGGCA	CTATCTCCAT	300
	TGGCTCCCCA	CCACAGAACT	TCACTGTCTC	CTTCGACACT	GGCTCCTCCA	ACCTCTGGGT	360
	CCCTCTGTG	TACTGCACAT	GCCCAGCCTG	CAAGACGCAC	AGCAGGTTC	AGCCTTCCCA	420
	GTCCAGCACA	TACAGCCAGC	CAGTCAATC	TTCTCCATT	CAGTATGGAA	CCGGGAGCTT	480
	GTCCGGGATC	ATTGGAGCCG	ACCAAGTCTC	TGTGGAAGGA	CTAACCCTGG	TTGGCCAGCA	540
20	GTTCGGAGAA	AGTGTACAG	AGCCAGGCCA	GACCTTTGTG	GATGCAGAGT	TTGATGGAAT	600
	TCTGGGCTCG	GGATACCCCT	CCTTGGCTGT	GGGAGGAGTG	ACTCCAGTAT	TTGACAACAT	660
	GATGGCTCAG	AACCTGGTGG	ACTTGGCCAT	GTTTCTGTCT	TACATGAGCA	GTAACCCAGA	720
	AGTGGTGGCG	GGGAGCGAGC	TGATTTTGG	AGGCTACGAC	CACCTCCATT	TCTCTGGGAG	780
	CCTGAATTGG	GTCCCACTCA	CCAAGCAAGC	TTACTGGCAG	ATTGCACCTG	ATAACATCCA	840
25	GGTGGGAGGC	ACTGTTATGT	TCTGCTCCGA	GGGCTGCCAG	GCCATTGTGG	ACACAGGGAC	900
	TTCCCTCATC	ACTGGCCCTT	CCGACAAGAT	TAAGCAGCTG	CAAAACGCCA	TTGGGGCAGC	960
	CCCGTGGAT	GGAGAATATG	CTGTGGAGTG	TGCCAACCTT	AACGTCATGC	CGGATGTCTC	1020
	CTTCACCAT	AACGGAGTCC	CCTATACCT	CAGCCCAACT	GCCTACACCC	TACTGGACTT	1080
	CGTGGATGGA	AGTGTACAG	GCAGCAGTGG	CTTCAAGGA	CTTGACATCC	ACCCTCCAGC	1140
30	TGGGCCCTCT	TGGATCCTGG	GGGATGTCTT	CATTGACAG	TTTACTCAG	TCTTGACCG	1200
	TGGGAATAAC	CGTGTGGGAC	TGGCCCCAGC	AGTCCCCTAA	GGAGGGGCT	TGTGTCTGTG	1260
	CTGCCTGTCT	TGACAGAGCT	TGAATATGTT	AGGCTGGGGC	ATTCTTTACA	CCTACAAAAA	1320
	GTTATTTTCC	AGAGAATGTA	GCTGTTTCCA	GGGTGCAAC	TTGAATTAAG	ACCAAAACAGA	1380
	ACATGAGAAT	ACACACACAC	ACACACATAT	ACACACACAC	ACACTTCACA	CATACACACC	1440
35	ACTCCACCA	CCGTCATGAT	GGAGGAATTA	CGTTATACAT	TCATATTTTG	TATTGATTTT	1500
	TGATTATGAA	AATCAAAAT	TTTCACATT	GATTATGAAA	ATCTCCAAAC	ATATGCACAA	1560
	GCAGAGATCA	TGGTATAATA	AATCCCTTTG	CAACTCCACT	CAGCCCTGAC	AACCCATCCA	1620
	CACACGGCCA	GGCCTGTTTA	TCTACACTGC	TGCCCACTCC	TCTCTCCAGC	TCCACATGCT	1680
	GTACCTGGAT	CATTCTGAAG	CAAATTCGGA	GCATTACATC	ATTTTGTCCA	TAAATATTTT	1740
40	TAACATCCTT	AAATATACAA	TCGGAATTCA	AGCATCTCCC	ATTGTCCAC	AAATGTTTGG	1800
	CTGTTTTTGT	AGTTGGATTG	TTTGTATTAG	GATTCAAGCA	AGGCCCATAT	ATTGCATTTA	1860
	TTTGAATGT	CTGTAAGTCT	CTTCCATCT	ACAGAGTTTA	GCACATTGTA	ACGTTGTCTG	1920
	TTGAAATCCC	GAGGTGTCTAT	TTGACATGGT	TCTCTGAAC	TATCTTTCCT	ATAAAATGGT	1980
	AGTTAGATCT	GGAGGTCTGA	TTTGTGGCA	AAAATACTTC	CTAGGTGGTG	CTGGGTACTT	2040
45	CTGTGTCAT	CCTGTGAGGA	GGCAGATAAT	GCTGGTGCT	CTCTATTGGT	AATGTTAAGA	2100
	CTGCTGGGTG	GGTTTGGAGT	TCTTGGCTTT	AATCATTCT	TACAAAGTTC	AGCATTTT	

Seq ID NO: 467 Protein sequence
 Protein Accession #: NP_001901.1

50

	1	11	21	31	41	51	
	MKTLLELLLV	LLELGEAQGS	LHRVPLRRHP	SLKKKLRRS	QLSEFWKSHN	LDMIQPTESC	60
55	SMDQSAKEPL	INYLDMVEYF	TISIGSPPQN	FTVIFDTGSS	NLWVPSVYCT	SPACKTHSRF	120
	QPSQSSTYSQ	PQGSFSIQYQ	TGSLSGIIGA	DQVSVEGLTV	VGQQFGESVT	EPGQTFVDAE	180
	FDGILGLGYP	SLAVSGTTPV	FDNMMAQNLV	DLPMFSVYMS	SNPEGGAGSE	LIFGGYDHS	240
	FSGSLNWVVP	TKQAYWQIAL	DNIQVGGTVM	FCSEGCQAIV	DTGTSITGTP	SDKIKQLQNA	300
	IGAAPVDGEY	AVECANLNMV	PDVTFPTINGV	PYTLSPATYT	LLDFVDGMQP	CSSGPGQLDI	360
60	HPPAGPLWIL	GDVFIHQFYS	VFDRGNRRVG	LAPAVP			

Seq ID NO: 468 DNA sequence
 Nucleic Acid Accession #: NM_018058.1
 Coding sequence: 319..1575

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70	TACACCGACA	AGTTGTTCAA	GTTCCGCAAT	AACCGGTGGG	AAGACATCCT	GAGCGATGAG	180
	GTCAACGTGG	CCCGTGGTGT	GGCCAGCCTC	TTTGCCGGAC	GCTCTGTGGC	CTGTGTGGAC	240
	AGAAAGGGCT	CTGGACGCTA	CTCTATCTAC	ATTGCCAATT	ACGCCCTACG	TAATGTGGGC	300
	CCTGATGCCC	TCATTGAAAT	GGACCCTGAG	GCCAGTGACC	TCTCCCGGGG	CATTCTGGCG	360
	CTCAGAGATG	TGGCTGCTGA	GGCTGGGGTC	AGCAAAATATA	CAGGGGGCCG	AGGCGTCAGC	420
	GTGGGCCCCA	TCCCTCAGCAG	CAGTGCCTCG	GATATCTTCT	GCGACAATGA	GAATGGGCTC	480
75	AACCTCCTTT	TCCACAACCG	GGGCGATGGC	ACCTTTGTGG	ACGCTGCGGC	CAGTGTGGGT	540
	GTGGACGACC	CCCACCAGCA	TGGGGGAGGT	GTCGCCCTGG	CTGACTTCAA	CCGTGATGGC	600
	AAAGTGGACA	TCGTCTATGG	CAACTGGAAT	GGCCCCCACC	GCCTCTATCT	GCAAAATGAGC	660
	ACCATGGGA	AGGTCCGCTT	CCGGGACATC	GCCTCACC	AGTTCTCCAT	GCCTCCCCCT	720
	GTCGCCACCG	TCATCACC	CGACTTTGAC	AATGACCAGG	AGCTGGAGAT	CTTCTTCAAC	780
80	AACATTGCCT	ACCGCAGCTC	CTCAGCCAAC	CGCTCTTCC	CGCTCATCCG	TAGAGAGCAC	840
	GGAGACCCCC	TCATCGAGGA	GCTCAATCCC	GGCGACGCCT	TGGAGCCTGA	GGGCCGGGGC	900
	ACAGGGGGTG	TGGTGACCGA	CTTCGACGGA	GACGGGATGC	TGGACCTCAT	CTTGTCCCAT	960
	GGAGAGTCCA	TGGCTCAGCG	GCTTCCCTC	TTCCGGGGCA	ATCAGGGCTT	CAACAACAAC	1020
	TGGCTGCGAG	TGGTGCCACG	CACCGGGT	GGGCGCTTTG	CCAGGGGAGC	TAAGGTCGTG	1080
85	CTCTACACCA	AGAAGAGTGG	GGCCACCTG	AGGATCATCG	ACGGGGGCTC	AGGCTACCTG	1140
	TGTGAGATGG	AGCCCGTGGC	ACACTTGGC	CTGGGGAAGG	ATGAAGCCAG	CAGTGTGGAG	1200
	GTACGCTGGC	CAGATGGCAA	GATGTTGAGC	CGGAACGTGG	CCAGCGGGGA	GATGAACCTA	1260

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 ACGAGGATGG CACAGCCTGC GTGGGGACTC TCGGCCAGTC ACCGGGGCCC CGCCCCACCA 1500
 5 CCCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560
 CACCGGTCTC COTAGATGGA GATCTCAATC TGGGGTCGGT GGTAAAGGAG AGCTCGGAGC 1620
 CCAGCTGCTG AGCAGGGGTG GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCCTGGGAG CTAGACCCCTC 1740
 CCCAAGCCCA TCCATGCACTA TTACTTAGCT AACCAATTAGG GAGACTCGTA AGGCCAGGCC 1800
 10 CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
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 15 AAATGGGGAT TAAGAAATAGA ATCTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
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 GGGCTTTGTC AACACGTG

Seq ID NO: 469 Protein sequence
Protein Accession #: NP_060528.1

1 11 21 31 41 51
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 25 FRDIASPKFS MSPVRTVIT ADFDNDQELE IFFNNIAYRS SSANRLPRVI RREHGDPLIE 180
 ELNPGDALEP EGRGTGGVVT DFDGDMMLDL ILSHGESMAQ PLSVFRGNQG FNNWLRVVP 240
 RTRVGAFARG ARVVLTKKS GAHLRIIDGG SGYLCMEFV AHFGLKDEA SSVVETWPDG 300
 KMVSRNVASG EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALET S PYVSTPMEAT 360
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Seq ID NO: 470 DNA sequence
Nucleic Acid Accession #: AJ279016
Coding sequence: 1..1962

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 40 AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180
 TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
 CAGAAGCGCG TGGTGAACAT CGCGGTGATG GAGCGCAGCT CACCCCTACT CGCGCTGCGG 300
 GACCGGCAGG GGAACGCCAT CGGGGTGACA GCCTGCGACA TCGACGGGGA CGGCCGGGAG 360
 GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG 420
 45 TTGTTCAAGT CCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
 CGTGGTGTGG CCAGCCTCTT TGCCGAGCGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
 GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGGCC TGATGCCCTC 600
 ATTGAATAGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
 GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
 50 CTCAGCAGCA GTGCCTCGGA TATCTTCTGC GACAATGAGA ATGGGCCTAA CTTCCTTTTC 780
 CACAACCGGG CGGATGGCAC CTTTGTGGAC GCTGCGGCCA GTGCTGGTGT GGACGACCCC 840
 CACCAGCATG GCGAGGTGT CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
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 55 GTCCGCTTCC GGGACATCGC CTCACCCAAG TTCTCCATGC CCTCCCCTGT CGGCACGGTC 1020
 ATCACCGCCG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCTAC 1080
 CGCAGCTCTC CAGCCAACCG CCTCTTCCGC GTCATCCGTA GAGAGCACGG AGACCCCTC 1140
 ATCGAGGAGC TCAATCCCGG CGAGCCTTGG GAGCCTGAGG GCCGGGGCAC AGGGGGTGTG 1200
 GTGACCGACT TCGACGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
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 CCCGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500
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 65 TTCTCCAGC AGGAAAATGG CCATTGCATG GACACCAATG AATGCATCCA GTTCCCATTC 1680
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 70 GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920
 CTGGGTGCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
 CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CCTAGACAGT 2040
 AGGGATGTAA AGGCCTGGGA GCTAGACCTT CCCCAGCCCC ATCCATGCAC ATTACTTAGC 2100
 TAACAATTAG GGAGACTCGT AAGGCCAGGC CCTGTGCTGG GCACATAGCT GTGATCACAG 2160
 CAGACAGGGT CGTGCCCTG ATGGCGCTTA CATTCAGTG GGTCTAATGA CCATATCTTA 2220
 75 GGACACAGAT GTGCCCAAGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280
 CCTGAGTTCA AATCTGATT CAGGAACTCA CAAAGCTATG TGACCTTACA CCAGTCACTT 2340
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Seq ID NO: 471 Protein sequence
Protein Accession #: CAC08451

1 11 21 31 41 51
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 85 FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQNAIGVT ACDIDGDGRE 120
 EIYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180

GRYSIIYANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNFPLF HNRGDGTVD AAASAGVDDP HQHGRGVALA DFNDRGKVDI 300
 VYGNWNGPHR LYLQMSHGHK VRFRDIASPK FSPMPSPVRTV ITADFDNDQE LEIPFNNIAY 360
 5 RSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDGFDGDM LILSHGESM 420
 AQLPSVFRGN QGFNNWLRV VPRTRFGAFA RGAKVVLTK KSGAHLRIID GSGYLCEME 480
 FVAHFLGKGD EASSVEVTPW DGMVSRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
 FSQQENGHCN DTNECIQFPF VCPDRKPCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT 600
 LGQSPGRPT TPTAAATAA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC

Seq ID NO: 472 DNA sequence
 Nucleic Acid Accession #: FGENESH
 Coding sequence: 1..4794

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 20 TCACCTACT ACAGCGTCGC GGACCGGCAG GGAACGCCA TCGGGGTGAC AGCCTGCGAC 240
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 25 GGGTGGGCA CGTACACCGA CAAGTTGTTT AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
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 30 GGCACTCTGG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAATA TACAGAAGGC 840
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 40 CTGAGAAGCT GGGAGGAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCACTCAGG 1440
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 65 GGTGAGGAG AAGGTTTAA AATCAGAAAG GGAGGGTTCC CAGGGCCAGG GGTGAGGGC 2940
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 75 CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC 3540
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 85 AACACAACT GGCTGCGAGT GGTGCCACGC ACCCGGTTTG GGGCTTTG CAGGGGAGCT 4140
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Seq ID NO: 473 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 PPTTPAGLLG LPPLSGRDFS SSLGQASPD S RQGERVPVPC CRGGLRPTHE PEPFLLRPKS 180
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 GGDPEEADDE HSGDGSTSQL CRLGWKDGQF KEEAAALVEE QREAGAAGVP RGRVRTALQT 360
 SKSHLADKNL FGPPCYYSVC APSPAHPFPA RQAPQHYPA PLVTQLMTHG RLAGKLARSV 420
 PHPRAPGMDP LCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK QAMSRCALR 480
 ELGGPWSQAT QHLPALEYD LGEPPILQRT DGDPRRRDS PKVTQECHLV ATMPALGGLE 540
 GPCRVAKREI GRETAVGRP LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA 600
 25 LAWNQMEKEE KIKHGDHEPR FRLRKAREAE FPPGSSEEPL LQPPSGLRGS PVLQVGLGLA 660
 SATHCGSMSP LGGRGVSVGP ILSSASDIF CDNENGNPFL FHNRGDGTFF DAAASAERRL 720
 AFIVHLKYHL CRDFPHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS 780
 LLTQGLASSA HRRTLSQLGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840
 LSSERVNVGV DDPHGVNNGV ALADFNDRGK VDIVYGNWNG PHRLYLQMS T HGVVRFRDIA 900
 30 SPKFSMPSPV RTVITADFDN DQELIFFNN IAYRSSSANR LFRCSILARG SSSLTAGGRN 960
 QGQEGRLIRR GGPFGPGGQA KVNTGPLMKK QKGRKDEWA RGCNAGQSL AKEPASAIAG 1020
 KKGNAQSV PRTQAPQDTK PHYHKKGLQG PITTRKRGY VQSLPGKAT GSNHYQEKGL 1080
 RGPITTRKRG YGVQSLPGK ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH 1140
 35 RKGLRAPITT RKRGVQVSL PGKATGSNH YQEKGLRGI TTRKRGYGLQ SLPGKATGS 1200
 NHYQEKGLQ PITTRKRGY VQSLPGKAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
 AMGSNHYQEK GLRAPITTRK RGYVQSLPG KGATGSNVIR REHGDPLIEE LNPGDALPE 1320
 GRGTGGVVTD FDGDGMLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVR TRGFAPARGA 1380
 KVVLYTKKSG AHLRIIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTWPDGK MVSRRNVASGE 1440
 40 MNSVLEILYP RDEDTLQDPA PLECGQGSQ QENGHCMDTN ECIQFPFVCP RDKFVCVNTY 1500
 GSYRCRTNKK CSRGYEPNED GTACVGTTELQ SRHTMTWKPR PKKELQLSQG ICTPVWSPFL 1560
 PGCRLLLKRA QLQAAPSTLL QKAPGIPPEAQ VYEQQQE

Seq ID NO: 474 DNA sequence
 Nucleic Acid Accession #: NM_003661.1
 Coding sequence: 1..1152

1 11 21 31 41 51
 | | | | |
 50 ATGAGTGCAC TTTCTCTTGG TGTGGGAGTG AGGGCAGAGG AAGCTGGAGC GAGGGTGCAA 60
 CAAAACGTTT CAAAGTGGGAC AGATACTGGA GATCCTCAAA GTAAGCCCTT CGGTGACTGG 120
 GCTGCTGGCA CCATGAGACC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC 180
 AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC 240
 GGATTCGTGG CTGCTGCTGA ACTGCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300
 55 GACAACCTTG CAAGACAAT GATCATGAAA GACAAAACT GGCACGATA AGGCCAGCAG 360
 TACAGAACT GGTTCCTGAA AGAGTTCTCT CGGTTGAAAA GTGAGCTTGA GGATAACATA 420
 AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAGGCAC CACCATCGCC 480
 AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCCTCGT CGGCATGGGT 540
 CTGGCACCCT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
 ATCACAGCCG CTTTGACCCG GATTACCAGC AGTACCATGG ACTACGAAA GAAGTGGTGG 660
 60 ACACAAGCCC AAGCCACAGA CTGTGTCATC AAAAGCCTTG ACAAAATTGA GGAGGTGAGG 720
 GAGTTTTTGG GTGAGAACAT ATCCAACCTT CTTTCTTAG CTGGCAATAC TTACCAACTC 780
 ACACAGGCGA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
 GTACCGCATG CTTACGCCTC ACGCCCCCGG GTCATGAGC CAATCTCAGC TGAAGCGGT 900
 65 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAG TGAGCAGAGG AGTCAAGCTC 960
 ACGGATGTGG CCCCTGTAAG CTTCTTTCTT GTGCTGGATG TAGTCTACCT CGGTACGAA 1020
 TCAAAGCACT TACATGAGG GGCAGAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080
 CAGGAGCTGG AGGAGAAGCT AACATTCTC AACATAATT ATAAGATTCT GCAGGCGGAC 1140
 CAAGAACTGT GA

Seq ID NO: 475 Protein sequence
 Protein Accession #: NP_003652.1

1 11 21 31 41 51
 | | | | |
 75 MSALFLGVGV RAEAEAGARVQ QNVPSGTD TG DPOSKPLGDW AAGTMDPESS IFIEDAIKYF 60
 KEKVSTQNL LLLTDNEAWN GPVAAELPR NEADELRKAL DNLRQMIMK DKNWHDKGG 120
 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLSSIS SGILTLVGM 180
 LAFPTGGSL VLEPEGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR 240
 80 EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300
 EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVEY SKHLHEGAKS ETAELKQVA 360
 QLEBEKLNIL NNNYKILQAD QEL

Seq ID NO: 476 DNA sequence
 Nucleic Acid Accession #: NM_014452.1
 Coding sequence: 1..1968

1 11 21 31 41 51

	ATGGGGACCT	CTCCGAGCAG	CAGCACCGCC	CTCGCTCTCT	GCAGCCGCAT	CGCCCGCGGA	60
	GCCACAGCCA	CGATGATGCG	GGGCTCCCTT	CTCCTGCTTG	GATTCTCTAG	CACCACCACA	120
5	GCTCAGCCAG	ACAGCAAGGC	CTCGAATCTC	ATTGGCACAT	ACGCCCATGT	TGACCGTGCC	180
	ACCGGCCAGG	TGCTAACCTG	TGACAAGTGT	CCAGCAGGAA	CCTATGTCTC	TGAGCATGTG	240
	ACCAACACAA	GCCTGCGCGT	CTGCAGCAGT	TGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
	AATGGCATAG	AGAAATGCCA	TGACTGTAGT	CAGCCATGCC	CATGGCCAAT	GATTGAGAAA	360
	TTACCTTGTG	CTGCCCTTGC	TGACCGAGAA	TGCATTGTCC	CACCTGGCAT	GTTCCAGTCT	420
10	AACGCTACCT	GTGCCCCCCA	TACGGTGTGT	CCTGTGGGTT	GGGGTGTGCG	GAAGAAAGGG	480
	ACAGAGACTG	AGGATGTGCG	GTGTAAGCAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCCT	540
	TCTAGTGTGA	TGAAATGCAA	AGCATACACA	GACTGTCTGA	GTCAGAACTT	GGTGGTGATC	600
	AAGCCGGGGA	CCAAGGAGAC	AGACAACGTC	TGTGGCACAC	TCCCCTCCTT	CTCCAGCTCC	660
	ACCTCACCTT	CCCTTGGCAC	AGCCATCTTT	CCACGCCCTG	AGCACATGGA	AACCCATGAA	720
15	GTCCCTTCTT	CCACTTATGT	TCCCAAAGGC	ATGAACCTCA	CAGAACTCAA	CTCTTCTGCC	780
	TCTGTTAGAC	CAAAGGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAAGC	840
	TCAGCAAGGG	GGAAGGAAGA	CGTGAACAAG	ACCCTCCCAA	ACCTTCAGGT	AGTCAACCAC	900
	CAGCAAGGCC	CCCACCACAG	ACACATCTGT	AAGCTGCTGC	CGTCCATGGA	GGCCACTGGG	960
	GGCGAGAAAT	CCAGCAGCGC	CATCAAGGGC	CCCAAGAGGG	GACATCCTAG	ACAGAACTTA	1020
20	CACAAGCATT	TTGACATCAA	TGAGCATTTC	CCCTGGATGA	TTGTGCTTTT	CCTGCTGCTG	1080
	GTGCTTGTGG	TGATTGTGGT	GTGCAGTATC	CGGAAAAGCT	CGAGGACTCT	GAAAAAGGGG	1140
	CCCCGGCAGG	ATCCCACTGC	CATTGTGGAA	AAGGCAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGAAAC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCTGAAG	1260
	CTTGTAGCAG	CCCAAGTGGG	AAGCCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
	AGTGAGAGGG	AGGTTGCTGC	TTTCTCCAAT	GGGTACACAG	CCGACCACGA	GCGGGCTTAC	1380
25	GCAGCTCTGC	AGCACTGGAC	CATCCGGGGC	CCCGAGGCCA	GCCTCGCCCA	GCTAATTAGC	1440
	GCCCTGCGCC	AGCACCGGAG	AAACGATGTT	GTGGAGAAGA	TTCGTGGGCT	GATGGAAGAC	1500
	ACCACCCAGC	TGGAACCTGA	CAAACTAGCT	CTCCCGATGA	GCCCCAGCCC	GCTTAGCCCG	1560
	AGCCCCATCC	CCAGCCCCAA	CGCGAAACTT	GAGAAATCCG	CTCTCTTAC	GGTGGAGCCT	1620
30	TCCCCACAGG	ACAAGAACAA	GGGCTTCTTC	GTGGATGAGT	CGGAGCCCCC	TCTCCGCTGT	1680
	GACTCTACAT	CCAGCGGCTC	CTCCGCGCTG	AGCAGGAACG	GTTCCTTTAT	TACCAAAGAA	1740
	AAGAAGGACA	CAGTGTGTGG	GCAGGTACGC	CTGGACCCCT	GTGACTTGCA	GCCTATCTTT	1800
	GATGACATGC	TCCACTTTCT	AAATCCTGAG	GAGCTGCGGG	TGATTGAAGA	GATTCCCCAG	1860
	GCTGAGGACA	AACTAGACCG	GCTATTGCGA	ATTATTGGAG	TCAAGAGCCA	GGAAGCCAGC	1920
35	CAGACCTCC	TGACTCTGT	TTATAGCCAT	CTTCTGACC	TGCTGTAG		

Seq ID NO: 477 Protein sequence
Protein Accession #: NP_055267.1

	1	11	21	31	41	51	
40	MGTSPPSSSTA	LASCSRIARR	ATATMIAGSL	LLGLFLSTTT	AQPEQKASNL	IGTYRHVDRA	60
	TGQVLTCDKC	PAGTYVSEHC	TNTSLRVCS	CPVGTFTRE	NGIEKCHDCS	QPCPWPMEIK	120
	LPCAALTDRE	CTCPPGMFQS	NATCAPHTVC	PVGWGVRRKG	TETEDVRCKQ	CARGTFSDVP	180
45	SSVMKCKAYT	DCLSQLNVVI	KPGTKETDNV	CGTLPSPFSS	TSPSPGTAIF	PRPEHMETHE	240
	VPSSTYVPKG	MNSTESNNSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPNLQVNVH	300
	QQGPHRHIL	KLLPSMEATG	GEKSSSTPIK	PKRGHPRQNL	HKHFDINEHL	PWMLVLFLL	360
	VLVVIVVCSI	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNREKWIYY	CNGHGIDILK	420
	LVAQVGSQW	KDIYQFLCNA	SEREVAAFSN	GYTADHERAY	AALQHWITRG	PEASLAQLIS	480
50	ALRQHRNDV	VEKIRGLMED	TTQLETDKLA	LPMSPSPLSP	SPIPSNAXL	ENSALLTVEP	540
	SPQDKNKGF	VDESEPLLR	DSTSSGSSAL	SRNGSFITKE	KKDTVLRQVR	LDPCLDQPIF	600
	DDMLHFLNPE	ELRVIEEIPQ	AEDKLDRLFE	IIGVKSQEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 478 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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60	GCTCTGCCCA	AGCCGAGGCT	GCGGGGCGGG	CGCCGCGGGG	AGGACTGCGG	TGCCCCGCGG	60
	AGGGGCTGAG	TTTGCCAGGG	CCCACTTGAC	CCTGTTTCCC	ACCTCCCGCC	CCCCAGGTCC	120
	GGAGGCGGGG	GCCCCCGGGG	CGACTCGGGG	GCGGACCGCG	GGGCGGAGCT	GCCGCCCGTG	180
	AGTCCGGCCG	AGCCACCTGA	GCCCGAGCCG	CGGGACACCG	TGCTCTCTGC	TCTCCGAATG	240
	CTGCGCACCG	CGATGGGCGT	GAGGAGCTGG	CTCGCCGCCC	CATGGGGCGC	GCTGCCGCTC	300
65	CGGCCACCGC	TGCTGCTGCT	CCTGCTGCTG	CTGCTCTGCT	TGCAGCCGCC	GCCTCCGACC	360
	TGGGCGCTCA	GCCCCCGGAT	CAGCTTGCCT	CTGGGCTCTG	AAGAGCGGCC	ATTCTCTAGA	420
	TTCGAAGCTG	AACACATCTC	CAACTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTACTGTG	GTGCTGAGTA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCTGCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCGG	AGAAGAAACA	GCAGTGCAGC	600
70	TTCAAGGGCA	AGGAGCCACA	GCGCGACTGT	CAAAACTACA	TCAAGATCCT	CCTGCCGCTC	660
	AGCGGCAGTC	ACTGTGTCAC	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACTACATC	720
	AACATGGAGA	ACTTCACCTT	GGCAAGGGAC	GAGAAGGGGA	ATGTCCTCCT	GGAAGATGGC	780
	AAGGGCCGTT	GTCCCTTCGA	CCCGAATTTC	AAGTCCACTG	CCCTGGTGGT	TGATGGCGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
75	AGCCTTCGCC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
	GCCTCAGCCT	ACATTCTCTA	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCTTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TTTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGACC	1140
	TCCTTCTCTA	AGGCCAGACT	GCTGTGCTCA	CGGCCCGACG	ATGGCTTCCC	CTTCAACGTG	1200
80	CTGCAGGATG	TCTTACAGTG	GAGCCCCAGC	CCCCAGGACT	GGCGTGACAC	CCTTTTCTAT	1260
	GGGGTCTTCA	CTTCCCAGTG	GCACAGGGGA	ACTACAGAAG	GCTCTGCCGT	CTGTGTCTTC	1320
	ACAATGAAGG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CCGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCCGGTG	CCCACACCCC	GGCCTGGAGC	GTGCATCACC	1440
	AACAGTCCCC	GGAAAGGGAA	GATCAACTCA	TCCCTGCAGC	TCCAGACCCG	CGTGGCTGAA	1500
85	TTCTCAAGG	ACCACTTCTT	GATGGACGGG	CAGGTCCGAA	GCCGCATGCT	GCTGCTGCAG	1560
	CCCCAGGCTC	GCTACCAAGC	CGTGGCTGTA	CACCGCGTCC	CTGGCCTGCA	CCACACCTAC	1620
	GATGTCCTCT	TCCTGGGCAC	TGGTGACGGC	CGGCTCCACA	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGACAA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAACTCG	1740

CTCCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCCTCAC ACTCGGCGT AGTCCAGGTG 1800
 CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGGACCCC 1860
 TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CACGTAGGCC TCTACCAAGC TCAGCTGGCC 1920
 5 ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCGTCT 1980
 TCGGTTGTGT CCCCCTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC 2100
 TGGTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCTCCT GCCACGTGCT ACCCACTGGG 2160
 GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGTGCTC ACTAGAGGAG 2220
 10 GGCTTCCAGC AGCTGGTAGC CAGTACTGTC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280
 CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGCACCA 2340
 GGTGGTGGCA AGGCCAGCTG GGGTGCAGAC AGGTCCCTACT GGAAGGAGTT CCGTGGTGAT 2400
 TGCACGCTCT TTGTGCTGTC CGTGTGCTC CCAGTTTAT TCTTGCTCTA CCGGCACCGG 2460
 AACAGCATGA AAGTCTCTCT GAAGCAGGGG GAATGTGCCA GCGTGCACCC CAAGACCTGC 2520
 15 CCGTGGTGC TGCCTCTGA GACCCGCCCA CTCACCGGCC TAGGGCCCCC TAGCACCOCG 2580
 CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640
 GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCCAGTGTGC 2700
 CCGGGCCCCC GGGTCCGCTT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT 2760
 TCCAGAGGAC GCTGCCCTGG CTTAGGGGTC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820
 TCCCTCCGCG TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG 2880
 20 GGCAGCTGG CCGTGTGCTC TCGGCTCAAG TAGCGAAGCT CCTACCAACC AGACACCCAA 2940
 ACAGCCGTGG CCCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCTTAGGTT GGTGGAACAG 3000
 TGCTCTTAT GTAACTGAG CCGTTTGTG TTTTAAACAA TCCAAATGTG AAATAAGAT 3060
 GAGAGGGAAG AGATAGCTG CAGTCAGCA CACACGGCTG CTCAGATTCA TGGCCTCCCA 3120
 25 GGGGTGCTGG GGATGCATCC AAAGTGGTGT TCTGAGACAG AGTTGGAAC CCTCACCAAC 3180
 TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
 CAGGACCCAG TTGGGCTGCG TGGCTTCTGC CTGTCCAGTC AGCCGAGGAT GTAGTTGTG 3300
 CTGCCGCTGT CCCACCACCT CAGGGACCCG AGGGCTAGGT TGGCACTGCG GCCTCACCA 3360
 GGTCTGTTGG TCGGACCCAA CTCCTGGACC TTTCAGCCT GTATCAGGCT GTGGCCACAC 3420
 30 GAGAGGACAG CCGGAGCTCA GGAGAGATT CTGTGACATG TACGCCTTTC CCTCAGAAAT 3480
 CAGGGAAGAG ACTGTGCGCT GCCTTCTCTC GTTGTGCGT GAGAACCCGT GTGCCCTTC 3540
 CCACCATATC CACCTCTGCT CCATCTTTGA ACTCAACAC GAGGAACATA CTGACCCCTG 3600
 GTCCTCTCCC CAGTCCCGAG TTCACCTCC ATCCCTCACC TTCCTCCTA CTAAGGGATA 3660
 TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTAATAAG 3720
 35 ATGCACCTTA TGTCTTTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 479 Protein sequence
Protein Accession #: XP_044533.3

1 11 21 31 41 51
 40 MLRTAMGLRS WLAAPWALP PRPPLLLLL LLLLQPPPP TWALSPRISL PLGSEERPFL 60
 RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120
 SFKGDQPDQR CQNYIKILL LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED 180
 45 VGRRCPPDPN FKSTALVVDG ELYTGVSSP QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
 KASAYIPESL GSLQGGDDKI YFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKAQLLC SRPDDGFPPN VLQDVPTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
 FTMKDQVRVF SGLYKEVNRE QQWYTVTHP VPTPRPGACI TNSARERKIN SLLQLPDRVL 420
 NFLKDHFLMD GQVRSRMLLL QPQARYQRYA VHRVPLHHT YDVLFLGTGD GRLHKAHSV 480
 50 PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 FYCAWSGSSC KHVSLYQPL ATRPWQDIE GASAKDLCSA SSVSPSPFVP TGEKPCEQVQ 600
 PQPNTVNTLA CPLLSNLATR LHLRNGAPVN ASASCHVLEP GDLLLVGTQO LGFQCWSLE 660
 EGGQQLVASY CPEVVEDGVA DQDDEGGSVP VIISTSRVSA PAGGKASWGA DRSYWKFLV 720
 MCTFLVLAFL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
 55 PLDHRGYSLS SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 480 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

1 11 21 31 41 51
 60 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG 60
 GCCCAGAAAGG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
 AGCACCTCTG CCGACGAGAT CCTCCGGAAG GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
 65 ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCTTGGCC AGAAGGTGAT GGAGAATAGC 240
 ATGCGGACAC CCGACATCTT AACCGGGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT 300
 CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
 ATCGTGGCGC TCAAGTCTCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
 70 CTGCGCAGAG AGATCGAAAT CCAGGCCAC CTGCACCATC CCAACATCCT CGTCTCTAC 480
 AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTGACGAGC AGCGAACAGC CACGATCATG 600
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGTGTA CTTGGGCTGG 720
 75 TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCTTGA CTACCTGCC 780
 CCGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGGTG CATTTGAGTG 840
 CTTTGTCTATG AGCTGCTGCT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC 900
 TATCGCGCTC TCGTCAAGST GAGCTTAAAG TTCCCGCTT CTGTGCCAC GGGAGCCAG 960
 80 GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020
 TCAGCCACCC CTTGGGTCGG GGCACACTCT CGGAGGGTGC TGCCCTCCCTC TGCCCTTCAA 1080
 TCTGTGCGCT GATGGTCCCT GTCAATCACT CGGGTGGTG TGTGTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGGATC CTTAATGTT CCCTTATCTG TTTTCTACCT CCTCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 481 Protein sequence
Protein Accession #: NP_004208

1 11 21 31 41 51

MAQKENSYPW	PYGRQTAPSG	LSTLPQVRVLR	KEPVTSPSALV	LMSRSNVQPT	AAPGQKVMEN	60
SSGTPDILTR	HFTIDDFEIG	RPLGKGFKN	VYLAREKKSH	FIVALKVLPK	SQIEKEGVEH	120
QLRREIEIQA	HLHHPNLRRL	YNYFYDRRRI	YLILEYAPRG	ELYKELQKSC	TFDEQRTATI	180
MEELADALMY	CHGKKVIHRD	IKPENLLLGL	KGELKIADFG	WSVHAPSLRR	KTMCGTLDYL	240
PPEMIEGRMH	NEKVDLWCTG	VLCYELLVGN	PPFESASHNE	TYRRIVKVDL	KFPASVPTGA	300
QDLISKLLRH	NPSERLPLAQ	VSAHPWVRAN	SRRVLPPSAL	QSV		

Seq ID NO: 482 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

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AAAACCACAA	AGATCCTTTT	TTGGCAAGTT	GTTACGGGAA	TTTAGACTTG	TAGCAGCTGA	120
CCGAAGGTCC	TGGAAGATAC	TGCTCTTTGG	TGTAATAAAC	TTGATATGTA	CTGGCTTCCT	180
GCTTATGTGG	TGCAGTTCTA	CTAATAGTAT	AGCTTTAACT	GCCTATACTT	ACCTGACCAT	240
TTTGTATCTT	TTTAGTTTAA	TGACATGTTT	AATAAGTTAC	TGGGTAACAT	TGAGGAAACC	300
TAGCCCTGTC	TATTCATTGG	GGTTTGAAAG	ATTAGAAGTC	CTGGCTGTAT	TTGCCCTCCAC	360
AGTCTTGGCA	CAGTTGGGAG	CTCTCTTTAT	ATTAAGAGAA	AGTGCAGAAC	GCTTTTGGGA	420
ACAGCCCGAG	ATACACACGG	GAAGATTATT	AGTTGGTACT	TTTGTGGCTC	TTTGTTTCAA	480
CCTGTTACAG	ATGCTTTCTA	TTCCGAATAA	ACCTTTTGCT	TATGCTCAG	AAGCTGCTAG	540
TACGAGCTGG	CTTCAAGAGC	ATGTTGCAGA	TCTTAGTCTG	AGCTTGTGTG	GAATTATTCC	600
GGGACTTAGC	AGTATCTTCC	TTCCCGCAAT	GAATCCATTT	GTTTTGATTG	ATCTTGCTGG	660
AGCAITTTGCT	CTTTGTATTA	CATATATGCT	CATTGAAATT	AATAATTATT	TTGCCGTAGA	720
CACCTGCCTCT	GCTATAGCTA	TTGCCCTGAT	GACATTTGGC	ACTATGTATC	CCATGAGTGT	780
GTACAGTGGG	AAAGTCTTAC	TCCAGACAAC	ACCACCCCAT	GTTATTGGTC	AGTTGGACAA	840
ACTCATCAGA	GAGGTATCTA	CCTTAGATGG	AGTTTITAGAA	GTCCGAAATG	AACATTTTGG	900
GACCCTAGGT	TTTGGCTCAT	TGGCTGGATC	AGTGCATGTA	AGAATTGAC	GAGATGCCAA	960
TGAACAAATG	GTCTTGTCTC	ATGTGACCAA	CAGGCTGTAC	ACTCTAGTGT	CTACTCTAAC	1020
TGTTCAAAT	TTCAAGGATG	ACTGGATTAG	GCCTGCCTTA	TTGTCTGGGC	CTGTTGCAGC	1080
CAATGTCCTA	AACTTTTCAG	ATCATCACGT	AATCCCAATG	CCTCTTTTAA	AGGGTACTGA	1140
TGATTTGAAC	CCAGTTACAT	CAACTCCAGC	TAAACCTAGT	AGTCCACCTC	CAGAAATTTT	1200
ATTTAAACACT	CCTGGGAAAA	ATGTGAACCC	AGTTATTCTT	CTAAACACAC	AAACAAGGCC	1260
TTATGGTTTT	GGTCTCAATC	ATGGACACAC	ACCTTACAGC	AGCATGCTTA	ATCAAGGACT	1320
TGGAGTTCCA	GGAATTTGGG	CAACTCAAGG	ATTGAGGACT	GGTTTITACAA	ATATACCAAG	1380
TAGATATGGA	ACTAATAATA	CAATGGACA	ACCAAGACCA	TGATAGACTC	TAACATTATT	1440
TTATAAGGAA	TATTGACTCC	TTGGCTTCCA	ATTTATTTAG	TAATCCAATC	TTGCATTGAC	1500
TGTTTAACTA	TTTACTCTAA	ATGTTAGATA	ATAGTAGTCT	TGTTCACTAT	TCATGAAACC	1560
TATGAAACTA	TTTITTTGTA	AAATGTATTT	GTGACAGTGA	AATCCTCGTA	AATGTTAAAG	1620
GCTTTAAATA	GGCTTCTCTT	AGAAAATGTG	TTTCTTTAAA	TTTGGATTTT	GGTATCTTTG	1680
GTTTTGTAGT	TGACTGCACT	GTGATGTGAC	CTTACCTTTA	TAAGAGCCAC	TTGATGGAGT	1740
AGATCTGTCA	CTTACTTAAG	ATACGATATT	TCTTTTTTTT	TCCGAGACGG	AGTCTTGCTC	1800
TGCCACTGTG	CCCGGCCAAT	ACATTATTAT	TAAGTTAAGG	CTGTACTTTA	TTAAGGCTTC	1860
CTTAGTTTTT	GTTTTGTGTT	GTTTTTTGAG	ATGGAGTCTC	ACTCTGTGCG	CCAGGCTGGA	1920
ATGCAGTGGC	ATGATCTCAG	CTCACTGCAA	CCTCTGCTTC	CTGAGTTCAA	ATGATTCTCC	1980
TGCCTCAGCC	TCCCGAGTAG	CTGGGATTAC	AGGCACCTGC	CACCACGCCC	AGCTAATTTT	2040
TGTATTTTAA	GTAAAGACCG	GGGATTTTAC	CATGTTGGCC	AGGCTGTGCT	TGAACCTCTG	2100
ACCTCATGAT	CCACCCACTC	TAGCCTCCCA	AAGTGTGGG	ATTAGGTGTG	AGCCACCGCA	2160
CCTGGCCGAT	ATTTTCTTTA	ATGAAATTTA	TAAATATGCT	TCTTGAATAA	TACACATTTT	2220
GGGAAAGGGA	AAAAATGCTG	TTCAAAAAGT	AAAGGTCTCT	TTTATAGCTT	TTCCAAAACCT	2280
AAATTGCTAAA	TTTTTCTTTG	AGGTTCTCCT	GAATTATGTC	TTACAAACTA	AAAGCAAAAA	2340
TTTTTAGCAG	AAATTTTGGA	ATACATTCTA	TCTAGCACAA	TTTGAATTTT	TAATTATCAA	2400
GATTTTGTGT	AAAGTTTCTC	TCCTTTAAAA	ATTTTAGTAC	ATTTGTAAT		

Seq ID NO: 483 Protein sequence
Protein Accession #: BAB70980.1

1	11	21	31	41	51	
MGTIHLFRKP	QRSFFGKLLR	EFRLVAADRR	SWKILLFGVI	NLICTGFLLM	WCSSTNSIAL	60
TAYTYLTIFD	LFSMLTCLIS	YWVTLRKPS	VYSFGFERLE	VLAFASTVL	AQLGALFILK	120
ESAERFLEQP	EHTGRLLVVG	TFVALCFNLF	TMLSIRNKPF	AYVSEAASTS	WLQEHVADLS	180
RSLCGIIPGL	SSIFLPRMNP	FVLIDLAF	ALCITYMLIE	INNYFAVDTA	SAIAIALMTF	240
GTMYPMVSYS	GKVLQTPP	HVIGQLDKLI	REVSTLDGVL	EVRNEHFWTL	GPGSLAGSVH	300
VRIRRDANEQ	MVLAHVNTNL	YTLVSTLTQ	IFKDDWIRPA	LLSGPVAANV	LNFSDDHHVIP	360
MPLLKGTDDL	NPVTSTPAKP	SSPPPEFSFN	TPGKNVNPVI	LLNTQTRPYG	FGLNHGHTPY	420
SSMLNQLGLV	PGIGATQGLR	TGFTNIPSR	GTNNRIGQPR	P		

Seq ID NO: 484 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

1	11	21	31	41	51	
ATGCGCGCGC	GGGAGCTGAG	CGAGGCGGAG	CCGCCCCCGC	TCCGGGCCCC	GACCCCTCCC	60
CCGCGGCGGC	GTAGCGCGCC	CCCAGAGCTG	GGCATCAAGT	GCGTGCTGGT	GGGCGACGGC	120
GCCGTGGGCA	AGAGCAGCCT	CATCGTCAGC	TACACCTGCA	ATGGGTACCC	CGCGCGCTAC	180
CGGCCACTG	CTCTGGACAC	CTTCTCTGGT	ACGTACGTTT	AATCGCCCGT	GCGGCGCGCT	240
GGCTGCGGCG	GGGCTGTGCA	CGGGGAGCT	GGGCGGGGCG	TCTCGGCGGG	AGGGCGCAGA	300
GGACCCCGGG	GAGGAGACTG	GAGCAGGCCC	CGAGGTGGCG	CTGGTGCGGC	CCAGGACGCT	360
CTTCTTAAC	CAGGCTCTCC	CCGCCCGCC	CCTGCAGTGC	AAGTCTGGT	GGATGGAGCT	420
CCGGTGCGCA	TTGAGCTCTG	GGACACAGCG	GGACAGGAGG	ATTTTGACCG	ACTTCGTTCC	480
CTTTGCTACC	CGGATACCGA	TGTCTTCTTG	GCGTGCTTCA	GCGTGGTGCA	GCCAGCTCC	540
TTTCAAAACA	TACAGAGAAA	ATGGCTGCC	GAGATCCGCA	CGCACAAACC	CCAGGCGCCT	600
GTGCTGCTGG	TGGGCACCCA	GGCCGACCTG	AGGACGATG	TCAACGTACT	AATTCAGCTG	660

GACCAGGGGG GCGGGGAGGG CCCCGTGCCC CAACCCAGG CTCAGGGTCT GGCCGAGAAG 720
 ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
 TTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAAGGTG TGCACACCT CTCGCGCTGC CGCTGGAAGA AGTTCCTCTG CTTCGTTTGA

Seq ID NO: 485 Protein sequence
 Protein Accession #: PGENESH predicted

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVKGSSSLIVS YTCNGYPARY 60
 RPTALDFTSG TVVQSPVRRP GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120
 LPNSGSPRPA PAVQVLVDGA PVRIELWDTA QEDFDRLRS LCYPDTDVFL ACFSVVQPSS 180
 FQNIETKWL P BIRTHNPQAP VLLVGTQADL RDDVNVLQL DQGGREGPVP QPQAQGLAEK 240
 IRACCYLECS ALTQNLKEV FDSAILSIE HKARLEKKLN AKGVRTL SRC RWKKFFCFV

Seq ID NO: 486 DNA sequence
 Nucleic Acid Accession #: XM_063832.2
 Coding sequence: 1..711

1 11 21 31 41 51
 | | | | |
 ATGCCGCGGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120
 GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTTCTCTGTG CAAGTCCTGG TGGATGGAGC TCCGTGCGC 240
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTC CTTTGCTTAC 300
 CCGGATACCG ATGCTTCTCT GGCCTGCTTC AGCGTGGTGC AGCCAGCTC CTTTCAAAAC 360
 ATCACAGAGA AATGGCTGCG CGAGATCCGC ACGCACAAAC CCCAGGCGCC TGTGCTGCTG 420
 GTGGGCACCC AGGCCGACCT GAGGACGAT GTCAACGTAC TAATTAGCT GGACAGGGG 480
 GGCGGGGAGG GCGCCGTGCC CCAACCCAG GCTCAGGGT TGGCCGAGAA GATCCGAGCC 540
 TGTGCTACCT TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAACTGAA TGCCAAAGGT 660
 GTGCGCACCC TCTCCCGCTG CCGCTGGAAG AAGTCTTCT GCTTCGTTTG A

Seq ID NO: 487 Protein sequence
 Protein Accession #: XP_063832.1

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVKGSSSLIVS YTCNGYPARY 60
 RPTALDFTSV QVLVDGAPVR IELWDTAGQE DFRLRLSLCY PDTDVFLACF SVVQSSSFQN 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPO AQGLAEKIRA 180
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAGK VRTL SRCRWK KFFCFV

Seq ID NO: 488 DNA sequence
 Nucleic Acid Accession #: NM_014398.1
 Coding sequence: 64..1314

1 11 21 31 41 51
 | | | | |
 GGCACCGATT CGGGGCTGCG CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
 ACCATGCCCC GGCAGCTCAG CGCGCGCGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
 CACGATGGCA GTCAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
 ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACCAGC TAAGCAAGCA 240
 CCTACCAAAA CTTTAGCAGC AAGATTCATG GATGGTCATA TCACCTTTCA AACAGCGGCC 300
 ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA ACTGTGCAAC CACCAGCCCA 360
 ATTACCTACA CCCTGGTCAC AACCCAGGCC ACACCCAAACA ACTCACACAC AGCTCCTCCA 420
 GTTACTGAAG TTACAGTCGG CCCTAGCTTA GCCCCTTATT CACTGCCACC CACCATCACC 480
 CCACCAGCTC ATACAGCTGG AACCAGTTCA TCAACCGTCA GCCACACAAC TGGGAACACC 540
 ACTCAACCCA GTAACCAAGC CACCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
 ACAACCGGTC AGAAGCTGTA TCAACCCACC CATGCCCCAG GAACAACGGC AGCTGCCACC 660
 AATACCAACC GCACAGCTGC ACCTGCCTCC ACGGTTCTCG GGCCACCCT TGCACCTCAG 720
 CCATCGTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
 TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
 AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA 960
 TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
 CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATT CTTCAAGTGC 1080
 GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGCAGG TGAACAAAC CGATGTCCAA 1140
 CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
 TACACAATTG TGCTTCTGT GATTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
 GGTGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
 CCGCGGGGGA ATGAAAATTA TGAATTTAG AGAACTCTTT CATCCCTTCC AGGATGGATG 1380
 TTGGGAAATT CCCTCAGAGT GTGGGTCTTT CAAACAATGT AAACCAACAT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500
 GTTTATTTTA TGAAAGATAT AGTAGCTGT TTTATTTCTA GTTCTCTTGA GAATATTTTA 1560
 GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGTCATATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680
 ATTTTATTTT ACCCTTGATC TTAACAAGC CTTTGCTTTG TTATCAAAAT GACTTTCATG 1740
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAC GGAGTTTCAC TCTTGTCAAC 1860
 CAGGCTGGAG TACAGTGCCA CGATCTCGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAAG 1920
 TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCAGCCTG 1980
 GCTAATTTTT GTATTTTTAT TATGACGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAA GTGCTGGAT TACAGGCATG 2100
 AGCCATTCGG CCCGCTTAA AATGTTTTTT TTAATCATCA AAAAGAACAA CATATCTCAG 2160

GTTGTCTAAG TGTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220
 CTTGATGACT CCTGCTCCAG AATGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAACAATA AGCAAGAGAG AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACCT AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA 2460
 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTCTCCCTA CACCAAGTTA 2520
 CCTACAAGAA CAATGCACAC ACACCTCGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCAG ATAACAAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTGA TGGGATTGCT TAGCTGGGCT 2760
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTGTGA TAATAGAGAA 2820
 ACTTCGTAA CCAACTGTTT TTTCTTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC 2880
 TTTCTGACTT CATATCCATA TTTCTATTG TTTCACTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAG AACTAAGTCA GGATGTTAAC 3000
 AGAAAAGTCC ACATAACCTT AGAATTCTTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060
 CCATGTTGAC TTTCTCATG TGTTCCTTGA TGACTCAGTA AGTTGGCAG GTCCTGACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAACT TACTTTGG

Seq ID NO: 489 Protein sequence
 Protein Accession #: NP_055213.1

1 11 21 31 41 51
 | | | | |
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPAKQAP 60
 HQTLAARFMD GHITFQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTQAT PNNSHAPPV 120
 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHHTGNIT QPSNQTTLPA TSLIALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKGTGIYQV LNSRLCTKA 240
 EMGIQLIVQD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLNFGGQGV NLTPKDEES 300
 YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSHKCV SEQSLQLSAH LQVKTTDVQL 360
 QAFDFEDDHF GNVDECSSDY TIIVLPVIGAI VVGLCLMGMG VYKIRLRQCS SGYQRI

Seq ID NO: 490 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
 | | | | |
 TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAAT 300
 AAAGGACAAC GATGCCTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGG ACCAAAACG GAAATACAGT CTTCCTGAAT GAATGACAAAT CAGAATTCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GAGTGTACAA AAGTGCTTTC ACGTTCCTAC TTGTGTATT ATACATTCAT 720
 GCATTCTTAG GCTAGAGAGC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTTCC 960
 CCAAAATATCA TGTAGCAGAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAA TTATACGCTA 1080
 TGGGATACCT GCAACAGTGC ACATATTCA TAACCAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTGTATAC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAGAAAAA TGTGTAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTTCATGC CTATATACTG TAAATTTTAG GTATACICAA GACTAGTTTA AAGAATCAAA 1440
 GTCAATTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAAAAAAA AAA

Seq ID NO: 491 Protein sequence
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 | | | | |
 MSVKGMALAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 492 DNA sequence
 Nucleic Acid Accession #: NM_000577.1
 Coding sequence: 41..520

1 11 21 31 41 51
 | | | | |
 GGCACGAGGG GAAGACCTCC TGTCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
 CCGACCTCTT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAACCA 120
 GAAGACCTTC TATCTGAGGA ACACCAACT AGTTGCCGGA TACTTGCAAG GACCAAAATG 180
 CAATTTAGAA GAAAAGATAG ATGTGATACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
 CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
 GGAGGACGTT AACATCTCTG ACCTGAGCGA GAACAGAAAG CAGGACAAAG GCTTCGCTT 360
 CATCCGCTCA GACAGTGACC CCACCACCAG TTTTGAAGTCT GCCGCTGCC CCGGTTGGTT 420
 CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
 CGTCATGGTC ACCAAATTC ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCTGT 540
 TCCCATTCCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCTGCCCC AGGGCTCCCG 600

GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
 CCTGGTCACA GGA CTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTCGCA CAAAGCCCTT CCATGTGCGC 780
 TCTGCATTCA GGATCAAAAC CGACCACTT GCGCAACCTG CTCTCTCTT GGCATGCCT 840
 CTTCTCTCCT CATTCCACCT TCCCATGCC TGGATCCATC AGGCCACTTG ATGACCCCA 900
 ACCAAGTGGC TCCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
 TTTAAGGGTT TGTGGAATAA GAAAATTAGG ATTTTCATGAT TTTT TTTT TTTT CAGTCCCGT 1020
 GAAGGAGAGC CTTTCATTG GAGATTATGT TCTTTGCGGG AGAGGCTGAG GACTTAAAT 1080
 ATTCTGCAAT TGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTTCCTCT CTTTTCCTC 1140
 TTTT TTTT TTTT ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCAT 1200
 ATTTT TTTT TTTT TCCTTTTAAA ACACITCCAT AATCTGGACT CCTCTGCCA GGCCTGCTG 1260
 CCCAGCTCC CAGCTCCATC TCCACTCCAG ATTTT TTTT TTTT GCTGCTGCA GTACTTTACC 1320
 TCCTATCAGA AGTTTCTCAG CTCCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGGTCTT 1380
 TCTTCTCTG TCGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCCTTGGAG 1440
 ACTTGTATGA AAGATGGCTG TGCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
 GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
 CTCTTGGCAG CTGATCAGCG AATGAATGCT GTATATGTTG GGTGCAAAAGT TCCCTACTTC 1620
 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAAT GCCTAAAAAA AAAAAAAA 1680
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 493 Protein sequence
Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPPIEP 60
 HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSNRK QDKRFAFIRS DSGPTTSPES 120
 AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE

Seq ID NO: 494 DNA sequence
Nucleic Acid Accession #: NM_002081.1
Coding sequence: 222..1898

1 11 21 31 41 51
 GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCGCGCCGC GCGCGCGCGC 60
 GGCTTTTGTG GTCTCGGCTT CCTCGGCGCG CGCGCGCTCT GGACCGCGAG CCGCGCGCGC 120
 CGGGACCTTG GCTCTGCCCT TCGCGGCGCG GAACCTCGCA GGACCGCGCC AGGATCCGAG 180
 AGAGCGCGCG GCGGGTGGCC GGGGCGCGCG CCGGCGCGCG CATGGAGCTC GGGGCGCGAG 240
 GCTGGTGGCT GCTATGTGCG GCGCAGCGCG TGGTGGCTG CCGCGCGCGG GACCGCGCCA 300
 GCAAGAGCGG GAGCTCGGCG GAGGTCGCGC AGATCTACGG AGCCAAAGGC TTCAGCCTGA 360
 GCGACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420
 CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 CCGCGCTCCG GGCAGCAGCG CGGCTCCTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540
 TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC 600
 CCGGCGCCTT CGGAGAGCTG TACACGACGA ACGCGAGGCG CTTCCGGGAC CTGTACTCAG 660
 AGCTGCGCGT GTACTACCGG GGTGCCAACC TGCACTGGA GGAGACGCTG GCGGAGTTCT 720
 GGGCGCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCTGTATG 780
 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGGCGCTGCG GCCCTTCGGG GAGGCGCGCA 840
 GAGAGCTGCG CCGTGGGCGC ACCCGTGCTT TCGTGGCTGC TCGCTCCTTT GTGCAAGGCC 900
 TGGGCGTGGC CAGCGACGCT GTCCGGAAG TGGCTCAGGT CCCCTTGGGC CCGGAGTGCT 960
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCGT GGGAGTCCCC GCGGCCAGGC 1020
 CCTGCGCTGA CTATTCCGA AATGTGCTCA AGGGCTGCGT TGCCCAACAG GCGGACCTGG 1080
 ACGCGAGTG GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140
 CATCGGCTGT GGAGAGTGTC ATCGGAGCGG TGCAACGCTG GCTGGCGGAG GCCATCAACG 1200
 CCCTCCAGGA CAACAGGAGC AGCTCACGG CCAAGTCTAT CCAGGCTGCG GGAACCCCA 1260
 AGGTCAACCC CCAGGCGCCT GGGCCTGAGG AGAAGCGCG CCGGGGCAAG CTGGCCCCGC 1320
 GGGAGAGGCC ACCTTCAGGC ACCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
 GCGACGTCCA GGACTTCTTG ATCAGCCTCC CAGGGACACT GTGCACTGAG AAGATGGCCC 1440
 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGATGGC CAGAGGCCGG TACCTCCCCG 1500
 AGGTGATGGG TGACGCGCTG GCCAACGAGA TCAACAACCC CGAGGTGGAG GTGGACATCA 1560
 CCAAGCGCGA CATGAGCCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCGGC 1620
 TGCGCAGCGC CTACAACGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGCGAGCG 1680
 GCTCGGCGAG CGGTGATGGC TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA 1740
 GCTCCAGCTC CCGGACGCGC TTGACCCATG CCCTCCGAGG CCTGTCAGAG CAGGAAGGAC 1800
 AGAAGACCTC GGCTGCCAGC TGCCCCCAGC CCCCGACCTT CCTCTGCCCC CTCCTCCTCT 1860
 TCCTGGCCCT TACAGTAGCC AGGCCCGGCT GCGGTAAC TCCCCAAGGC CCCAGGGACA 1920
 GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGACG ATATTTAATT CACCTCAGCC 1980
 TGGAGAGGCC TGGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040
 GTCCCAAGCC CAGGCGTGGC CTGCGCTGCC TTTCTGCTTT TTAATTTTGT ATGAGGTCTT 2100
 CAGGTGAGCT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC 2160
 TCCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGACCGCGC CAGAAGCAGC CCCTCGAGGC 2220
 CTACAGAGGA GGCCTCAAAG CAACCGCTG GAGCCACAG CGAGCCTGTG CCTTCTCTCC 2280
 CGCTCTCTCC CATGGGCTG CACAGCAGAG CCCACAGGCC AGCCCTGGCC CACCCCCAG 2340
 CCTCCAGAGA AGCCCCGAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400
 TCTGAGATGA TGCATGATGC CCTCCCTCA GCGCAGGCTG CAGAGCCCGG CCCACCTTCC 2460
 CTGCGCCCTT GAGGGGCTG GAGGTCTGCA GGGTGAACGC TGAGACAGCA CCACTGCTGA 2520
 GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCAGTGAGG GGCCCTCCAT GCGCAGATGA 2580
 GGGGCCACTG ACCCACTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAG 2640
 GGAGGCGAGC TGGGCTCTGC CAATGTGGGC TGCCCCCTCG ACACAGGGCT CACAGGGCAG 2700
 GCCTTGCTGG GGTCCAGGGC TGTGGAGGA CCCCAGGGC TGAGGAGCAG CCAGGACCCG 2760
 CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCTCC CTGTTACAGG TGACACAGGT 2820
 CAGGGCTCAG AGTGACCTC GGCTGTCAAC TGCTCACAGG GATGCTGGTG GCTGGTGAGA 2880
 CCCCAGCTG CACACGGGAA TGCTTAGGTC CCTTCCCGAC CCAGCCAGCT GCACTGCAGG 2940
 GCAAGGGGAG CTGGATAGTT AAGGGCTTTT CCAACATGAT ATCCATTTAC TGACACTTCC 3000
 TGCTCTTGTG TGTGGAGAGC TGTTCGCTCC TCCAGATGG CTTGGAGGC CCGCAGGGCC 3060
 CACCTTGGAC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120

CTGGACGGGC CCTCCTTCCC TCCTGTGCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180
 TGTGGTGTGG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
 TCCTGAACCG ACTGACCCTG AGGAGGCCGC TTAGTGCTGC TTGCTTTTC ATCACCCTCC 3300
 CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAAGTCCC CATGGCTTGT TCTCTGGAAC 3360
 CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
 CCTTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
 TCTCTGGAAG GGCAGCCCT GAGTGTCTAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
 CCTTCTCTCA CAAGGTCCTC CCACCGCTCA GTGTACGGCG GTGACGTGTG TTCTTTTGAG 3660
 TCCTTGTATG AATAAAGGC TGGAAACCTA AA

Seq ID NO: 495 Protein sequence
 Protein Accession #: NP_002072.1

1 11 21 31 41 51
 MELRARGWWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSVDP QAEISGEHLR 60
 ICPOGYTCTT SEMEENLANR SHAELETALR DSSRVLQAML ATQLRSFDDH FQHLLNDSER 120
 TLQATFFGAF GELYTONARA FRDLYSELRL YVRGANLHLE ETLAEFWARL LERLFFKQLHP 180
 QLLLPDDYLD CLGKQAEALR PFGEAPRELRL LRATRAFAVA RSFVQGLGVA SDVVRKVAQV 240
 PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVL I 300
 TDKFWGTSGV ESVGISVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 360
 RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA 420
 RGRYLPVVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD 480
 ASDDGSGSGS

Seq ID NO: 496 DNA sequence
 Nucleic Acid Accession #: NM_001650.2
 Coding sequence: 40.1011

1 11 21 31 41 51
 GGGGCAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCACAGCA 60
 AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCITTCAAA 120
 GGGGTCTGGA CTCAAGCTTT CTGGAAAGCA GTCACAGCGG AATTCTGGC CATGCTTATT 180
 TTTGTTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
 GTCGACATGG TTCTCATCTC CCTTTGCTTT GGACTCAGCA TTGCAACCAT GGTGCAGTGC 300
 TTTGGCCATA TCAGCGGTGG CCACATCAAC CTGCGAGTGA CTGTGGCCAT GGTGTGCACC 360
 AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420
 ATGGAGCAGG GAATCCTCTA TCTGGTCACA CCTCCAGTG TGGTGGGAGG CCGGGAGTGC 480
 ACCATGGTTC ATGGAATCTT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540
 TTTCAATGGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACCGACTGA TGTCACTGGC 600
 TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTTGC AATCAATTAT 660
 ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720
 GAAAACCATT GGATATATTG GGTGTGGCCC ATCATAGGAG CTGTCTCTCG TGGTGGCCTT 780
 TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840
 AAAGCTGCCC AGCAAACAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900
 GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA 960
 GAGGAGAAGA AGGGGAAGA CCAATCTGGA GAGGTATTGT CTTAGTATG ACTAGAAGAT 1020
 CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCCTCAG ATTTCTCTCC ACCCATTAAG 1080
 GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTTGTG GTTTCATGTC ATATTACTCA 1140
 GTCTAAACAA TAAATTTTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
 TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATATAT ACCTATTTTA 1260
 TCTAGTTACC TTTCATTAAC AACCAATTTT AACCGTGTGT CAAGATTGGG TTAAGTCTTG 1320
 CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCCTT CTCTACTGGA ATATTGGTAT 1380
 AGTCAATTCT TATTGAATA TTTATCTAT TAAACTGAGT TTAACATGG C

Seq ID NO: 497 Protein sequence
 Protein Accession #: NP_001641.1

1 11 21 31 41 51
 MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG 60
 GTEKPLPVDV VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120
 AQCLGAIIGA GILYLVTPPS VVGGLGVMTV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
 KRTDVTGSIA LAIGFSAVIG HLFAINYTGA SMNPARSFGP AVIMGNWENH WIYVWGP IIG 240
 AVLAGGLYEF VFCPDVEFKR RFKEAFSKAA QQTGSGYMEV EDNRSQVETD DLILKPGVVH 300
 VIDVDRGEKE KGKQSGSEVL SSV

Seq ID NO: 498 DNA sequence
 Nucleic Acid Accession #: AB020684.1
 Coding sequence: 1..1744

1 11 21 31 41 51
 CCCCCTGTGC ATTAATACAT TAAAAAGATT CAATCTTTAC CCTGAGGTAA TTTTGGCCAG 60
 TTGGTACCGG ATTTATACCA AAATAATGGA CTTGATTGGT ATTCAAACCA AGATATGTTG 120
 GACGGTTACC AGAGGAGAAG GACTCAGTCC TATTGAAAGC TGTGAAGGAT TGGGAGATCC 180
 TGCTTGCTTT TATGTTGCTG TAATTTTAT TTTAAATGGA CTAATGATGG CATTATCTCT 240
 CATATATGGC ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGATTACAG TGTGTGCTT 300
 CTTTTTCAAT CATGGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
 CTCATATCCA TTCTTTGTTT TTCAGATGTT GCTAGTGACT CATATCTCA GGGCTACAAA 420
 ACTTTATAGA GGAAGCTTGA TTGCACTCTG CATTTCCAAT GTATTTTCA TGCTTCCTTG 480
 GCAGTTTGCT CAGTTTGTAT TTCTTACTCA GATTGCATCA TTATTTCAG TATATGTTGT 540
 CGGGTACATT GATATATGTA AATTACGGAA GATCATTAT ATACACATGA TTTCTCTTGC 600
 ACTTTGTTTT GTTTTGATGT TTGGGAACCT AATGTTATTA ACTTCTTATT ATGCTTCTTC 660
 TTTGGTAATT ATTTGGGGTA TTCTGGCAAT GAAACACAT TTCCTGAAA TAAATGTATC 720

	TGAACCTAGT	TTATGGGTGA	TTCAAGGATG	TTTTTGGTTA	TTTGGAACTG	TCATACCTAA	780
	ATACTTGACA	TCTAAAATTT	TTGGTATTGC	AGATGACGCT	CATATTGGCA	ACTTACTAAC	840
	ATCAAAATTC	TTTAGTTATA	AGGATTTTGA	TACTTTATTG	TATACCTGTG	CAGCGGAGTT	900
5	TGACTTTATG	GAAGAAAGAGA	CTCCACTGAG	ATACACAAAG	ACATTATTGC	TCCAGTTGTT	960
	TCCTGTAGTG	TTTGTGTGTA	TTGTTAGAAA	GATTATTAGT	GATATGTGGG	GTGTCTTAGC	1020
	TAAACAACAG	ACACATGTAA	GAAGAACACCA	GTTTGATCAT	GGAGAGCTGG	TTTACCATGC	1080
	ATTGCAATTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	ATGAGACTAA	AACTCTTCTT	1140
	GACACCACAC	ATGTGTGTAT	TGGCATCACT	GATCTGCTCA	AGACAGCTAT	TTGGATGGCT	1200
10	CTTTTGCAAA	GTACATCCTG	GTGCTATTGT	GTTTGCTATA	TTAGCAGCAA	TGTCAATACA	1260
	AGGTTTCAGCA	AATCTGCAAA	CCCAGTGGAA	TATTGTAGGG	GAGTTCAGCA	ATTTGCCCCA	1320
	AGAAGAACTT	ATAGAAATGA	TCAAATATAG	TACTAAACCA	GATGCAGTGT	TTGCGGGTGC	1380
	CATGCCACAG	ATGGCAAGTG	TTAAGCTCTC	TGCACCTCGG	CCCATTGTGA	ATCATCCACA	1440
	TTATGAAGAC	GCAGGCTTGA	GAGCCAGAAC	AAAAATAGTA	TACTCAATGT	ATAGTCGGAA	1500
	AGCAGCCGAA	GAAGTGAAGC	GAGAACTGAT	AAAGTTAAAA	GTGAACCTAT	ACATTCTAGA	1560
15	AGAGTCATGG	TGTGTAAAGAA	GATCCAAGCC	TGGTTCAGCT	ATGCTGAAAA	TTTGGGATGT	1620
	AGAAGATCCT	GCCAATGCTG	GGAAAACTCC	CTTATGTAAC	CTCTTGGTGA	AGGATTCCAA	1680
	ACCCTCACTC	ACCCATGTTA	TCCAGAACAG	TGTTTACAAA	GTCTTAGAAG	TTGTAAAGAA	1740
	ATGACTGCTA	CATGACCTGC	TGCCTACGGA	GAACCTACATC	TGTAATGGTT	TTAATGTTTT	1800
	GCTAAGTCAT	GTGTTGTGTA	TATCCCAAAA	ACTTTTATAG	GTAACCTGTT	TCAAATAGAA	1860
20	AACGTTTTAT	TTGTTCAATT	TGAAATGTCAT	TCTAATTATA	AAAATGACTT	ACACCTTTAT	1920
	CAATTGGTTA	CTATTTCAT	GCACCCCTTA	AAATTTGCTA	TGCAAAATGAG	TATATGCTTG	1980
	TACTTGACTT	TAATATTGTT	GCTAAAGTGA	GCAAAGCTAC	CTGTATAAAG	AAAACACAGT	2040
	GGGTTGTGAC	AAGGATGACA	TGAAAATACA	GGACAATTCT	GACAATGTAG	GGGCTGATTT	2100
	TATAGTGTAA	GAACATATAA	TGCCCTTTCG	TTCTTTTTTC	TGCCTCTTGC	TCTTGTCTTT	2160
25	TGGCATTTC	AGTGATTGTA	AGTTCCTCGG	TCATGTCAGC	CCCTGTCATC	AACTTGAGTT	2220
	ACAGTAGATG	GGGACAGCAT	GGAGTGTGTT	CTATATAAAA	CTATCTGTTT	GTTTACTTTC	2280
	CTTGTGCGCT	TTTTGTCTCT	TGTTCTCTTG	TTAATGAAGC	TTTTCCCTGC	CATTATTAAAT	2340
	CCAAACTCTT	GGACCTTGTG	GTTAGGAAAT	TCCCTTAACT	TCCAGCCATA	TGGCATTATC	2400
	GTGCTCTCTT	CTCTCTCTCT	CTTCTCTCTC	CTTCCCTCAT	TTTTCTGTCA		2460
30	AATAAGTACT	GTTTACTCAT	TTAGTTGCTT	ATCAAGTACT	TATCTTGGT	TTTAAAAAAA	2520
	ATTAATGGTA	ACTGTATTTT	TCTCATTTTT	AGCATTTATC	AAATGTTTAT	ATTTTAAATAC	2580
	CTTTAAACCA	CTTTAAAGTT	TTTTCATGTT	TAATTATAGT	TTAAGAAAAA	ACTATTTTGA	2640
	ACAACCCCAA	ATATAGTGCA	TCTAGAAACT	AATGTATATT	TGATTAGACA	TCATTTATAG	2700
	TGGAACAGTA	GACTGTAGTA	CATGGTAATT	TTTCTTTTAC	TATTAAGATA	CAATAAAACA	2760
35	TGACTAATTT	TGCTGTCAAA	AATGTAAAGA	ATAATGATAA	ATGGAGTTTT	TTATATTTTA	2820
	CTTTTAAAGT	TGCTGTCTTT	TAATAAGACA	AAGCCTTAAG	CCTTATGTTA	TAATTTTGGT	2880
	TCTAAAAACC	ATCATTTTCAG	TATAAGGAAT	AAGTATATTT	CGTCTCCTC	TTTAGTTTTT	2940
	TTCTTCTCTAT	TTATTTTAT	TTTGAAAAAT	TTCTACACCT	TCTTTGAATT	CCTTGTATGA	3000
	ATTTTGTGTT	CTTAGAAGTT	AATTTGTGTG	AAATGAGATT	CTTCAAAACG	ATGAAACCTC	3060
40	ATAGCTCTGA	GAAGAGGTTT	TAGGGTTTTA	AATCTAAGC	AAAGCGTGAC	TATGGCTGAC	3120
	AGACTACACA	CTTAATTATA	CAGCTTCTCT	TTCTTAACCA	CAGGCAGATT	AACCTCATTG	3180
	TGGATTGTCC	TTCAGACCTT	AGTCTCTCAG	CATGGTTTCT	GGTGCCCACT	CCTGGAAGCC	3240
	GCTGTTCCCT	TTCTACCTTC	TTACCAAGAG	CCAAGGGCAG	GCCTGGTCCC	GGGGAAGCAG	3300
45	CAGCTTGCTG	ACATAAGTCA	GCTGCAAGG	CTGAGGAGTG	TGCCCTCAGA	GAAGCACCGC	3360
	CCCCCAGTCT	TGTGCCAGCG	CCTAGAGCCG	CAGCTCCAG	GGATGCTCCT	TCCCTGGAGG	3420
	CAGCCCAAGG	GAGGAGCTCT	GGCAGCGTTC	TTCAGATTG	TGGCCACTGT	TTCTCATTG	3480
	CTGGTTGACT	GTTTTTATTT	CTTAGGCTTT	TGCTAGTTTT	AGAAAAATAGG	GAAGCAGCCC	3540
	TTGATTGTG	GATTAAGAGC	AACATTTGAG	CGATGATGCA	CAACAGTCCA	GGAAAAATGG	3600
	CGGTGGACAG	TTGAGGCTGA	GGATGGGAGT	TGACATGAGC	AGGGAGAGGG	AGGTGCGCGC	3660
50	TGCTTATCTG	TGATTGTGTC	TCACTTGAGT	GTGGCTGATT	GTGTACATCC	AGCAGTTACA	3720
	ATTTTAAAAA	ATTATACTTT	TACATTTIAT	TTATATTTTT	CTCACCCCCA	GTAATTTCTT	3780
	TCCAAAGAAG	TTACATGTGA	ATAAGTAGAA	ATTCTGTATA	GGAAAAAAGC	ATTAAAAATA	3840
	CTATTATAAC	TGCTTCATTT	GCTGGGAACC	ATTAAAAAGT	ATATAAATTA	GCTTTTCCCA	3900
	GAAGGATCCT	TTTGTAGCAG	TGTTTATGAA	TGTAACCCCC	AGCAAAATAT	GGCTATATAT	3960
55	TAGGGGAGCC	AGTTTGGAGC	AGAGGCTGGA	AGGTCCCTGC	TATGCAGCCG	TGGCCACAGC	4020
	TCGCAGCCCA	AGCAGCTGTG	AGCATCCACA	CCTTTGATGG	CAATGCAGAT	TGGTAGCAGG	4080
	TTCCATAGGC	GTACAAAACA	GTATTAAAGC	TCAGTGTGTT	GCATATTGTT	AGCATTTACA	4140
	AAATATTTTG	CTTTAGTATG	AGGAAAGTAA	GGATGGGCAA	AGAAGCGATC	AAAATAGCTA	4200
	TTGCTACAAC	ATTTTCGAAA	ACAAAGTTGG	GGCTGTATTT	CTTTAAAAAG	ATAAGCCTCT	4260
60	AAAAATGCTT	GGCAAAAAAA	ATATAGTGTG	AAAAATAGGC	AGTGATATTA	ATGAGAAAAAT	4320
	GAAAGTATGT	ATCAGGAATA	AAGTGATATT	GCATAGGAGT	ATTGTATTTT	TATGAATTTT	4380
	ATGCCAGTTG	TTTACATGTA	CTATATATGT	TAAATTAATA	AAAATCATGA	GAAATG	

Seq ID NO: 499 Protein sequence
Protein Accession #: BAA74900.1

	1	11	21	31	41	51	
70	PLVINTLKRF	NLYPEVILAS	WYRIYTKIMD	LIGIQTKICW	TVTRGEGLSP	IESCEGLGDP	60
	ACFYVAVIFI	LNGLMMALFF	IYGTLYSGSR	LGGLVTVLCP	FFNHGECTRV	MWTPPLRESP	120
	SYPFVLVQML	LVTHILRATK	LYRGLIALC	ISNVFFMLPW	QFAQFVLLTQ	IASLFAVYVV	180
	GYIDICKLRK	IYIHMISLA	LCFVLMFGNS	MLLTSYYASS	LVIIWGLIAM	KPHFLKINVS	240
	ELSLWVIQGC	PWLFGTIVLK	YLTSKIFGIA	DDAHIGNLLT	SKFFSYKDFD	TLTYTCAAEF	300
75	DFMEKETPLR	YTKTLLPVV	LVVFVAIVRK	IISDMWGLA	KQQTIVRHQ	FDHGLVYHA	360
	LQLLAYTALG	ILIMRLKFLP	TPHMCVMASL	ICSRQLFGWL	FCKVHPGAIV	FAILAAMSIQ	420
	GSANLQQTWN	IVGEFNLNPQ	EELIEWIKYS	TKPDVAFAGA	MPTMASVKLS	ALRPVNHHPH	480
	YEDAGLRART	KIVYSMYSRK	AAEEVKRELI	KLKVNYIYLE	ESWCVRRSKP	GCSMPFIWDV	540
	EDPANAGKTP	LCNLLVKDSK	PHFTTVFQNS	VYKVLVVEKE			

Seq ID NO: 500 DNA sequence
Nucleic Acid Accession #: NM_001276.1
Coding sequence: 127..1278

	1	11	21	31	41	51	
85	AGTGGAGTGG	GACAGGTATA	TAAAGGAAGT	ACAGGGCCTG	GGGAAGAGGC	CCTGTCTAGG	60
	TAGCTGGCAC	CAGGAGCCGT	GGGCAAGGGA	AGAGGCCACA	CCCTGCCCTG	CTCTGCTGCA	120

	GCCAGAAATGG	GTGTGAAGGC	GTCTCAAACA	GGCTTGTGG	TCCTGGTGCT	GCTCCAGTGC	180
	TGCTCTGCAT	ACAACTGGT	CTGCTACTAC	ACCAGCTGGT	CCCAGTACCG	GGAAGGCGAT	240
	GGGAGCTGCT	TCCAGATGC	CCTTGACCGC	TTCTCTGTA	CCCACATCAT	CTACAGCTTT	300
5	GCCAATATAA	GCAACGATCA	CATCGACACC	TGGGAGTGA	ATGATGTGAC	GCTCTACGGC	360
	ATGCTCAACA	CACTCAAGAA	CAGGAACCCC	AACCTGAAGA	CTCTCTTGTC	TGTGGGAGGA	420
	TGGAACCTTG	GGTCTCAAAG	ATTTTCCAAG	ATAGCCTCCA	ACACCCAGAG	TCGCGGAGCT	480
	TTCATCAAGT	CAGTACCGCC	ATTCTGCGC	ACCCATGGCT	TTGATGGGCT	GGACCTTGCC	540
	TGGCTCTACC	CTGGACGGAG	AGACAAACAG	CATTTTACCA	CCCTAATCAA	GGAATGAAG	600
10	GCCGAATTTA	TAAAGGAAGC	CCAGCCAGGG	AAAAAGCAGC	TCCTGCTCAG	CGCAGCACTG	660
	TCGTGGGGGA	AGGTCAACAT	TGACAGCAGC	TATGACATTG	CCAAGATATC	CCAACACCTG	720
	GATTTTCATTA	GCATCATGAC	CTACGATTTT	CATGGAGCCT	GGCGTGGGAC	CACAGGCCAT	780
	CACAGTCCCC	TGTTCCGAGG	TACGAGGAT	GCAAGTCTTG	ACAGATTGAG	CAACACTGAC	840
	TATGCTGTGG	GGTACATGTT	GAGGCTGGGG	GCTCCTGCCA	GTAAGCTGGT	GATGGGCATC	900
	CCCACTTCG	GAGGAGCTT	CACCTGGCT	TCTTCTGAGA	CTGGTGTGG	AGCCCCAATC	960
15	TCAGGACCGG	GAATTCACAG	CCGGTTCACC	AAGGAGGCAG	GGACCCCTGC	CTACTATGAG	1020
	ATCTGTGACT	TCCTCCGCGG	AGCCACAGTC	CATAGAACCC	TCGGCCAGCA	GGTCCCCTAT	1080
	GCCACCAAGG	GCAACCAAGT	GATAGGATAC	GACGACCAAG	AAAGCGTCAA	AAGCAAGGTG	1140
	CAGTACCTGA	AGGATAGGCA	GCTGGCAGGC	GCCATGGTAT	GGGCCCTGGA	CCTGGATGAC	1200
20	TTCCAGGGCT	CCTTCTGCGG	CCAGGATCTG	CGCTTCCCTC	TCACCAATGC	CATCAAGGAT	1260
	GCACCTGCTG	CAACGTAGCC	CTCTGTTCTG	CACACAGCAC	GGGGGCCAAG	GATGCCCGT	1320
	CCCCCTCTGG	CTCCAGCTGG	CCGGGAGCCT	GATCACCTGC	CCTGCTGAGT	CCCAGGCTGA	1380
	GCCTCAGTCT	CCCTCCCTTG	GGGCCTATGC	AGAGGTCCAC	AACACACAGA	TTTGAGCTCA	1440
	GCCTCTGTGG	GAGGAGAGGT	AGGGATGGGG	CTGTGGGGAT	AGTGAGGCAT	CGCAATGTAA	1500
25	GACTCGGGAT	TAGTACACAC	TTGTTGATGA	TTAATGGAAA	TGTTTACAGA	TCCCCAAGCC	1560
	TGGCAAGGGA	ATTTCTTCAA	CTCCCTGCCC	CCTAGCCCTC	CTTATCAAAG	GACACCATTT	1620
	TGGCAAGCTC	TATCAACAAG	GAGCCAAACA	TCCTACAAGA	CACAGTGACC	ATACTAATTA	1680
	TACCCCTGTC	AAAGCCAGCT	TGAAACCTTC	ACTTAGGAAAC	GTAATCGTGT	CCCCTATCCT	1740
	ACTTCCCTCT	CCTAATTCCA	CAGCTGCTCA	ATAAAGTACA	AGAGTTTAAAC	AGTGTGTTGG	1800
30	CGCTTTGCTT	TGCTCTCATC	TTGAGCGCCC	ACTAGACCCA	CTGGAATCAC	CTCCCCATC	1860
	TCCTCTGGGT	TCCTTCTCT	GAGCCTTGGG	ACCCCTGAGC	TTGAGAGAT	GAAGGCCGCC	1920
	ATGTT						

Seq ID NO: 501 Protein sequence
Protein Accession #: NP_001267.1

35	1	11	21	31	41	51	
	MGVKASQTGF	VVLVLLQCCS	AYKLVCYYTS	WSQYREGDGS	CFPDALDRFL	CTHIIYSFAN	60
40	ISNDHIDTWE	WNDVTLYGML	NTLKNRNPNL	KTLLSVGGWN	PGSQRFSKIA	SNQSRRTFI	120
	KSVPPPLRTH	GFDGLDLAWL	YPRRDQKHQF	TTLIKEMKAE	FIKEAQPGKK	QLLLSALSA	180
	GKVTIDSSYD	IAKISQHLDF	ISIMTYDFHG	AWRGTTGHHS	PLFRGQEDAS	PDRFSNTDYA	240
	VGMYLRLGAP	ASKLVMIPT	FGRSFTLASS	ETGVGAPISG	PGIPGRFTKE	AGTLAYEIC	300
	DFLRGATVHR	TGQQQVPYAT	KGNQWVGYYD	QESVSKSVQY	LKDRQLAGAM	VWALDLDDFQ	360
45	GSFCGQDLRF	PLTNAIKDAL	AAT				

Seq ID NO: 502 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

50	1	11	21	31	41	51	
	GCTGCCTAGG	GTCTGGAAAG	CTCGGGCACC	CTCCCTCTCC	GGGGCTCCTG	CTCCCACCCC	60
	TCCGGCCCCC	CACCGTCCG	GCTCCTCCAG	GCTGGGCTCG	TGGCCGCGGT	GCTTTTAATT	120
55	TTCCCCCAGC	TCAGAATCTT	GCTGCTCGGC	CCCCAGGAGA	GCAACAACTC	AACGGGAACG	180
	ATGTGGAAGG	TGTCACTCT	GCTCTTCGTT	TTGGGAAGCG	CGTCGCTCTG	GGTCTGGGCA	240
	GAAGGAGCCA	GCACAGGCCA	GCCAGAAGAT	GACACTGAGA	CTACAGGTTT	GGAAGGCGGC	300
	GTTGCCATGC	CAGGTGCCGA	AGATGATGTG	GTGACTCCAG	GAACCAGCGA	AGACCGCTAT	360
	AAGTCTGGCT	TGACAACTCT	GGTGGCAACA	AGTGTCAACA	GTGTAACAGG	CATTGCGATC	420
60	GAGGATCTGC	CAACTTCAGA	AAGCAAGTC	CACGCGCAAG	AACAAAGTCC	AAGCGCCACA	480
	GCCTCAAACG	TGGCCACCAG	TCACTCCACG	GAGAAAGTGG	ATGGAGACAC	ACAGACAACA	540
	GTTGAGAAAG	ATGGTTTGTC	AACAGTGACC	CTGGTTGGAA	TCATAGTTGG	GGTCTTACTA	600
	CCCATCGGTT	TCATTGGTGT	AATCATCGTT	GTGGTTATGC	GAAAAATGTC	GGGAAGGTAC	660
	TCGCCCTAAA	GAGCTGAAGG	GTTACGCCCT	GCTTGCCAAC	GTGCTTTAAA	AAAAGACCGT	720
65	TTCTGACTCT	GTGGCCCTGT	CCCTGAGCTC	GTGGGGAGAA	GATGACCCCTG	GGAACATTTG	780
	CGGGCCCATC	CAGATTCCAC	GGTGACTTTC	CGTTTGCCAA	ATTAACCGAG	GAAAGACCTT	840
	TCACCAGATT	TGTTCTTTAA	ACTTT				

Seq ID NO: 503 Protein sequence
Protein Accession #: NP_006465.1

70	1	11	21	31	41	51	
	MWKVSALLFV	LGSASLWVLA	EGASTGQPED	DTETTGLEGG	VAMPGAEDDV	VTPGTSEDYR	60
75	KSLGTLTVAT	SVNSVTGIRI	EDLPTSESTV	HAQEQSPSAT	ASNVTASHST	EKVDGDTQTT	120
	VEKDGLSTVT	LVGIIVGVLL	AIGFIGGIIV	VVMRKMSGRY	SP		

Seq ID NO: 504 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

80	1	11	21	31	41	51	
	CACTGCTCTG	AGAATTGTG	AGCAGCCCCCT	AACAGGCTGT	TACTTCACTA	CAACTGACGA	60
85	TATGATCATC	TTAATTTACT	TATTTCTCTT	GCTATGGGAA	GACACTCAAG	GATGGGGATT	120
	CAAGGATGGA	ATTTTTCATA	ACTCCATATG	GCTTGAACGA	GCAGCCGGTG	TGTACCACAG	180
	AGAAGCACGG	TCTGGCAAAAT	ACAAGCTCAC	CTACGCAGAA	GCTAAGGCGG	TGTGTGAATT	240
	TGAAGGCGGC	CATCTCGCAA	CTTACAAGCA	GCTAGAGGCA	GCCAGAAAAA	TTGATTTC	300

5
10
15
20

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TGCTGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATG TGAAGCCAGG 360
GCCCCAAGT GGAATTGGAA AACTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
TGAAGATGG GATGCTTATT GCTACAACCC ACACGCAAGG GAGTGTGGTG GCGTCTTTAC 480
AGATCCAAAG CAATATTTTA AATCTCCAGG CTTCACAAAT GAGTACGAAG ATAACCAAAT 540
CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTAGATTT 600
TGACCTTGAA GATGACCCAG GTTGCTTGCC TGATTATGTT GAAATATATG ACAGTTACGA 660
TGATGTCCAT GGCCTTGTGG GAAGATACG TGGAGATGAG CTTCAGATG ACATCATCAG 720
TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
CCAAATCAA TATGTTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAAG 840
TACTACTCT ACTGGAATA AAAACTTTT AGCTGGAAGA TTAGCCACT TATAAAAAA 900
AAAAAAGGA TGATCAAAC ACACAGTGT TATGTTGAA TCTTTTGAA CTCCTTTGAT 960
CTCACTGTTA TTATTACAT TTATTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020
TAGGGAATA TGGAATAAT AGGAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
ACTGCATAGA AATAACAAGC GTTAACATT TCATATTTT TTCTTTCAGT CATTTTCTA 1140
TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTGCGT TTGAAATTT GGAATCCGTC 1200
TCTATGTACA GTTTGTATT ATACTTTTA AATCTTGAAC TTTATAACA TTTTCTGAAA 1260
TCATTGATTA TTCTACAAA ACATGATTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
TGTTTTATGC ATTATTAAAG CCTGCTCTA TTGTTGGAAT TTCAGGTCAT TTTCATAAAT 1380
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Seq ID NO: 505 Protein sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
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EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCQPGKGTI IDYGIRLNRS 120
ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
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Seq ID NO: 506 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

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GGGGATTCAA GGATGGAATT TTTCATAACT CCATATGGCT TGAACGAGCA GCCGGTGTGT 180
ACCAACAGAGA AGCACGGTCT GGCATAATACA AGCTCACCTA CGCAGAAAGCT AAGGCGGTGT 240
GTGAATTGGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG 300
GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360
AGCCAGGGCC CAATCTGGAC TTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA 420
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GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
GAGGTTTCCA AATCAAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840
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CTGTCTCTAT GTACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTT 1260
TGAAATCATT GTATTATCTA CAAAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320
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Seq ID NO: 507 Protein sequence
Protein Accession #: NP_009046.1

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ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
QIKYVAMPDV SKSSQKNTS TTSTGNKNFL AGRFSLH

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Seq ID NO: 508 DNA sequence
Nucleic Acid Accession #: NM_001044.1
Coding sequence: 129..1991

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GTGTGCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCCGG 180
CTAAGGAGCC CAATGCCGTG GGGCCGAAGG AGGTGGAGCT CATCTTGTG AAGGAGCAGA 240
ACGGAGTGCA GCTCACCAGC TCCACCCTCA CCAACCCGCG GCAGAGCCCC GTGGAGGCCC 300
AGGATCGGGA GACCTGGGCG AAGAAGATCG ACTTCTCTCT GTCCGTCAAT GGCTTTGCTG 360
TGGACCTGGC CAACGTCTGG CGGTTCCCTT ACCTGTGCTA CAAAAATGGT GCGCGTGCCT 420

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	TCCTGGTCCC	CTACCTGCTC	TTTCATGGTCA	TTGCTGGGAT	GCCACTTTTC	TACATGGAGC	480
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	TGAAAGGTGT	GGGCTTCACG	GTTCATCCTCA	TCTCACTGTA	TGTGGGCTTC	TTCTACAACG	600
5	TCATCATGCG	CTGGGCGCTG	CACATATCTCT	TCTCCTCCTT	CACCACGGAG	CTCCCCTGGA	660
	TCCACTGCAA	CAACTCTCTG	AACAGCCCCA	ACTGCTCGGA	TGCCCCATCT	GGTGACTTCA	720
	GTGGAGACAG	CTCGGGCCTC	AACGACACTT	TTGGGACCAC	ACCTGCTGCC	GAGTACTTTG	780
	AACGTGGCGT	GCTGCACCTC	CACCAGAGCC	ATGGCATCGA	CGACCTGGGG	CCTCCGCGGT	840
	GGCAGCTCAC	AGCCTGCGTG	GTGCTGGTCA	TCGTGCTGCT	CTACTTCAGC	CTCTGGAAGG	900
10	GGGTGAAGAC	CTCAGGGAAG	GTGGTATGGA	TCACAGCCAC	CATGCCATAC	GTGGTCTCTCA	960
	CTGCCCTGCT	CCTGCGTGGG	GTACCCCTCC	CTGGAGCCAT	AGACGGCATC	AGAGCATACC	1020
	TGAGCGTTGA	CTTCTACCGG	CTCTGCGAGG	CGTCTGTTTG	GATTGACGCG	GCCACCCAGG	1080
	TGTGCTTCTC	CCTGGGCGTG	GGGTTCGGGG	TGCTGATCGC	CTTCTCCAGC	TACAACAAGT	1140
	TCACCAACAA	CTGCTACAGG	GACGCGATTG	TCACCACCTC	CATCAACTCC	CTGACGAGCT	1200
15	TTCTCTCCGG	CTTCTGCTGC	TTCTCCTTCC	TGGGGTACAT	GGCACAGAAG	CACAGTGTGC	1260
	CCATCGGGGA	CGTGGCCAAG	GACGGGCCAG	GGCTGATCTT	CATCATCTAC	CCGGAAGCCA	1320
	TGCCCACGCT	CCCTCTGTCC	TCAGCCTGGG	CCGTGGTCTT	CTTCATCATG	CTGCTCAGCC	1380
	TGGGTATCGA	CAGCGCCATG	GTGGTATGGA	AGTCAGTGAT	CACCGGGCTC	ATCGATGAGT	1440
	TCCAGCTGCT	GCACAGACAC	CGTGAGCTCT	TCACGCTCTT	CATCGTCTGT	GCGACCTTCC	1500
20	TCCTGTCCCT	GTCTGCGCTC	ACCAACGGTG	GCATCTACGT	CTTCACGCTC	CTGGACCATT	1560
	TTGCAGCCCG	CACGCTCCAT	CTCTTTGGAG	TGCTCATCGA	AGCCATCGGA	GTGGCCTGGT	1620
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	TGTAATGGCG	GCTGTGCTGG	AAGCTGGTCA	GCCCTGTGTT	TCTCCTGTTC	GTGGTCTGTG	1740
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25	ACGCGCTGGG	CTGGGTCTAT	GCCACATCTT	CCATGGCCAT	GGTGCCCATC	TATGCGGCCT	1860
	ACAAGTTCTG	CAGCCTGCGT	GGGTCTCTTC	GAGAGAAACT	GGCCTACGCC	ATTGCACCCG	1920
	AGAAGGACCG	TGAGCTGGTG	GACAGAGGGG	AGGTGCGCCA	GTTCAACGCT	CGCCACTGGC	1980
	TCAGGTGTGA	GAGGGAGCAG	AGACGAAGAC	CCCAGGAAGT	CATCTGCAA	TGGGAGAGAC	2040
	ACGAACAAAC	CAAGGAAATC	TAAGTTTCGA	GAGAAAGGAG	GGCAACTTCT	ACTCTTCAAC	2100
30	CTCTACTGAA	AACACAAACA	ACAAAGCAGA	AGACTCCTCT	CTTCTGACTG	TTTACACCTT	2160
	TCCGTGCCGG	GAGGCGACCT	CGCCGTGTCT	TGTGTTGCTG	TAATAACGAC	GATGATCTGT	2220
	GCAGCGAGGT	CCACCCCGTT	GTGTGCTCTG	CAGGGCAGAA	AAACGTCTAA	CTTCATGCTG	2280
	TCGTGTGAG	GCTCCTCTCC	TCCCTGCTCC	CTGCTCCCGG	CTCTGAGGCT	GCCCAGGGG	2340
	CACGTGTGTT	TCAGGCGGGG	ATCAGCATCC	TTGTAGACGC	ACCTGCTGAG	AATCCCGGTG	2400
35	CTCACAGTAG	CTTCTAGAC	CATTTACTTT	GCCCATATTA	AAAAGCCAAG	TGCTCTGCTT	2460
	GGTTTAGCTG	TGCAGAAGGT	GAAATGGAGG	AAACCAAAA	TTTCATGAAA	GTCTTTTCCC	2520
	GATGCGTGGC	TCCCAGCAGA	GGCCGTAAAT	TGAGCGTTCA	GTTGACACAT	TGCACACACA	2580
	GTCTGTTTCA	AGGCATTGGA	GGATGGGGGT	CCTGGTATGT	CTCACCAGGA	AATTCTGTTT	2640
	ATGTTCTTGC	AGCAGAGAGA	AATAAACTC	CTTGAAACCA	GCTCAGGCTA	CTGCCACTCA	2700
40	GGCAGCTGT	GGGTCTTGT	GGTGTAGGGA	ACGGCCTGAG	AGGAGCGTGT	CCTATCCCCG	2760
	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	GACGCATGCA	GGGCCCCCAC	2820
	AGGAGCATGT	CCTATCCCTG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCCGG	2880
	AACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCCGG	GACGCATGCA	GGGCCCCCAC	2940
	TGAGCGTGT	ACTACCCCGG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCGGACGC	ATGCGAGGAG	CCCAAGGAG	CGTGTACTAC	CCCAAGGAGC	ATGCGAGGAG	3060
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	CCCAAGGAGC	ATGCGAGGAG	CCCAAGGAGC	ATGCGAGGAG	CGTGTACTAC	CCCAAGGAGC	3180
	TGAGCGTGT	ACTACCCCGG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	3240
	CATCAATAAC	AACAGTTTTT	ATGTTTGGCA	ATGGCTTTTT	AAAATCATAT	TTACCTGTGA	3300
50	ATCAAAACAA	ATTCAAGAA	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTTTG	3360
	TTTCAAGAAA	TAATAGTCAA	TACTAGTGA	AGGATGTTGG	CCAAAAGCTG	CTTTCCATGG	3420
	CACACTGCCC	TCTGCCACTG	ACAGGAAAGT	GGATGCCATA	GTTTGAATTC	ATGCCTCAAG	3480
	TCGGTGGGCC	TGCCTACGTG	CTGCCGAGG	GCAGGGGCGG	TGCAGGGCCA	GTCATGGCTG	3540
	TCCCTGCAA	GTGGACGTGG	GCTCCAGGGA	CTGGAGTGTA	ATGCTCGGTG	GGAGCCGTCA	3600
55	GCCTGTGAAC	TGCCAGGCAG	CTGCAGTTAG	CACAGAGGAT	GGCTTCCCCA	TTGCCTTCTG	3660
	GGGAGGGACA	CAGAGGACGG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAGTC	AGCACAGAGA	3720
	GCGGCTTCCC	CATTGCTTTC	TGGGAGGGA	CACAGAGGAC	AGTTTCCCCA	TGCGCTTCTG	3780
	GTGTGTTAAG	ACAGCACAGA	GAGCGGCTTC	CCCATCGCCT	TCTGGGGAGG	GGCTCCGTGT	3840
	AGCAACCCAG	GTGTGTGCTG	TGTCTGTGTA	CCAATCTCTA	TTCAGCATCG	TGTGGGTCCC	3900
60	TAAGCACAAT	AAAAGACATC	CACAATGGAA	AAAAAAAAG	GAATTC		

Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

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	ETWKKIDFL	LSVIGFAVDL	ANVWRFPYLC	YKNGGGAFLV	PYLLFMVIAG	MPLPFYMEAL	120
	GQFNREGAAG	VWKICPILKG	VGFTVILISL	YVGFFYNVII	AWALHYLFSS	FTTELPWIHC	180
70	NNSWNSPNC	DAHPSDSSGD	SSGLNDTFGT	TPAAEYFERG	VLHLHQSHGI	DDLGPWRWL	240
	TACLVLVIVL	LYFSLWKGVK	TSGKVWVITA	TMPIVVLTA	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV	WIDAATQVCF	SLGVGFGLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
	GFVVFSLFLY	MAQKHSVPIG	DVAKDGPGLI	PIIYPEAIAT	LPLSSAWAVV	FFIMLLTLGI	420
	DSAMGMESV	ITGLIDEFQL	LHRHRELFTL	FIVLATFLLS	LFCVTNGGIY	VFTLLDHFAA	480
75	GTSILFGLI	EAIGVAVFYG	VGFSDDIQQ	MTGQRPSLYW	RLCWKLVSFC	FLFVIVVSI	540
	VTFPPHYGA	YIFPDWANAL	GWVIATSSMA	MVPIYAAKYP	CSLPGSPREK	LAYAIAPKED	600
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Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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	CTGTCACTGC	GCTTCTGAT	GCTGTCCAT	CCCCAGAGGT	TGCCCGGAT	GCAGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGA	GATGACCCAC	TGGCGAGGA	GGATCTGCC	240

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 CGCCCTTGGC CCGGGGTGTC CCCAGCCTGC GCGGGCGGCT TCCAGTCCCC GGTGGATATC 540
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Seq ID NO: 511 Protein sequence
 Protein Accession #: NP_001207.1

1 11 21 31 41 51
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 DPQEPQNNAH RDKEGDDQSH WRYGGDPWP RVSPACAGRF QSPVDIRPQL AAPCPALRPL 180
 ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGRY RALQLHLHWG AAGRPGSEHT 240
 VEGHRFPAEI HVVHLSTAFR RVDEALGRPG GLAVLAAFLB EGPEENSAYE QLLSRLBEIA 300
 EEGSETQVPG LDISALLPSD FSRYPQYEGS LTPPCAQGV INTVFNQVIM LSAQLHLTSL 360
 DTLWGPDSR LQLNFRATQP LNRGVIBASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
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Seq ID NO: 512 DNA sequence
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 CTGTGTTCTG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTGGA 3360
 AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTCGTCTGGT GGAGCCAGCC 3420
 15 AGTGGCAGAA TCTTTATTGA TGAGGTGGAT ATCTGCATTC TCAGCTTGGG AGACCTCAGA 3480
 ACCAAGCTCA CTGTGATCCC ACAGGATCCT GTCCTGTTTG TAGGTACAGT AAGGTACAA 3540
 TTGGATCCCT TTGAGAGTCA CACCGATGAG ATGCTCTGGC AGGTCTGGA GAGAACATTC 3600
 ATGAGAGACA CAATAATGAA ACTCCAGAA AAATTACAGG CAGAAGTCAC AGAAAATGGA 3660
 GAAAACTTCT CAGTAGGGGA ACGTCAGCTG CTTTGTGTGG CCCGAGCTCT TCTCCGTAAT 3720
 20 TCAAAGATCA TTCTCCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGAC TGACACCTG 3780
 GTTCAGAAAC CCATCAAAGA TGCCTTCAAG GGCTGCACTG TGCTGACCAT CGCCACCGC 3840
 CTCACACAG TTCTCAACTG CGATCACGTC CTGGTTATGG AAAATGGGAA GGTGATTGAG 3900
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 GCAGAAGTCA GATTGTAG

25 Seq ID NO: 513 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 30 MVGEGPYLIS DLDQRGRRRS FAERYDPSLK TMIPVRPCAR LAPNPVDDAG LLSFATPSWL 60
 TPVMVKGYRQ RLTVDTLPPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVKPQR 120
 TRVLMDIVAN ILCIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEFTKVFFW 180
 ALAWAINYRT AIRLKVALLST LVFENLVSEK TLTHISVGEV LNILSSDSYS LFEAALFCPL 240
 35 PATIPILMFV CAAYAFFILG PTALIGISVY VIFIPVQMF AKLNSAFRRS AILVTDKRVQ 300
 TMNEFLTICR LTKMYAWEKS FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360
 TLSCHILLRR KLTAPVAFSV IAFNVMKFS IAILPFSSIA MAEANVSLRR MKKILIDKSP 420
 PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNK RHLCKQRSE AYSESPPAK 480
 40 GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSKAD 540
 KDESRLRLTW PQEVDRTORA AKYLKILGI CGNVGSGKSS LLAALLGQM LQKGVVAVNG 600
 TLAYVSQQA IFHGNVRENI LFGKYDHQR YQHTVRVCG LKDLNLDPY DLTETGERGL 660
 NLSGGQRQRI SLARAVYSR QLYLLDDPLS AVDAHVGKHV FECCIKTTLR GKTVVLVTHQ 720
 LQPLESCDEV ILLEGEICE KGTHELMEE RGRYAKLIHN LRGLQFKDPE HLYNAAMVEA 780
 FKESPAEREE DAGIIGYLLS LFTVFLFLM IGSAAFSNWW LGLWLDKGSR MTCGPQGNRT 840
 45 MCEVGAFLAD IQGHVYQWVY TASMVFLVF GVTKGFFVTK TTLMASSSLH DTVFDKILKS 900
 PMSFFDTTPT GRLMNRFSKD MDELDRVLEF HAENFLQOFF MVVFILVILA AVFPAVLLV 960
 ASLAVGFFIL LRIPHRGVEE LKKVENVSRS PWFTHITSSM QGLGIHAYG KKESCITYTS 1020
 SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKWD 1080
 50 PSCGEITFRD YQMRVDRNTP LVLDLNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140
 SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTVRYN LDPFESHTDE MLWQVLETF 1200
 MRDTIMKLPE KLAQEVTEENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMSDKTDL 1260
 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGKIVIE FDKPEVLAEK PDSAFAMLLA 1320
 AEVRL

55 Seq ID NO: 514 DNA sequence
 Nucleic Acid Accession #: Z31560
 Coding sequence: 1-966

1 11 21 31 41 51
 60 CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCGCGG CCCGCAGCAA 60
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 AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CGGCGACGG 180
 CGCAAGATGG CCCAGAGAAA CCCCAAGATG CACAACTCGG AGATCAGCAA GCGCCTGGGC 240
 65 GCCGAGTGA AACTTTTGTG GGAGACGGAG AAGCGGCGGT TCATCGACGA GGCTAAGCGG 300
 CTGGAGCGCG GCGCGAGGAT GGAGCAACCG GATTATAAAT ACCGGGCCCC GCGGAAAAAC 360
 AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGCG GGTGCTGGC CCCCGGCGG 420
 AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCCGCGCTGG GCGCGGCGGT GAACCAAGCG 480
 ATGGACAGTT ACGCGCACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC 540
 70 CAGCTGGGCT ACCCGCAGCA CCCGGGCTC AATGCGCAGC GCGCAGCGCA GATGCAGCCC 600
 ATGCACCGCT ACGACGTGAG CGCCCTGCAG TACAACTCCA TGACCAAGCTC GCAGACCTAC 660
 ATGAACGGCT CGCCCACTCA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT 720
 CTTGGCTCCA TGGGTTCCGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCC TGTGTTTACC 780
 TCTTCTCCC ACTCCAGGGC GCCCTGCCAG GCCGGGGACC TCCGGGACAT GATCAGCATG 840
 75 TATCTCCCGC GCGCGAGGAT GCGGGAACCC GCGGCCCCCA GCAGACTTCA CATGTCCAG 900
 CACTACCAGA GCGGCGCGGT GCCCGGCACG GCCATTAAAC GCACACTGCC CCTCTCACAC 960
 ATGTGAGGGC CGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAAGAAAA ACGAGGGAAA 1020
 TGGGAGGGGT GCAAAGAGG AGAGTAAGAA ACAGCATGGA GAAACCCGG TACGCTCAAA 1080
 AAAAA

80 Seq ID NO: 515 Protein sequence
 Protein Accession #: CAA83435

1 11 21 31 41 51
 85 HSARMYNMME TELKPPGPQQ TSGGGGNGST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR 60
 RKMAQENPKM HNSETSKRLG AEWKLLSETE KRPFIDEAKR LRLAHMKHEP DYKVRPRRT 120
 KTLMKDKYT LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGSYSMMQD 180

QLGYPOHPGL NAHGAQMOP MHRVDVLSAQ YNSMTSSQTY MNGSPTYSMS YSQQGTGMA 240
 LGSMGSSVVK EASSSPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAEPPEP AAPSRHMSQ 300
 HYQSGFVPGT AINGTLPLSH M

5 Seq ID NO: 516 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29..541

10 1 11 21 31 41 51
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 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAAGAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTTCT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 15 TCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGT GCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GGCTTTAGCT TGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAAT CCTTATATTC TGAACGCGCA 480
 20 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTATTAT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTG TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAA TAAATCTAAA 720
 TCTTCAAAA AAAAAAATAA AAATGGGGCC GCAATT

25 Seq ID NO: 517 Protein sequence
 Protein Accession #: AAB50564

30 1 11 21 31 41 51
 MMAGMKIQLV CMLLLAFSSW SLCSDEEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNVLNS PAETGEVHE EELVARRKLP TALDGFSLA MLTIYQLHKI CHSRAFQHWE 120
 LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY

35 Seq ID NO: 518 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109..2940

40 1 11 21 31 41 51
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 AGCATTGCAG GTCTATTGTC CAACCTGAAG TTTGTGACTC TCCTGGTTCG CTTAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAGACA ATGGGTATAA TGGATTGCTC 240
 45 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG 300
 ATAAGTAAAG CTTCATTTTA CCTATTAAAT GCTACCAAGA GAAGAGTATT TTTAGAAAT 360
 ATAAAGATT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGCATAATGT GAATGGTACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCTTAC AATACAGAGG GTGTGGAAAA GAGGGAAAT ACATTCATTT CACACCTAAT 540
 50 TTCTACTGTA ATGATAACTT AACAGCTGGC TACGATCAC GAGGCCGAGT GTTGTGCCAT 600
 GAATGGGCCC ACCTCGTGTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTCTAC 660
 ATAAATGGGC AAAATCAAT TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGGTCTTGG CCCCAGAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTCACT TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 55 AGTTTATCTT CTGTGGTTGA ATTTTGTAA GCAAGTACCC ACAACCAAGA AGCACCAAC 900
 CTACAGAAC AGATGTGCAG CCTCAGAAAT GCATGGGATG TAATCAGAGA CTCTGCTGAC 960
 TTTTACACCA GCTTTCCCAT GAGCTTCCAC CTCCTCCAC ATTCTCGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGAG TCCTTCAACT ACAACAGGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA 1140
 60 ATTCTACCT TCGTGGGCTA TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCAGGATA 1200
 CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCAGTGA 1260
 TCAGCTAAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTGTA GGTGGTTGAA 1320
 AAATCGAATG GAAAGCTTGA TGGCTCTGTG ATGATATTAG TGACAGCGG AGATGATAAG 1380
 CTTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCATTGCC 1440
 CTGGGTTTAT CTGACGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
 65 TTCTTTGTTT CAGATATATC AAATCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTC 1560
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 AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
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 70 GGACGAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
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 75 GAGCCAGAGA CTGGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
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 80 CCACATGCA AATATTGA CTTGGAAGCT GTAAAAGTAG AAGAGGAAT GACCCTATCT 2460
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 85 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700
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 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
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 TCATTAGATT ACTTTGATTA ATTTTCTTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG 3360
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Seq ID NO: 519 Protein sequence
 Protein Accession #: NP_006527.1

1 11 21 31 41 51
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 GDDPYTLQYR GCGKEGKYIH FTFNPLNDN LTAGYGSRRG VVHEWAHLR WGVFDEYNND 180
 KPFYINGQNO IKVTRCSSDI TGFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
 MFMQSLSSVV EPCNASTHNQ EAPNLQNMCM SLRSADWVIT DSADPHHSFP MNGTELPPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAEPYLM QIVEIHTFVG IASFDSKGEI 360
 RAQLHQINSN DDRKLIVSVL PTTVSAKTDI SICSLKKGF EVVEKLNGKA YGSVMILVTS 420
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLELSRLT GGLKFFVPDI SNSNSMIDAF 480
 SRISSTGDI FQHQLLEST GENVKPHQL KNTVTVDNTV GNDTFLVTV QASGPPEIIL 540
 FDPDGRKYIT NNFITNLTPR TASLWIPGTA KPGHWYTLN NTHSLQALK VVTSRASNS 600
 AVPPATVEAF VERDSLHFFH PVMYANVKQ GFYPILNATV TATVEPETGD PVTLRLDDG 660
 AGADVIKNDG IYSRYFFSFA ANGRYSLVKH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
 IQMNAPRKSV GRNBEERKNG FSRVSSGGSF SVLGVPAGPH PDVFPPCKII DLEAVKVEE 780
 LTLSWTAPGE DFDQQAQSY EIRMSKSLQN IQDDFNAIL VNTSKRNPOQ AGIREIFTFS 840
 PQISTNGPEH QNNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
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Seq ID NO: 520 DNA sequence
 Nucleic Acid Accession #: NM_000228.1
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1 11 21 31 41 51
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 CTGTGTTGGA GAGCCCGGT TCTCCGAGCT TCATCTACCT GTGGACTGAC CAAGCCTGAG 240
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 CCTCCAGCG CCTACTATGC TGTGTCCAG CTCCGTCTGC AGGGGAGCTG CTTCTGTCTC 840
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Seq ID NO: 521 Protein sequence
 Protein Accession #: NP_000219.1

1 11 21 31 41 51
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 MEFGQMPAG MEPIERSDFG KTWVYQYLA ADCTSTFPV RQGRPSWQD VRCQSLPQR 180
 NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYVA 240
 VSQLRLQGSC FCHGHADRC PKPGASAGPS TAVQVHDCV CQHNTAGPNC ERCAFFYNR 300
 PWRPAEQDA HECQRCDNG HSETCHFDPA VFAASQAGY GVCNCRDHT EGKNCERCQL 360
 HYFRNRPGA SIQETCISCE CDPDGAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420
 TYANPQGCHR CDCNIGSRR DMPCDEESGR CLCLPNVVG KCDQCAPYHW KLASGQCEP 480
 CACDPHNSPQ PTVQPVHRAV PCREGFGLM CSAAAIRQCP DRTYGDVATG CRACDCFRG 540
 TEGFGCDKAS GRCLCRPGLT GPRCDQCRG YCNRYPCVA CHPCFQTYDA DLREQALRF 600
 LRLRNATASLW SGPGLLEDRGL ASRILDAKSK IEQIRAVLSS PAVTEQEVQ VASAILSLR 660
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Seq ID NO: 525 Protein sequence
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Seq ID NO: 527 Protein sequence
 Protein Accession #: NP_077741.1

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	GAAGCGCCAT	TTGCTAGAGA	TATTTCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGGTTACA	1440
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	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGA	CCCAAACTAC	CAACAACTCT	2340
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25	GAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
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	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTAAAAAT	TGCATCGATG	TAATCAGAAT	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
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30	AATAATTGG	AACCCAAAT	TATTACATTA	GCAGAAGCAT	GCACAAAGAG	ATAATGTCTC	2760
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75	CTAGTGCCGA	TAAACTTTCT	CAAGAGCAAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
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	ATTAAAAAGTA	TTAGAAGGTG	GTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180

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Seq ID NO: 529 Protein sequence
 Protein Accession #: NP_001932.1

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 Coding sequence: 115..2223

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TAAAGCATT GCAACAGTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
AAATACAAAA ATGAGCTGGG CTGTGTGGCG CGCACCTGTA GTCCCAAGTA CTGGGAGGC 2460
TGAGGCAGGA GAATCGCTTG AATCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
ACTGCACTCT AGTCTGGCAA CAGAGCAAGA CTCCATCTCA AAAAGAAAAG AAAAGAGAGC 2580
TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
AACTTTAATG AACTAACTGA CAGCTTCATG AAATGTGCTA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTTCTTA AATGTCTTGT 2760
TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTTACAG CAATTTGATA 2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
AGACTGGGA AACTATTCTA GAATATTATG ATGTATGGT AATATAGTTA TTGCACAAGT 2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

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Seq ID NO: 533 Protein sequence
Protein Accession #: NP_004354.1

45
50
55
60

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1 11 21 31 41 51
| | | | |
MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEKGE VLLLVHNLPO 60
HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGPF 120
TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWV 180
NNQSLPVSFR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP 240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGTFQQS TQELFIPNIT VNNSGTYTCQ 300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVWNN 360
QSLPVSFRLQ LSNDRNLTLL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGPDPTI 420
SPSYTYRPG VNLSSLCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
NSASGHSRRT VKTITVSABL KPSSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
PDSSYLSGAN LNLCHSASN PSPQYSWRIN GIPQHTQVL FIAKITPNNN GTYACFVSNL 660
ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGA LI

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Seq ID NO: 534 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

65
70
75
80

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1 11 21 31 41 51
| | | | |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCTGTTGC TTCCAGGGCC TGCTGATTTT 60
TGAAATGTG ATTATTGGTT GTTGGCGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTCTATC TGATGTTTAT 300
AGTATATGCC TTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
ACCAACCTCT TTCTGGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GGCCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
TGAGAATAAT TTCTGTAAGC ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCTCTC AACCTGGAGG CTGTGAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CTGGTGTGAG 720
ATTTGCCATT CTCTGCTGGA CTTTGTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA

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Seq ID NO: 535 Protein sequence
Protein Accession #: NP_008883.1

85

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1 11 21 31 41 51
| | | | |

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MAKDNSTVRC FQGLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAHW 60
 IGIFVIGICLP CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFPTPNL 120
 FLKQMLERYQ NNSPNNDDTL WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
 DADYPWPRQC CVMNMLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 536 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
 CAATACAGCT AAGGAATTAT CCCTTGTAAG TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCACTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
 TCCGGTGGC CATGTTGAAT CCCCCTAACC GCTGCTTGA AGATACTGAC TGCCAGGAA 420
 TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTCCCCAG TGAAGGGAGC 480
 CGGTCTTGC TGCACTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCTT CCCCCTCCA CACTGTCCAT TCTTCTCTCC ATTCCAGATG CCCACGGCTG 600
 GAGCTGCCTC TCTCATCCAC TTCCAATAA A

Seq ID NO: 537 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTVKGKVP FNGQDPVKGQ VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCPIL IRCAMLNPPN RCLKDTDCPG IKKCEGSCG MACFPVQ

Seq ID NO: 538 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

1 11 21 31 41 51
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGCCCGTCCG GGCAGCTGCT TCAACCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCTCTCTTC TCCAGGTTTG 120
 CTGGCTCAG TCGCGGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTGGAGGCG GAGGGCGCG AGCAGGAGCC CGGCCAGGCG CTGGGGAAG TATTCTAGG 240
 CTGCCCTGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCTGAAGAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCAA TATCTGTCCC 420
 TGAATAATGG AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTCTACA GCATCACGG GCGGGGGGCA GACAGCCCC CTGAGGGTGT 540
 CTTCGTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCCTCA TCGTAGCCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCAG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAACCAAGG ACCCACAGA CCTCATGTTT ACCATTACG GGAGCACAGG 900
 CACCATCAG GTCATCTCCA GTGGCTGGA CCGGGAAGAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAA GCAGTGGGCC ATGAGGTGCA GAGGTGACG GTCATGATC TGGACGCCCC 1140
 CAACTACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCACC ATCCACCTG AGAGCAACCA GGGCATCTG ACAACAGGA AGGGTTTGA 1260
 TTTTAGGGCC AAAAACCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
 GCTGAAGCT CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCGTGTGTT GTCCACCTCG CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGCTACCG 1500
 CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 TGTGGGCAAC CTCGAGCTGA AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCCACT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGAAGGGGAG GTTTCATCCT 2040
 CCGTGTGCTG GGGGTGTGTC TGGCTCTGCT GTTCTCTCTG CTGGTGTGTC TTTTGTGGT 2100
 GAGAAAGAAG CGGAAGATGA AGGAGCCCTC CTAATCTCCA GAAGATGACA CCGGTGACAA 2160
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTCTCT CGCAATGACG TGGCACCAAC 2280
 CATCATCCCG ACACCCATGT ACCGTCCTCG GCCAGCCAA CAGATGAAA TCGGCAACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACA GCCCGGCCCT ACACACCCCT 2400
 CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC 2460
 CTCGCCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG CCGGCCTGCC TGCAGGGCTG 2580
 GGGACCAAAC GTGAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCACTGAG 2640
 GACTTCGGAG CTTGTGAGG AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACCTTAGAGT GGTGCTTCTC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTGTACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
 TCTTACCTCG CTAATAATGC TCAACCCCTG GTCCCTGGGC TGGCCTGCT GTGACTGACC 2880
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940

TTTTITTAAT GCTATCTTCA AAACGTTAGA GAAAGTCTCT CAAAAGTGCA GCCCAGAGCT 3000
 GCTGGGCCCA CTGGCGCTCC TGCATTTCTG GTTCCAGAC CCCAATGCCT CCCATTCGGA 3060
 TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGGCC CCTTATTTT TATTTTCCCT 3120
 GTTGCCTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAAACT TTCCACAGAA AAAAA

Seq ID NO: 539 Protein sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVPMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSEK ILRRHKRDWV VAPISVPENG 120
 KGFFPQRLNQ LKSNKDRDRTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREBIAK 180
 YELFGHVAUSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TMDMDGSGST TAVAVVEILD ANDNAPMFDQ QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP 360
 AWRYATYLING GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSGQVAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDK HGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLALLVRK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
 GLEARPEVL RNDVAPTII PPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEAGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKLA DMYGGGEDD

Seq ID NO: 540 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..672

1 11 21 31 41 51
 ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GCGCGCGGCC CCGGGGCGGG 60
 CGGGGCTCCC CTACCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
 AAGGGCGGGG AGGGGCGCGC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180
 CTGCTGCGCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
 GCGAGACAAC GAGATCCAGA GGACTCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300
 TGTGATGTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATAGG 360
 ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG 420
 AAGCAGTGCT CGCTGGTTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
 CTCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAGTGTG GTAAATTCG CTAAGTCAAT 540
 TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600
 AGCTGTGGT GGTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGCGCTC 660
 AGCTGTCTT GA

Seq ID NO: 541 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MRLQRPRQAP AGRRRAPRGG RGSFYRDPDG RGARRLRFRQ KGEGEAPRAD PPWAPLGTMA 60
 LLLALLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCERENTF EQCNPRRCKW 120
 TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEBPMPPFY LKCKKIRYCN 180
 LBGPPINSSV FKEYAGSMGE SCGLWLAIL LLLASIAAGL SLS

Seq ID NO: 542 DNA sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

1 11 21 31 41 51
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
 TGCGGGCCCC AAGCGGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG 120
 GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG 180
 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240
 TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGTCT AAGGAGGCG GCTCGCCGGG 300
 CTGGGCGCTG GTGGTGTGGG CCGCGTGGCG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
 CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTACA TGCTGGAGGT 420
 CTACGGCTCG CTGCCCGCTC TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC 480
 ATCGCAGTAC ATCGTGGCCC TGGTCTTTCG CACCTACCTG CTCAGCCGCG TCTTCCCCAC 540
 CTGCCCGGTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGTCTAC 600
 GGCGGTGAAC TGCTACAGCG TGAAGGCGCG CACCCGGGTC CAGGATGCCT TTGCCCGCGC 660
 CAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCAT TGAAGGCACC AAACCTGGATG TGGGGAACAT 780
 TGTGTGGCA TTATACAGCG GCCTCTTTCG CTATGAGGGA TGAATTACT TGAATTTCGT 840
 CACAGAGGAA ATGATCAACC CTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
 CATCTGACG CTGGTGTACG TCGTGACCAA CCTGGCCTAC TTCACCAACC TGTCCACCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCTTGATC ATCCCGCTCT TCGTGGGCTC GTCTGCTTC GGCTCCGTC ATGGGTCCCT 1080
 GTTCACATCC TCGAGGCTCT TCTTCTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTGCTGTCA CGTGTGTGAT 1200
 GACGCTGCTC TAGCCTTCT CCAAGGACAT CTTCTCGGTC ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTC TCGTGGGCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
 CCTCTTCCTG ATCGCGCTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
 CATCATCCTC AGCGGGCTGC CGTCTACTT CTTGCGGGTC TGGTGGAAAA ACAAGCCCAA 1500
 GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560

CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 543 Protein sequence
Protein Accession #: XP_035292.2

1	11	21	31	41	51	
MAGAGPKRRA	LAAPAAEKE	EAREKMLAAK	SADGSAPAGE	GEGVTLQRNI	TLINGVAIIIV	60
GTIIGSGIFV	TPTGVLKEAG	SPGLALVWVA	ACGVFSIVGA	LCYAEELGTI	SKSGGDYAYM	120
LEVVGSLPAP	LKWIIELLII	RPSSQYIVAL	VFATYLLKPL	FPTCFVPEEA	AKLVACLCLV	180
LLTAVNCYSV	KATRVRQDAF	AAAKLLALAL	IILLGFVQIG	XGDVSNLDPN	FSPEGTKLDV	240
GNIVLALYSG	LFAYGWNLYL	NFVTEEMINP	YRNLPALIII	SLPIVTLVYV	LTNLAYFTTL	300
STEQMLSSAA	VAVDGNYHL	GVMWIIIPVF	VGLSCFGSVN	GSLFTSSRLF	FVGSREGHLP	360
SILSMIHPQL	LTPVPSLVPT	CVMTLLYAFS	KDIFSVINPF	SFFNWLCVAL	AIIGMIWLRH	420
RKPELERPIK	VNLALPVFFI	LACLFLIAVS	FWKTPVECGI	GFTIILSGLP	VYFFGVWVKN	480
KPKWLLQGIF	STTVLCQKLM	QVVPQET				

Seq ID NO: 544 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

1	11	21	31	41	51	
TAAAAGCAA	AAGAATTCGC	GGCCGCGTCG	ACACGGGCTT	CCCCGAAAAC	CTTCCCCGCT	60
TCTGGATATG	AAATTCACAG	TGCTTGCTGA	GTCCTATTGC	CGGCTGCTGG	GAGCCAGGAG	120
AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGCGTGG	GTCCACCATG	AACTGGAGTA	180
TCCTTGAGGG	ACTCCTGAGT	GGGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
TGTCTCTGGT	CTTCATCTTC	CGCGTCTGG	TGTACCTGGT	GACGGCCGAG	CGTGTGTGGA	300
GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTCGCCAGCC	CGGCTGCTCC	AACGTCTGCT	360
TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGGTGA	420
CATGCCCTCT	ACTGCTCGTG	GTCTGCACG	TGGCTTACCG	GGAGGTTTCA	GAGAAGAGGC	480
ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG	540
GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT	600
TTCTCTATGT	GTTCCTACTC	TTCTACCCCA	AATATATCCT	CCCTCCTGTG	GTCAAGTGCC	660
ACGCAGATCC	ATGTCCCAAT	ATAGTGGACT	GCTTCTATCT	CAAGCCCTCA	GAGAAGAACA	720
TTTTTACCCT	CTTCATGGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
TCATCTACCT	GGTGAGCAAG	AGATGCCACG	AGTGCCTGGC	AGCAAGGAAA	GCTCAAGCCA	840
TGTGCACAGG	TCATCACCCC	CACGGTACCA	CCTCTTCTCG	CAAAACAAGAC	GACCTCCTTT	900
CGGGTGACCT	CATCTTCTGT	GGCTCAGACA	GTCTCTCTCC	TCTCTTACCA	GACCGCCCCC	960
GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGGTCTG	GCAGGTTGGG	1020
CCTGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGG	GGAGCTAAGC	1080
CATGAGGTAG	GGGCAGGCAA	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCTTAGTCC	1140
TCAACTCCAG	CCACCTGCCC	CAGCTCGACG	GCACTGGGCC	AGTTCCCCCT	CTGCTCTGCA	1200
GCTCGGTTTC	CTTTTCTAGA	ATGGAAATAG	TGAGGGCCAA	TGC		

Seq ID NO: 545 Protein sequence
Protein Accession #: NP_005259.1

1	11	21	31	41	51	
MNWSIFEGLL	SGVNKYSTAF	GRIWLSLVFI	FRVLVYLVT	ERVWSDHDKD	FDCNTRQPGC	60
SNVCFDEFFP	VSHVRLWALQ	LILVTCPSLL	VVMHVAYREV	QEKRHREAHG	ENSGRLYLNP	120
GKKRGGGLWWT	YVCSLVFKAS	VDIAFLYVPH	SFYPKYILPP	VVKCHADPCP	NIVDCFISKP	180
SEKNIFTLFM	VATAATCILL	NLVELIYLV	KRCHECLAAR	KAQAMCTGHH	PHGTTSSCKQ	240
DDLSSGLDIF	LGSDSHPPLL	PDRPRDHVK	TIL			

Seq ID NO: 546 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

1	11	21	31	41	51	
CGGGCGAAGC	AGCGCGGGCA	GCGAGATGCA	GCACCGAGGC	TTCCTCTCTC	TCACCTCTCT	60
CGCCCTGCTG	GCGCTCACCT	CCGCGGTCCG	CAAAAAGAAA	GATAAGGTGA	AGAAGGGCGG	120
CCCGGGGAGC	GAGTGCCTG	AGTGGCCCTG	GGGGCCCTGC	ACCCCCAGCA	GCAAGGATTG	180
CGGCGTGGGT	TTCCGCGAGG	GCACTGCGG	GGCCAGACCC	CAGCGCATCC	GGTGCAAGGT	240
GCCCTGCAAC	TGGAAGAAGG	AGTTTGAGC	CGACTGCAAG	TACAAGTTTG	AGAACTGGGG	300
TGCGTGTGAT	GGGGGCACAG	GCACCAAGT	CCGCCAAGGC	ACCCTGAAGA	AGGCGCGCTA	360
CAATGCTCAG	TGCCAGGAGA	CCATCCGCGT	CACCAAGCCC	TGCACCCCCA	AGACCAAGC	420
AAAGGCCAAA	GCCAAGAAAG	GGAAGGGAAA	GGACTAGACG	CCAAGCCTGG	ATGCCAAGGA	480
GCCCTGGTG	TCACATGGGG	CCTGGCCACG	CCCTCCCTCT	CCCAGGCCCG	AGATGTGACC	540
CACCACTGCC	TTCTGTCTGC	TGCTTAGCTT	TAATCAATCA	TGCCCTGCCT	TGTCCTCTCT	600
ACTCCCCAGC	CCCACCCCTA	AGTGCCCAAA	GTGGGGAGGG	ACAAGGGATT	CTGGGAAGCT	660
TGAGCCTCCC	CCAAAGCAAT	GTGAGTCCCA	GAGCCCGCTT	TTGTTCTTCC	CCCAATTTC	720
ATTACTAAGA	AACACATCAA	ATAAACTGAC	TTTTTCCCCC	CAATAAAGC	TCTTCTTTT	780
TAATAT						

Seq ID NO: 547 Protein sequence
Protein Accession #: NP_002382.1

1	11	21	31	41	51	
MQHRGFLLLT	LLALLALTSA	VAKKDKVKK	GGPGSECAEW	AWGPCTPSSK	DCGVGFREGT	60
CGAQTQIRIC	RVPCNWKKEF	GADCKYKFEN	WGACDGGTGT	KVRQGTLLKA	RYNAQCQETI	120
RVTKPCTPKT	KAKAKAKGK	GKD				

Seq ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1

Coding sequence: 1..786

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5 1 11 21 31 41 51
| | | | | |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60
GGGAAGTGTG GGATCACAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTTCCCG GTGTCCCACA TCCGGCTGTG GGCCTCCAG 240
10 CTGATCTTGG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTCC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
15 TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGTC 540
TTTATTCTTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TCGCTCTGTG 600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTATAG 660
AGATCAAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
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AGCTAA
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Seq ID NO: 549 Protein sequence
Protein Accession #: NP_006774.1

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25 1 11 21 31 41 51
| | | | | |
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KNVCYDHFPP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRGE KRNDFKDIED 120
IKKKHVRIEG SLWWTYTSSI PFRIIFEAAP MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
FISRPTKTV FTTFMISASV ICMLLNVAEL CYLLKVCFR RSKRAQTQKN HPNHALKESK 240
30 QNEMNELISD SGQNAITGFP S
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Seq ID NO: 550 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

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40 AGGACCTGGA GCTCCCAAGG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCCT CTCTGAGGGT CCACATCACC TCCTGTGTGC 240
CCACCCCGGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGAGAGG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGCGCAACGA GGCACACGCT CTCGATACTG ACTACGACAA TTTCTGTGTT CTCTGCCTAC 420
45 AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
AGGACGATGA GATCATGCAG GGATTTCATCA GGGCTTTCAG GCCCCTGCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCGCCT 600
CCAGGAAGAC CAGACTCCCA CCCTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCC 660
50 TTTCAAAGAA TAACCACAGC TCAGAAGAGC ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TTCTGCTGCA CACTGCAC CATTGCCATG GAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G
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Seq ID NO: 551 Protein sequence
Protein Accession #: NP_002562.1

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55 1 11 21 31 41 51
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WENNSCVEKK VLGEKTNPK KFKINYTVAN BATLLDITDYD NFLFLCLQDT TPIQSMCMQ 120
60 YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPF RF
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Seq ID NO: 552 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

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70 CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTGCACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGTGCGCCAG GGCAGGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300
TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCTGACTCA AGTCACCCCC CAAGACGAGC 360
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG 420
75 TCTACAAAGC TCCGAGGAG CCAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTAAG 540
TCATCTGGTA CAAGAATGGC CGGCCCTCGA AGGAGGAGAA GAACCGGTC CACATTAGT 600
CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCAGTGC 720
80 GGAACCATAT GAAAGAGTCC AGGGAAGTCA CGTCCCTGT TTTCTACCGG ACAGAAAAAG 780
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GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGTCCCT GGTGCTGGAG CCTGCCGGA 960
AGGAACACAG TGGGCGCTAT GAATGTCAGG CCTGGAACCT GGACACCATG ATATCGCTGC 1020
85 TGAGTGAACC ACAGGAACCT CTGGTGAACT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080
CCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
ACCTCGAGTT CAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAGG GGCCTGTGTC 1200
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	TTCAAGTTGCA	TGACCTGAAA	CGGGAGGCAG	GAGGCGGCTA	TCGCTGCGTG	GCGTCTGTGC	1260
	CCAGCATACC	CGGCCTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTITT	GGCCCCCTT	1320
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5	GTGAAGCGTC	AGGGCACCCC	CGGCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCTGTA	GCACCCTGAA	TGTCTCGTG	ACCCCGGAGC	1500
	TGTTTGAGAC	AGGTGTGTAA	TGCAAGGCTT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCTTCTGGA	GCTGTCAAT	TTAACCACCC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
	TCAGCACTTC	CACTGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
10	TGCGGAGGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCGGTGCT	GGGCGCTGTC	CTCTATTTCC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGGAA	GCAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAAGCT	GATGTTGAAG	1860
	TTAAGTCAGA	TAAGCTCCCA	GAAGAGATGG	GCCTCCTGCA	GGGCGAGCAG	GGTGACAAGA	1920
	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
15	CAGCTCCCTT	CCCTGCCTGG	ACCATTCCTA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCTCACC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TAGGACCTTG	AGGACCTCAC	TTGGCCCTGG	AAGCCGCTTT	TCAGGGACCA	2160
	GTCCACCACC	ATCTCCTCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
	CCGAGCGGGT	AGGAGAGTTT	CTTGACAGAAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
20	AAATACCTGG	CTCTGCTGAG	CGGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC		2340
	CAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CACTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GCCTGCTCAT	GTGTAAGTGC	GCTGTTCACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTGTC	TGCCACCAAC	CTCCTGCTCG	CCTCTTCAAA	GTCTCCTGTG	2520
	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAGA	TACGTGCCGG	2580
25	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGCT	AGGACGAGAC	CATCTGGCT	AACACGGTGA	AACCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	GCGTAGTGGT	TGGCACCTAT	AGTCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGT	AGAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
	CAGTGCACCT	CAGCCTGGGC	AACACAGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAA	2880
30	ACGCGTACCT	GCGGTGAGGA	AGCTGGGCGC	TGTTTTCGAG	TTACAGGTGAA	TTAGCCTCAA	2940
	TCCCGTGTGT	CACTTGCTCC	CATAGCCCTC	TTGATGGATG	ACGTAAAACT	GAAAGGCAGC	3000
	GGGGAGCAGA	CAAGATGTAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGTTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAGGG	CCCAAATGAG	3120
	AGAATGTATC	TTAGGATGAG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
35	CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
	TTGTTTCCTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCACAGAA	AATCATAAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
	AGAGATCAGG	GGTTACTCTC	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
40	CTACCTTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATGCG	TTTCCGTCCA	CTT		

Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

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	GLPRLVCAFL	LAACCCCPRV	AGVPGEAEQP	APELVEVEVG	STALLKCGLS	QSQGNLSHVD	60
	WFSVHKERT	LIFRVQGGG	QSEPEYEQR	LSLQDRGATL	ALTQVTPQDE	RIFLCQGRKP	120
50	RSQERYQLR	VYKAPEEPNI	QVNPLGIPVN	SKEPEVATC	VGRNGYPIQ	VIWYKNGRPL	180
	KEENRNVHIQ	SSQTVESSGL	YTLQSLKQAQ	LVKEDKDAQF	YCELNYRLPS	GNHMKESREV	240
	TVPVFYFTEK	VWLEVEPVGM	LKEGDRVEIR	CLADGNPPPH	FSISKQNPST	REAEETNTD	300
	NGVLVLEPAR	KEHSGRYECQ	AWNLDTMISL	LSEPQELLVN	YVSDVRVSPA	APERQEGSSL	360
	TLTCEAESSQ	DLEFQWLREE	TDQVLERGPV	LQLHDLKREA	GGGYRCVASV	PSIPGLNRTQ	420
55	LVKLAIFGPP	WMAFKERKVV	VKENMVLNLS	CEASGHPRPT	ISWNVNGTAS	EQDQDPQRLV	480
	STLNVLTPE	LLETGVBECTA	SNDLGKNTSI	LFLELVNLT	LTPDSNTTGT	LSTSTASPH	540
	RANSTSTERK	LPEPESRGVV	IVAVIVCIV	LAVLGAVLYF	LYKKGKLP	RSQKEITLP	600
	PSRKTSLVVE	VKSDKLPPEM	GLLQSSGDK	RAPGDQGERY	IDLRH		

Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

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	CGAAGGCTGC	CCAGAGAGGT	GGAGTCGGTA	GCGGGGCGCG	GAACATGAGG	CAGTCTCTCC	180
	TATTCCTGAC	CAGCGTGGTT	CCTTTCGTGC	TGGCGCGCGG	ACCTCCGGAT	GACCCGGGCT	240
70	TCGGCCCCCA	CCAGAGACTC	GAGAAGCTTG	ATTCTTTGCT	CTCAGACTAC	GATATTCTCT	300
	CTTTATCTAA	TATCCAGCAG	CATTTCGGTAA	GAAAAAGAGA	TCTACAGACT	TCAACACATG	360
	TAGAAACACT	ACTAACTTTT	TCAGCTTTGA	AAAGGCATTT	TAAATTATAC	CTGACATCAA	420
	GTACTGAACG	TTTTTCACAA	AATTTCAAGG	TCGTGGTGGT	GGATGGTAAA	AACGAAAGCG	480
	AGTACACTGC	AAATGGCAG	GACTTCTTCA	CTGGACACGT	GGTTGGTGAG	CCTGACTCTA	540
75	GGGTTCTAGC	CCACATAAGA	GATGATGATG	TTATAATCAG	AATCAACACA	GATGGGCGCG	600
	AATATAACAT	AGAGCCACTT	TGGAGATTGG	TTAATGATAC	CAAAGACAAA	AGAATGTTAG	660
	TTTATAAATC	TGAAGATATC	AAGAAATGTT	CACGTTTGCA	GTCTCCAAAA	GTGTGTGGTT	720
	ATTTAAAGT	GGATAATGAA	GAGTTGCTCC	CAAAAGGGTT	AGTAGACAGA	GAACCACTG	780
	AAGAGCTTGT	TCATCGAGTG	AAAAGAAGAG	CTGACCCAGA	TCCCATGAAG	AACACGTGTA	840
80	AATTATTGGT	GGTAGCAGAT	CATCGCTTCT	ACAGATACAT	GGGCAGAGGG	GAAGAGAGTA	900
	CAACTACAAA	TTACTTAATA	GAGCTAATTG	ACAGAGTTGA	TGACATCTAT	CGGAACACTT	960
	CATGGGATAA	TGCAGGTTTT	AAAGGCTATG	GAATACAGAT	AGAGCAGATT	CGCATTCTCA	1020
	AGTCTCCACA	AGAGGTAAAA	CCTGGTGAAG	AGCACTACAA	CATGGCAAAA	AGTTACCCAA	1080
	ATGAAGAAAA	GGATGCTTGG	GATGTGAAGA	TGTTGCTAGA	GCAATTTAGC	TTTGATATAG	1140
85	CTGAGGAAGC	ATCTAAAGTT	TGCTTGGCAC	ACCTTTTCAC	ATACCAAGAT	TTTGATATGG	1200
	GAACTCTTGG	ATTAGCTTAT	GTTGGCTCTC	CCAGAGCAAA	CAGCCATGGA	GGTGTGTC	1260
	CAAGGCTTA	TTATAGCCCA	GTTGGGAAGA	AAAATATCTA	TTTGAATAGT	GGTTTGACGA	1320
	GCACAAAGAA	TTATGGTAAA	ACCATCCTTA	CAAAGGAAGC	TGACCTGGTT	ACAACTCATG	1380

	AATTTGGACA	TAATTTTGGG	GCAGAACATG	ATCCGGATGG	TCTAGCAGAA	TGTGCCCGGA	1440
	ATGAGGACCA	GGGAGGGA	TATGTCATGT	ATCCCATAGC	TGTGAGTGGC	GATCACGAGA	1500
	ACAATAAGAT	GTTTTCAAA	TGCAGTAAAC	AATCAATCTA	TAAGACCATT	GAAAGTAAAG	1560
5	CCGAGGAGTG	TTTTCAAGAA	CGCAGCAATA	AAGTTTGTGG	GAACCTCGAGG	GTGGATGAAG	1620
	GAGAAGAGTG	TGATCTCTGC	ATCATGTATC	TGAACAACGA	CACCTGCTGC	AACAGCGACT	1680
	GCACGTTGAA	GGAAAGGTGC	CAGTGCAGTG	ACAGGAACAG	TCCTTGCTGT	AAAAACTGTC	1740
	AGTTTGAGAC	TGCCAGTAAG	AAGTGCAGG	AGGCGATTAA	TGCTACTTGC	AAAGGCGTGT	1800
	CCTACTGCAC	AGGTAATAGC	AGTGAGTGCC	CGCCTCCAGG	AAATGCTGAA	AATGACACTG	1860
10	TTTGTCTGGA	TCTTGGCAAG	TGTAAGGATG	GGAAATGCAT	CCCTTTCTGC	GAGAGGGAAC	1920
	AGCAGCTGGA	GTCTGTGTGA	TGTAATGAAA	CTGACAACTC	CTGCAAGGTG	TGCTGCAGGG	1980
	ACCTTTCTGG	CGCTGTGTG	CCCTATGTCG	ATGCTGAACA	AAAGAACTTA	TTTTTGAGGA	2040
	AAGGAAAGCC	CTGTACAGTA	GGATTTTGTG	ACATGAATGG	CAATGTGTAG	AAACGAGTAC	2100
	AGGATGTAAT	TGAACGATT	TGGGATTTC	TTGACAGCT	GAGCATCAAT	ACTTTTGGA	2160
15	AGTTTGTAGC	AGACAACATC	GTTGGGTCTG	TCCTGGTTTT	CTCCTTGATA	TTTTGGATTG	2220
	CTTTCAGCAT	TCTTGTCCAT	TGTGTGGATA	AGAAATTGGA	TAAACAGTAT	GAATCTCTGT	2280
	CTCTGTTTCA	CCCCAGTAAC	GTCGAAATGC	TGAGCAGCAT	GGATTCTGCA	TCGGTTGCGA	2340
	TTATCAAACC	CTTTCCTGCG	CCCCAGACTC	CAGGCCGCTC	GCAGCCTGCC	CCTGTGATCC	2400
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20	CCAGCACAGA	CTCCCATATG	GACGAGGATG	GGTTTGAGAA	GGACCCCTTC	CCAAATAGCA	2520
	GCACAGCTGC	CAAGTCAATT	GAGGATCTCA	CGGACCATCC	GGTCGCCAGA	AGTGAAAAGG	2580
	CTGCCTCCTT	TAACTGTCAG	CGTCAGAAATC	GTGTTAACAG	CAAAGAAACA	GAGTGTCTAT	2640
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	TTTGAATCTC	CTGCAGGTAA	ACAGTTCTTG	TGTGGTTTGG	CCCTTCTCCT	TTTGAAAAGG	2820
25	TAAGGTGAAA	GTGAATCTAC	TTATTTTGAG	GCTTTCAGGT	TTTAGTTTTT	AAATATCTT	2880
	TTGACCTGTG	GTGCAAAAGC	AGAAAATACA	GCTGGATTGG	GTTATGAATA	TTTACGTTTT	2940
	TGTAAATTA	TCCTTTATAT	TGATAACAGC	ACTGACTAGG	GAAATGATCA	GTTTTTTTTT	3000
	ATACACTGTA	ATGAACCGCT	GAATATGAAG	CATTTGGCAT	TTATTTGTGA	GAAAAGTGGG	3060
30	ATAGTTTTTT	TTTTTTTTTT	TTTTTTTTTG	CTTCAACTAA	AAACAAAGGA	GATAAAATTA	3120
	GTATACATTG	TATCTAAAT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	TTTTATGTAG	3180
	CAGGGAAT	ATATATCTAA	ATTTAGAAAT	CATTTGGGTT	AATATGGCTC	TTCATAAATC	3240
	TAAGACTAAT	CTGCAGAAC	TAACCACTAC	CTTACAGTGA	GGGCTATACA	TGGTAGCCAG	3300
	TTGAATTTAT	GAATCTACC	AACTGTTTAG	GGCCCTGATT	TGCTGGGCAG	TTTTCTGTGA	3360
35	TTTTATAAGT	ATCTTCATGT	ATCCCTGTTA	CTGATAGGGA	TACATGTCTT	AGAAAATCA	3420
	CTATTGGCTG	GGAGTGGTGG	CTCATGCCCTG	TAATCCAGC	ACTTGGAGAG	GCTGAGGTTG	3480
	CGCCACTACA	CTCCAGCCTG	GGTGACAGAG	TGAGATCTGC	CTC		

Seq ID NO: 555 Protein sequence
Protein Accession #: NP_003174.2

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	QTSHTVELL	TFSALKRHPK	LYLTSSTERF	SQNFKVVVD	GKNESEYTA	WQDFPTGHV	120
45	GEPSRVLAH	IRDDVVIIR	NTDGAENIE	PLWRFVNDK	DKRMLVYKE	DIKNVSRQLS	180
	PKVGYLQVD	NEELLPKGLV	DREPPELVH	RVKRRADPD	MKNCTKLLV	ADHRFPYRMG	240
	RGEESTTNY	LIELIDRVDD	IYRNTSWDNA	GFKGYGQIE	QIRILKSPQE	VKPEKHYNM	300
	AKSPNEEKD	AWDVKMLLEQ	FSFDIAEEAS	KVCLAHLPTY	QDFDMGLGL	AYVGSPPRNS	360
	HGGVCPKAY	SPVGKKNIYL	NSGLTSTKNY	GKTLTKEAD	LVTTHELGH	FGAEHDPDGL	420
50	AECAPNEDQ	GKVMYPIAV	SGDHENKMF	SNCSSQSIYK	TIESKAQECF	QERSNKVCGN	480
	SRVDEGECD	PGIMYLNNDT	CCNSDCTLKE	GVQCSDRNSP	CKKNCQFETA	QKKCQEAINA	540
	TKGVSYCTG	NSSECPPPGN	AENDTVCLDL	GKCKDGKIP	FCEREQQLES	CACNETDNNS	600
	KVCCRDLSGR	CVFVYDAEQK	NLFRLKGP	TVGFCDMNGK	CEKRVQDVIE	RPWDFIDQLS	660
55	INTFGKFLAD	NIVGSVLVFS	LIFWIPFSIL	VHCVDKKLDK	QYESLSLFHP	SNVEMLSMD	720
	SASVRIIKPF	PAPQTPGRILQ	PAPVIPSAPA	APKLDHQRM	TIQEDPSTDS	HMEDGFEEKD	780
	PFNSSTAARK	SFEDLTDHPV	ARSEKAASEK	LQRQNRVNSK	ETEC		

Seq ID NO: 556 DNA sequence
Nucleic Acid Accession #: NM_021832.1
Coding sequence: 164..2248

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	GAAGGCTGCC	CAGAGAGGTG	GAGTCGGTAG	CGGGGCCGGG	AACATGAGGC	AGTCTCTCCT	180
	ATTCTGTACC	AGCGTGGTCT	CTTCTGTGCT	GGCGCCGCGA	CCTCCGGATG	ACCCGGGCTT	240
	CGGCCCCAC	CAGAGACTCG	AGAAGCTTGA	TTCTTTGCTC	TCAGACTACG	ATATTCTCTC	300
70	TTTATCTAAT	ATCCAGCAGC	ATTCCGTAAG	AAAAAGAGAT	CTACAGACTT	CAACACATGT	360
	AGAAACACTA	CTAATTTTT	CAGCTTTGAA	AAGGCATTTT	AAATTATACC	TGACATCAAG	420
	TACTGAACGT	TTTTACAAA	ATTTCAAGGT	CGTGGTGGTG	GATGGTAAAA	ACGAAAGCGA	480
	GTACACTGTA	AAATGGCAGG	ACTTCTTCAC	TGGACACGTG	GTTGGTGAGC	CTGACTCTAG	540
	GGTTCTAGCC	CACATAAGAG	ATGATGATGT	TATAATCAGA	ATCAACACAG	ATGGGGCCGA	600
75	ATATAACATA	GAGCCACTTT	GGAGATTTGT	TAATGATACC	AAAGACAAAA	GAATGTTAGT	660
	TTATAAATCT	GAAGATATCA	AGAATGTTTC	ACGTTTGACG	TCTCCAAAAG	TGTGTGGTTA	720
	TTTAAAGTGT	GATAATGAAG	AGTTGCTCCC	AAAAGGGTTA	GTAGACAGAG	AACCACCTGA	780
	AGAGCTTGTG	CATCGAGTGA	AAAGAAGAGC	TGACCCAGAT	CCCATGAAGA	ACACGTGTAA	840
	ATTATTGGTG	GTAGCAGATC	ATCGCTTCTA	CAGATACATG	GGCAGAGGGG	AAGAGAGTAC	900
80	AACACACAA	TACTTAATAG	AGCTAATGTA	CAGAGTTGAT	GACATCTATC	GGAAACCTTC	960
	ATGGGATAAT	GCAGGTTTTA	AAGGCTATGG	AATACAGATA	GAGCAGATTG	GCATTCTCAA	1020
	GTCTCCACAA	GAGGTAAAC	CTGGTGAAAA	GCACTACAA	ATGGCAAAAA	GTTACCCAAA	1080
	TGAAGAAAAG	GATGCTTGGG	ATGTGAAGAT	GTTGCTAGAG	CAATTTAGCT	TTGATATAGC	1140
	TGAGGAAGCA	TCTAAAGTTT	GCTTGGCACA	CCTTTTCA	TACCAAGATT	TTGATATGGG	1200
85	AACTCTTGGA	TTAGCTTATG	TTGGCTCTCC	CAGAGCAAA	AGCCATGGAG	GTGTTGTGCC	1260
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	CACAAAGAA	TATGGTAAAA	CCATCTTAC	AAAGGAAGCT	GACCTGGTTA	CAACTCATGA	1380
	ATTGGGACAT	AAATTTGGAG	CAGAACATGA	TCCGATGGT	CTAGCAGAA	GTGCCCGGAA	1440

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15
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Seq ID NO: 557 Protein sequence
 Protein Accession #: NP_068604.1

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Seq ID NO: 561 Protein sequence
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 CAACATGGCG AAACCCCATC TCTACTAAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720
 GGCCTGTAAT CCCAGTTCTG TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCGGGGACG 780
 GAGGTTGCAG TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840
 15 CATCTCAAAA AAAAAAAGAA AAGAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900
 TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGA TGCTGTGCTT 960
 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTTCACTGT TGGGAGATGG 1020
 TGATATTTTC AACCTACTT CCTAAACATC TGTCTGGGTG TCCTTTAGTC TTGAATGTCT 1080
 TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140
 20 CAGTTGAAGA GGTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGT CAGTGCCCAT 1200
 TTCTCATTTT ACATTTTAAA GTCGTCTCTC CAACATAGTG TGTATTGGTC TGAAGGGGGT 1260
 GGTGGGATCG CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320
 TTTTCTTAA CTAATAAGT GGAATATATA TTTCAAAAAA AAAAAAAAAA AA

25 Seq ID NO: 563 Protein sequence
 Protein Accession #: NP_037464.1

30 1 11 21 31 41 51
 MKHVLNLYLL GVLTLISIF VRVMSLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60
 RSM

35 Seq ID NO: 564 DNA sequence
 Nucleic Acid Accession #: NM_023915.1
 Coding sequence: 250..1326

40 1 11 21 31 41 51
 GGACGAGGGG TTTCGTTTTC ATGCTTTACC AGAAAATCCA CTTCCCTGCC GACCTTAGTT 60
 TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
 GTGAATGGAC AGCCAGGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 CCACGCGCTC AATCGTCCCC AAGTGTCTCC TGACACGCAT CTTTGTCTAC AGTGCAATC 240
 AACTGAAGAA TGGGGTTCAA CTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 45 CAAGAGAGTC ACAATTCAAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCCTTCA 360
 AATGAATTG ACACAATTGT CTTGCCGTG CTTTATCTCA TTATATTGT GGCAAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
 TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCAAT 660
 50 GATCGCTATC TAAAGATGCT CAAGCACTTC GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGGTTT TATCTGTTTG TGTGTTGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
 ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAGT 840
 CCTTTGGGGG TCAAATGGGA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
 55 AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAAATCC TTTTACTTTT 1080
 AGTCACCTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAAGAA 1140
 ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTCATG 1200
 60 TGTAGTGCAT TTTCAAGAAG GCTGTTCAAA AAATCAATA TCAGAACCAAG GAGTGAAAGC 1260
 ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380
 TTCAATTATC TAAAAA AAAA AA

65 Seq ID NO: 565 Protein sequence
 Protein Accession #: NP_076404

70 1 11 21 31 41 51
 MGFNLTAKL PNNEHLGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFFHI RNKTSIFIFL KNIVVADLIM TLTFPPRIVH DAGFGPWYFK FILCRYTSVL 120
 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTFTKV LSVCVVWIMA VLSLPNIILT 180
 NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRKRRH NQSIRVVAV FFTCFPLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
 75 PLSACNVCLD PIIFYFMCRS FSRLFPKSN IRTRESIRS LQSVRRSEVR IYYDYTDV

80 Seq ID NO: 566 DNA sequence
 Nucleic Acid Accession #: NM_005365.1
 Coding sequence: 1..948

85 1 11 21 31 41 51
 ATGTCTCTCG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60
 GAGGACTTGG GCCTGATGGG TGCACAGGAA CCCACAGCG AGGAGGAGGA GACTACCTCC 120
 TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCCAGAGT 180
 CCTCAGGGAG GCGCTTCCTC CTCCATTTC GTCTACTACA CTTTATGGAG CCAATTGAT 240
 85 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGACCC AGCTCAGCTG 300
 GAGTTATATG TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360

CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
 AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAAGCCT CCGAGTTCAT GCAGGTGATC 480
 TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACGTCT 540
 CTTGGCCTCT CGTGGGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCGCCCTC 600
 CTGATCATTTG TCCTGGGTGT GATCCTAACC AAAGACAAC TCGCCCTGA AGAGGTATC 660
 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG 720
 CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAACT ACCTGGAGTA CCGCAGGTG 780
 CCCGGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
 AGCTATGAGA AGGTATATAA TTATTGGTTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 567 Protein sequence
 Protein Accession #: NP_005356.1

1 11 21 31 41 51
 MSLEQRSPHC KPDEDLEAQE EDLGLMGAQE PTGEEEEETS SSDSKEEEVS AAGSSSPPPQS 60
 PQGGASSSIS VYITLWSQFD EGSSSQEEEE PSSSVDP AOL EFMFQEA LKL KVAELVHFL 120
 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI PGTDVKEVDP AGHSYILVTA 180
 LGLSCDSMLG DGHSMPKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240
 PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL V MLNAREPICY 300
 PSLYEEVLGE EQEGV

Seq ID NO: 568 DNA sequence
 Nucleic Acid Accession #: NM_014400
 Coding sequence: 86..1126

1 11 21 31 41 51
 GGTACTCAT CTGGGCTCA GGTAAAGAGG CCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
 GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCC GCCAGG AAAGCAGGTG CCCAGGCCAT 120
 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTGC GGAGGAGCGC AGGCCCTGGA 180
 GTGCTACAGC TGCGTGCA GAAGCAGATGA CGGATGCTCC CCGAACAGA TGAAGACAGT 240
 GAAGTGGCGC CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300
 CGGACAATTC TCGCTGGCAG TGCSGGGTTG CGGTTCCGGA CTCGCCGGA AGAATGACCG 360
 CGGCCTGGAT CTTACGGGCT TCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
 CTGCAAGGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
 ATACCCGCCC AACGGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
 GGGTACATCG CCGCCGCTG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
 CTTGACGGC AACGTCACCT TGACGGCAGC TAATGTGACT GTGTCCTTGC CTGTCCGGGG 660
 CTGTGTCCAG GATGAATCTT GCACTCGGGA TGGAGTAACA GGCCAGGAGT TCACGCTCAG 720
 TGGCTCCTGT TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
 CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCCTCAAC 840
 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAACCCAT 900
 GCCAGGCCCA ACCAGTCAGA CTCCGAGACA GGGAGTAGAA CACGAGGCTT CCGGGATGA 960
 GGAGCCCAAG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
 TCCTGCAAAA GGGGGGCCCT AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCC CTTCTGTGG CCGTGGCTGC TGGTGTCTA CTGTGAGCTT CTCACCTGG 1140
 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTGTT 1200
 CCCACCACTG GACTGGGCTG GCCAGCCCC TGTTTTCCA ACATTCCTCA GTATCCCCAG 1260
 CTTCTGCTGC GCTGTTTTC GGCCTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320
 GGGTGTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380
 TCCTCTTGTG ATGTAGGAG AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
 AGGATGCTAA GCTTCTACT CACTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
 GTGGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCTT ACTCCCGCA TCTTTGGGGA 1560
 ATCGGTTCCC CATATGTCTT CTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
 CTTATGTCTG TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680
 TTGTATAGTG AAAAAAA

Seq ID NO: 569 Protein sequence
 Protein Accession #: NP_055215

1 11 21 31 41 51
 MDPARKAGAQ AMIWTAGWLL LLLLRGGAQA LECYSCVQKA DDGCSNPKMK TVKCAPGV DV 60
 CTEAVGAVET IHQFSLAVX GCGSGLPGKN DRGLDLHGLL AFILQLQCAQ DRNNAKLNLT 120
 SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVLT 180
 AANVTVSLPV RGCVDPEFT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPLVR 240
 LPPPEPTTVA STTSVTTSTS APVRPTSTTK PMPAPTSQTP RQGVHEASR DEEPRLTGGA 300
 AGHQDRSNSG QYPAKGPPQQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 570 DNA sequence
 Nucleic Acid Accession #: NM_005329.1
 Coding sequence: 1..1662

1 11 21 31 41 51
 ATGCCCGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
 GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTTCATCCA CACGGAAAAG 120
 CACTACCTGT CTTTGGCCTT GTACGGCGCC ATCCTGGGCC TGCACTGCTT CATTGAGAGC 180
 CTTTTCGCTT TCCTGGAGCA CCGGCGCATG CGACGTGCGG GCCAGGCCCT GAAGCTGCCC 240
 TCCCCGGCGC GGGGCTCGGT GGCATGTGTC ATTGCGCGCT ACCAGGAGGA CCCTGACTAC 300
 TTGCGCAAGT CCTGCGCTC GGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
 GTGGTGGATG GCAACGCCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
 GCGGGCACCG AGCAGGCCCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
 GGTGAGACCG AGGCCAGCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC 540
 AGCACCTTCT CGTGATCAT GCAGAAAGTG GGAGGCAAGC CGAGGTCAT GTACACGGCC 600

TTCAAGGCCCT TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
 GATCCAGCCT GCACCATCGA GATGCTTCGA GTCCTGGAGG AGGATCCCCA AGTAGGGGGA 720
 GTGCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTCT CCTGAGCAGC 780
 GTGCGGTACT GGATGGCCTT CAACGTGGAG CGGGCTGCGC AGTCCTACTT TGGCTGTGTG 840
 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCCTGGAG 900
 GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
 ACCAACCCGAG TGGTCAACGG TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
 ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT 1080
 TACTTCCGGG AGTGGCTCTA CAACCTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC 1140
 TACGAGTCAG TGGTCAACGG TTCTTCTCCC TTCTTCTCTA TTGCCACGGT TATACAGCTT 1200
 TTCTACCGGG GCCGCATCTG GAACATTCTC CTCTTCTCTG TGACGGTGCA GCTGGTGGGC 1260
 ATTATCAAGG CCACCTATCG CTGCTTCCTT CGGGGCAATG CAGAGATGAT CTTCATGTCC 1320
 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCCGGCCA AGATCTTTGC CATTGCTACC 1380
 ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTTATGGC 1440
 CTCATTCCCTG TGTCCATCTG GGTGGCAGTT CTCCTGGGAG GGCTGGCCTA CACAGCTTAT 1500
 TGCCAGGACC TGTTCACTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGGC TATACTGTAT 1560
 GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620
 AAGAAGCCGG AGCAGTACAG CTGCTCTTTT GCTGAGGTGT GA

Seq ID NO: 571 Protein sequence
 Protein Accession #: NP_005320.1

1 11 21 31 41 51
 MPVQLTTALR VVGTSLFALA VLGGILAAYV TGYQFIHTEK HYLSPGLYGA ILGLHLIIQS 60
 LPAPLEHRRM RRAGQALKLP SPRRGSVALC IAAAYQEDPDY LRKCLRSAQR ISFPDLKVVVM 120
 VVDGNRQEDA YMLDIFHEVL GGTEQAGFFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180
 STFSCIMQKW GKGREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQPLE 300
 DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTWSKS 360
 YFREWLYNSL WFKHHLNMT YESVVTGFPF FFLIATVIQL FYRGRIWNIL LFLLLTVQLVG 420
 IKAITYACFL RGNABMIFMT LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVNVFNG 480
 LIPVSIWVAV LLGGIAYTAY QDLFSETEL AFLVSGAILY GCYVWALLML YLAIIARRCG 540
 KKPEQYSLAF AEV

Seq ID NO: 572 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-7095

1 11 21 31 41 51
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAACA ATTTCCTTCG CTCCCTCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCCT CGCTTGCAAT 180
 CAGCTCCTCT GTGTTTGGCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTGTGTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAAG 300
 AAATATCCAA CATGTAATAG CCCAAAAACA TCTCCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAAGGTT GGGATAAAAC ATCATTGGAA 420
 AACACATTCA TTCATAACAC TGGGAAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480
 GTCAGCGGAG GAGTTTCAGA AATGGTGTTT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTCACTCGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAA 660
 GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTTG 720
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT 780
 TTAGATCCAT TCATACCTGT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC 840
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAAG CCAAGTTGGT GTTTTGTG AGTTTCTTAC AATGCAACAA 960
 TCTGGTTATG TCATGCTGAT GGACTACTTA CAAAACAATT TTGAGAGCA ACAGTACAAG 1020
 TTCTCTAGAC AGGTGTTTTC CTCTACACT GGAAGGAAAG AGATTATAGA AGCAGTTTGT 1080
 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTACA 1140
 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGAGT TTTGTACCAG 1200
 CAGTTGGATG CAGTGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
 GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
 TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380
 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAAGT AAGAAAATAT CAAGGAGGAG 1440
 GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500
 AACCAATCA GGAAGGAGGA ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG 1560
 ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620
 AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAAGTAC TAAATTAGCC 1680
 ACAGAAAAAG ATATTTCTCT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
 GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAAAGT TTCTTAGATC TCCCATATG 1800
 AACTTGTGCG GCACTGACAG ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860
 AGTTTATTGA CCAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
 GCAACTTCTG CATCTCTGAG AACATATCCC AAGGGTATAT ATTTCTCTCC 1980
 GAAAACCCAG AGACAATTAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040
 GAAGATTCAA CTTTCATCAG TTCAGAAGAA TCACTAAAG ATCCTTCTAT GGAGGGAAAT 2100
 GTGTGGTTTC AGTCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160
 AGCTTCTTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220
 TCCTTTCTG CAGGCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280
 CATATTCTTA CCTTCTGCTA CTTCCTCACT GAGGTAACAC CTCATGCTTT TACCCATCC 2340
 TCCAGACAAC AGGATTTGGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCAACG 2400
 GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460
 ACCCTTTTGT TGCTTGACAA TACAGATCTC AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520
 TCGGCCTTGC ATGCTAGGCC TGTATTCTCC AGTGTGATG TGTCAATTGA ATCCATCTG 2580
 TCTTCTATG ATGGTGACCT TTGTCTTCCA TTTTCTCTG CTTCCTTCAG TAGTGAATTG 2640
 TTTGCCATC TGCATCAACT TTCTCAAACT CTTCCACAAG TTACTTCAGC TACCGAGAGT 2700
 GATAAGGTGC CCTTGCATGC TTCTCTGCCA GTGGCTGGGG GTGATTGCT ATTAGAGCCC 2760

	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	TCCTTTATAA	ACGCTTATGT	TTTCTCAAGT	TGAACCACCC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCCTTGCTC	2940
5	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCGCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACCTA	TCAGGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	OGTTAAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAAACT	TTCTTCACTT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
10	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAAATGAG	3300
	ACTGAACTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCCTAGCA	CCAGGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACTTTTCAG	TTCAACCTAC	ACATACTGTC	3540
15	TCTCAAGCAT	CTGGTGACAC	TTGCTTAAAT	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAG	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TTAAACACTG	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
20	AGTGAAAAA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTGTGTTA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAAC	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTATAT	AAATTGATGA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
25	CATTCCGATG	AAATTTTAAAC	CTCCACCAAA	AGTTCTGTGA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TTGGTCTCTG	TACATTGTGA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
	GGGCATGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCGTGAAC	CTCAACAAGG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAAG	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
30	AGAGGTAGTG	ATGGCTTATC	CATTATAAG	TGTATGTGAT	GCTCATCCTA	TAGAGAATCA	4500
	CAGGAAAAGG	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAATAAT	4560
	CCAATCTCAT	ACTCATCTAT	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGATATC	4620
	TCAGACGTGC	AAACTCGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
35	CCTCTCAGCC	CTGATCTTAA	AGCATGGGCA	GTTCGTACAA	GTGATGAAGA	AAGTGGATCA	4800
	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTGTGA	4860
	GACACTAATG	AAAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCAC	AGTCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCACCGTT	4980
40	TCAGAGGAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAGATG	ATGTCGGAGC	AATTCCTAAT	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
45	CATGCAAGTG	CTGGGTTTAC	TGAAGAAATT	GAGACACTGA	AAGAGTTTTA	CCAGGAAAGT	5340
	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACACAAG	5400
	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
50	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTT	5580
	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	5640
	AAAGGAAGGA	GAAATATGTA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCCCTATT	ATACTGTGAG	GAATTTTACT	5760
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
	ACACAGTATC	ACTACACGCA	TGGGCTGTAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
55	CTGACCTTTG	TGAGAAAGAG	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGT	5940
	CACTGCGATG	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	6000
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTCCAAA	6060
	AGAAATTTAT	TGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	6120
	GCCATACTTA	GTAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCCTA	TGTTAATGCA	6180
60	CTCCTCATTC	CTGGACGAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
	CAGTCAAAAT	TACAGCAAGT	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAGAG	6300
	AATCGAAGTT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	6360
	GGAGAAGGCA	CAGACTACAT	CAATGCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTCATCATTA	CCAGCACCCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
	GACCATAATG	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
65	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATGTGT	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAAGAG	TCTATCTAAT	GAGGAAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
	CCAAATCCAG	ATAGCCCCAT	TAGTAAAACT	TTTGAACTTA	TAAGTGTTAT	AAAAGAAGAA	6780
70	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
	ACTTCTGTG	CTCTGACAAC	CCTTATGCAC	CAACTAGAAA	AAGAAAATTC	CGTGGATGTT	6900
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	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
	TCCACCTCTC	TGGACAGTAA	TGGTGCAGCA	TTGCCTGATG	GAAATATAGC	TGAGAGCTTA	7080
	GAGTCTTTAG	TTTAAACAG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTTCTCT	7140
75	TTCTTAAAT	TAGGCAAGAA	AAATCAGTCTA	GTTCGTGTTAT	CTGTGATTTT	CCCATCACTT	7200
	GACAGTAACT	TTCATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTAA	CAATGTGTGC	7260
	CTTTTTGCAA	GACTTGTAAAT	TACTTATTA	TGTTTGAAC	AAAATGATTG	AATTTTACAG	7320
	TATTTCTAAG	AATGGAAATG	TGGTATTTTT	TTCTGTATTG	ATTTTAAAC	AAAATTTCAA	7380
	TTTATAGAGG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAATTTTAA	7440
80	GCTGTATTTG	TAGCAATTAT	CAGGTTTGCT	AGAAAATATA	CTTTTAATAC	AGTAGCCCTGT	7500
	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAAATACT	GCCCTAGTGT	CTCCATGGAC	CAAATTTATA	7620
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	GTTTAGTTTA	TAGACGTGAT	TCAATTAGCTG	GTCTTACTCT	ACCAAGTTTTT	TGACATTGTA	7740
85	TTGTGTTACC	TAAGTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAAAATA	7800
	GAAATACCTT	CATTTTGAAG	GAAGTTTFTA	TGAGAATAAC	ACCTTACCAA	ACATTTGTCA	7860
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Seq ID NO: 573 Protein sequence:
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQVNVNLLKKL	KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
10	FKASKITFW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGLRLALS	180
	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPPILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVISISBSQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEIEHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTGDGYD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPFE	420
	LIGTEEIIKE	EEEGKDIIEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
15	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPFHT	VEGTASASLND	540
	GSKTVLRSFH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	ENSPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVSGGR	ESFLQTNYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFTP	SSRQDLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
20	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSS	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPLHASL	PVAGGDLLE	PSLAQYSDVL	STTHAASETL	EFSGESGVLY	900
	KTLMPQSVEP	PSDDAMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVITYQG	960
	SLFSFGSHIP	IKSSLLITPT	ASDLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVAEFTYT	TSVFGDDNKA	LSKSEIIYGN	ETELQIPSFN	EMVYPSESTV	MPNMYDNVVK	1080
25	LNASLQETSV	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	NNFSVQPTH	VSQASGDTSL	1140
	KPVLANSSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLKTVLP	1200
	AVPSDPIIVE	TPKVDKISST	MLHLIVNSA	SSENMLHSTS	VPVFDVSPTS	HMSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVVPISLYSD	ELFQTANLEI	NQAHPPKGRH	VFATPVLSID	1320
	EPLNTLINKL	IHSDEILTST	KSSVTGKVFA	GIPTVASDTP	VSTDHSPVIG	NGHVAITAVS	1380
30	PHRDGSVTST	KLLFPKATS	ELSHSAKSDA	GLVGGGEDGD	TDDGDGDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVMNDS	THENSIMDQN	NPISYSLSEN	SEEDNRVTSV	SSDSQTMMDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTSAL	LPLSPESKAW	AVLTSDEESG	SGQGTSDSLN	1560
	ENETSTDFSF	ADTNEKDADG	ILAAGDSEIT	PGFPQSPTSS	VTSENSEVFH	VSEAEASNSS	1620
	HESRIGLAEG	LESEKKAIVP	LIVVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	1680
35	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCITVDLGI	1740
	TADSSNHDPN	KHKRYNINIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGPKLSTAEF	FLRMIWEHNV	EVIVMITNLV	EKGRKCDQY	WPADGSEEEY	NFLVTQKSVQ	1860
	VLAYTIVRNF	TLRNTKIKKG	SQGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFRKAAAY	1920
	AKRHAVGPVV	VHCSAGVGR	GTIYVLDLML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
40	QYVFIHDTLV	EAILSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKQCNRE	KNRTSSIIPV	ERSRVGISSL	SGEGTDYINA	SYIMGYQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDQGNMAED	EFVYWPKNDE	PINCESFKVT	LMAEEHKCLS	2160
	NEEKLIQDPF	ILEATQDDYV	LEVRHFQCPK	WPNFDSPISK	TFELISVIKE	EAANRDGPMI	2220
	VHDEHGGVTA	GTCALTTLM	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVL	2280
45	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESIV			

Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-4518

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	CAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCACTC	TGAGAAGCAG	AGGAGCCGCA	120
55	CGGCGAGGGG	CGGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCATT	180
	CAGCTCCTCT	CTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGTAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTTGAA	420
60	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCACTCTG	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATCGCGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTGT	720
65	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATAGTCTT	GAACCTCTCT	CCAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCTTGACCA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCTTAC	AATGCAACAA	960
70	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAG	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCTATG	AGCAGTTTGT	1080
	AGTTCTAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTATCA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTCT	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
75	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCTCTAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATCTG	ATTGTGAATC	CTGCTAGAGA	CAGTGCTAGA		1500
	AACCAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAGACCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
80	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAAGTG	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGACGA	ATCTTTAAAT	ACAGTTTCTA	TAACAGAAAT	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
85	GCACTTCTCT	CTATCCCATC	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCGA	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TACTATAAGG	ATCCTTCTAT	GGAGGGAAAT	2100

	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTCTCG	CAGGCCCACT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
5	CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
	TGCTCTAGTG	TTCTTGTGGG	TATTTCTATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
10	TTTTACTTAG	AGGACAGTAC	ATCCCCCTAGA	GTATATATCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTCCG	AGCAATTCCA	ATAAGCACT	TTCCAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGT	TAAGCTAGCA	2880
15	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
	TACACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAATG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTTCTGG	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCCCT	ATTATACTGT	GAGGAATTTT	3180
20	ACTCTAAGAA	ACACAAAAAT	AAAAAAGGGC	TCCCAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
	GTACACAGAT	ATCATACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTGTTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAAC	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATT	AACACGAAGG	AACGTGCAAC	ATATTTGGCT	TCTTAAACA	CATCCGTTCA	3480
25	CAAAGAAATT	ATTTGGTACA	AACGTAGGAG	CAATATGTCT	TCATTATGA	TACACTGGTT	3540
	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGTC	ATATTCATGC	CTATGTTAAT	3600
	GCATCTCTCA	TTCTTGAACC	AGCAGGCAAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
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	AAGAATCGAA	CTTCTTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTTATCCCTG	3780
30	AGTGGAGAAG	CTTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGSTCACT	3840
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	CTTATGGCTG	AAGAACACAA	ATGCTATCT	AATGAGGAAA	AACCTATAAT	TCAGGACTTT	4080
35	ATCTTAGAAG	CATACACAGG	TGATTATGTA	CTTGAAGTGA	GGCAGTTTCA	GTGCTCTAAA	4140
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40	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTGA	GCACAAGGCA	GGAAGAGAAT	4440
	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTGCGCTG	ATGGAAATAT	AGCTGAGAGC	4500
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	CCTGACAGTA	ACTTTCATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
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	ATTGTTTAGT	TTAATGACGT	AGTTCATTAG	CTGGTCTTAC	TCTACCAGTT	TTCTGACATT	5160
	GTATTGTGTT	ACCTAAGTGA	TTAATCTTGT	TTTCTCATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGAAATAC	CTTCATTTTG	AAAGAAGTTT	TTATGAGAAT	AACACCTTAC	CAACATTGT	5280
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Seq ID NO: 575 Protein sequence:
Protein Accession #: Eos sequence

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65	FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSFEEAV	KGKGLRLALS	180
	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
70	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPPE	420
	LIGTEEIIKE	EEEGKDIEEG	AIYNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPPTH	VEGTSASLND	540
	GSKTVLRSFH	MNLSGTAEAL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
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	PIKHPFKHVA	DLHASSGFTE	EPETLKEFYQ	EVQSCTVDLG	ITADSSNHDP	NKHKNRYINI	900
	VAYDHSRVKL	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPKSTAE	DFWRMIWEHN	960
80	VEVIVMITNL	VEKGRRKCDQ	YWPADGSEFY	GNFLVTQKSV	QVLAAYTVRN	FTLRNTKIKK	1020
	GSQGRGPGSR	VVTQYHYTQW	PDGMVPEYSL	PVLTFVRKAA	YAKRHAVGPV	VVHCSAGVGR	1080
	TGTYIVLDSM	LQQIQHEGTV	NIFGFLKHIR	SQRNYLVQTE	EQYVFIHDTL	VEAILSKETE	1140
	VLDSHIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIQQSD	YSAALKQCNR	EKNRTSSIIIP	1200
	VERSRVGISS	LSGEGTYDIN	ASYIMGYYSQ	NEFIITQHPL	LHTIKDFWRM	IWDHNAQLVV	1260
85	MIPDQGNMAE	DEFVYWPNDK	EPINCESFKV	TLMAEEHKCL	SNEKLIQD	FILEATQDDY	1320
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Seq ID NO: 576 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

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	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
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	GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
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	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
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Seq ID NO: 577 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 578 DNA sequence
 Nucleic Acid Accession #: EOS sequence
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Seq ID NO: 579 Protein sequence:
Protein Accession #: EOS sequence

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	ISENISQGYI	FSSNPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	EGNVWFPSST	540
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70	FPTEVTPHAF	TPSSRQQLDV	STVNVVYSQT	TQPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
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	IPIKHPPKHV	ADLHASSGFT	EEPETLKEFY	QEVQSCVVDL	GITADSSNHP	DNKHKNRYIN	780
	IVAYDHSRVK	LAQLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAQGPKLSTA	EDFWRMIWEH	840
	NVEVIVMITN	LVEKGRKCD	QYWPADGSEE	YGNFLVTQKS	VQVLAYYTVR	NFTLRNTRIK	900
75	KGSQKGRPSG	RVVTQYHYTQ	WPDMGVPEYS	LPVLTFVRKA	AYAKRHAVGP	VVVHCSAGVG	960
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	PVERSRRVGS	SLSGEGTDTY	NASYIMGYQQ	SNEFIITQHP	LLHTIKDFWR	MIWDHNAQLV	1140
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Seq ID NO: 581 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 583 Protein sequence
 Protein Accession #: NP_002842.1

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Protein Accession #: NP_005679.1

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5
10

VPWSVYGVYI	QAAGGPLAFI	VIMALFMLNV	GSTAFSTWML	SYWIKQSGSN	TTVTRGNETS	900
VSDSMKDNPH	MQYYASIYAL	SMAVMLILKA	IRGVVVFVKGT	LRASSRLHDE	LPRRILRSPM	960
KFFDTTPTGR	ILNRPFSKMD	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAGV	FPWFLVAVGP	1020
LVILFSVLHI	VSRVLIRELK	RLDNITQSPF	LSHITSSIQG	LATHAYNKG	QEFLLHRYQEL	1080
LDDNQAPFFL	PTCAMRWLAV	RLDLISIALI	TTTGLMIVLM	HGQIPPAYAG	LAISYAVQLT	1140
GLFQPTVRLA	SETEARFTSV	ERINHIYIKL	SLEAPARIKN	KAPSPDWQPE	GEVTFENAEM	1200
RYRENLPVLV	KKVSPTIKPK	EKIGIVGRGT	SGKSSLGMAL	FRLVELSGGC	IKIDGVRISD	1260
IGLADLRSLK	SIIPQEPVLF	SGTVRSNLDP	FNQYTEDQIW	DALERTHMKE	CIAQLPLKLE	1320
SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLLIQE	TIREAFADCT	1380
MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKVG	

Seq ID NO: 586 DNA sequence

Nucleic Acid Accession #: NM_001327.1

Coding sequence: 89..631

15
20
25
30

1	11	21	31	41	51	
AGCAGGGGCG	GCTGTGTGTA	CCGAGAATAC	GAGAATACCT	CGTGGGCCCT	GACCTTCTCT	60
CTGAGAGCCG	GGCAGAGGCT	CCGAGGCCAT	GCAGGCCGAA	GGCCGGGGCA	CAGGGGGTTC	120
GACGGGCGAT	GCTGATGGCC	CAGGAGGCCC	TGGCATTCTC	GATGGCCAG	GGGGCAATGC	180
TGGCGGCCCA	GGAGAGGGCG	GTGCCACGGG	CGGCAGAGGT	CCCCGGGGCG	CAGGGGCAGC	240
AAGGGCCTCG	GGGCGGGGAG	GAGGCGCCCC	CGCGGGTCCG	CATGGCGGCG	CGGCTTCAGG	300
GCTGAATGGA	TGCTGCAGAT	GCGGGGCCAG	GGGGCCGGAG	AGCCGCCTGC	TTGAGTTCTA	360
CCTCGCCATG	CCTTTCGCGA	CACCCATGGA	AGCAGAGCTG	GCCCGCAGGA	GCCTGGCCCA	420
GGATGCCCCA	CCGCTTCCCG	TGCCAGGGGT	GCTTCTGAAG	GAGTTCAGTG	TGTCGGGCAA	480
CATACTGACT	ATCCGACTGA	CTGCTGCAGA	CCACCGCCAA	CTGCAGCTCT	CCATCAGCTC	540
CTGTCTCCAG	CAGCTTTCCT	TGTTGATGTG	GATCACGCAG	TGCTTCTGCG	CCGTGTTTTT	600
GGCTCAGCTC	CCCTCAGGGC	AGAGGCGCTA	AGCCCGAGCT	GGCGCCCTTT	CCTAGGTCAT	660
GCCTCTCTCC	CTAGGGAATG	GTCCAGCAC	GAGTGGCCAG	TTCATTGTGG	GGGCGCTGAT	720
GTTTGTGCTG	GGAGGAGGAC	GGCTTACATG	TTTGTTCCTG	TAGAAAATAA	AACTGAGCTA	

Seq ID NO: 587 Protein sequence

Protein Accession #: NP_001318.1

35
40

1	11	21	31	41	51	
MQAEGRGTTG	STGDADGPGG	PGIPDGPGGN	AGGPGEAGAT	GGRGPRGAGA	ARASGPGGGA	60
PRGPHGGAAS	GLNGCCRCGA	RGPE SRLLEF	YLAMPFATPM	EAELARRSLA	QDAPPLPVPG	120
VLLKEPTVSG	NILTRLTLAA	DHRQLQLSIS	SCLQLLSLLM	WITQCFLPVF	LAQPPSGQRR	

Seq ID NO: 588 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 52..459

45
50
55

1	11	21	31	41	51	
CCTCGTGGGC	CCTGACCTTC	TCTCTGAGAG	CCGGGCAGAG	GCTCCGGAGC	CATGCAGGCC	60
GAAGGCCAGG	GCACAGGGGG	TTCAGCGGGC	GATGCTGATG	GCCCGAGAGG	CCCTGGCATT	120
CCTGATGGCC	CAGGGGGGCA	TGCTGGCGGC	CCAGGAGAGG	CGGGTGCCAC	GGGCGGCAGA	180
GGTCCCGCGG	CGCGAGGGGC	AGCAAGGGCC	TCCGGGCGCA	GAGGAGGCGC	CCCGCGGGGT	240
CCGATGCGCG	GTGCCGCTTC	TGCGCAGGAT	GGAAGGTGCC	CCTGCGGGGC	CAGGAGGGCG	300
GACAGCGGCC	TGCTTCAGTT	CCGACTGACT	GCTGCAGACC	ACCGCCAACT	GCAGCTCTCC	360
ATCAGCTCTC	GTCTCCAGCA	GCTTCCCTG	TTGATGTGGA	TCACGCACTG	CTTCTGCCCC	420
GTGTTTTTGG	CTCAGGCTCC	CTCAGGGCAG	AGGCGCTAAG	CCCAGCCTGG	CGCCCCCTCC	480
TAGGTCATGC	CTCCTCCCTC	AGGGAATGGT	CCCAGCACGA	GTGGCCAGTT	CATTGTGGGG	540
GCCTGATTGT	TTGTGCTGCG	AGGAGGACGG	CTTACATGTT	TGTTTCTGTA	GAAAATAAAG	600
CTGAGCTA						

Seq ID NO: 589 Protein sequence

Protein Accession #: Eos sequence

60
65

1	11	21	31	41	51	
MQAEGGQTGG	STGDADGPGG	PGIPDGPGGN	AGGPGEAGAT	GGRGPRGAGA	ARASGPRGGA	60
PRGPHGGAAS	AQDGRCPGCA	RRPDSRLQLF	RLTAADHRQL	QLSISSCLQQ	LSLLMWITQC	120
FLPVFLAQAP	SGQRR					

Seq ID NO: 590 DNA sequence

Nucleic Acid Accession #: NM_005562.1

Coding sequence: 90..3671

70
75
80
85

1	11	21	31	41	51	
ACAGCGGAGC	GCAGAGTGAG	AACCACCAAC	CGAGGCGCGG	GGCAGCGACC	CCTGCAGCGG	60
AGACAGAGAC	TGAGCGGGCC	GGCACCGCCA	TGCCTGCGCT	CTGGCTGGGC	TGCTGCCTCT	120
GCTTCTCGCT	CCTCTGCCCC	GCAGCGCGGG	CCACCTCCAG	GAGGGAAGTC	TGTGATTGCA	180
ATGGGAAGTC	CAGGCAGTGT	ATCTTTGATC	GGGAACCTCA	CAGACAAACT	GGTAATGGAT	240
TCCGTGCGCT	CAACTGCAAT	GACAACTAGT	ATGGCATTCA	CTGCGAGAAG	TGCAAGAATG	300
GCTTTTACCG	GCACAGAGAA	AGGGACCGCT	GTTTGCCCTG	CAATTGTAACT	TCCAAGGTT	360
CTCTTAGTGC	TGATGTCTGC	AACCTGGAC	GGTGACAGTG	TAAACCAAGT	GTGACAGGAG	420
CCAGATGCGA	CCGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAAG	480
ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCCGTG	540
ACGCGGGCCG	CTGTGCTGCG	AAGCCAGCTG	TTACTGGAGA	ACGCTGTGAT	AGGTGTCGAT	600
CAGGTTACTA	TAATCTGGAT	GGGGGAACCC	CTGAGGGCTG	TACCCAGTGT	TTCTGCTATG	660
GGCATTGACG	CAGCTGCCCC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
TTATCAAGA	TGTTGATGGC	TGGAAGGCTG	TCCAACGAAA	TGGGTCTCCT	GCAAAGCTCC	780
AATGGTCACA	GCGCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840

	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCTT	900
	TTGACTACCG	TGTGGACAGA	GGAGGCGAGC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
	GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
5	TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCAGC	1080
	TGAGTTACTT	TTAGTATCGA	AGGTTACTGC	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCGCCCTG	1200
	TCTCTGGAGC	CCCAGCACCC	TGGGTGAAC	AGTGATATATG	TCTGTGTTGG	TACAAGGGGC	1260
	AATTCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTG	AGCGAGACTG	GGGCTTTTGG	1320
10	GCACCTGTAT	TCCTTGTAA	TGTCAAGGGG	GAGGGGCTTG	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTTCAGG	GGATGAGAAT	CCTGACATTG	AGTGATGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCCGCA	CGACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTGAGCTGCT	1500
	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTCACCGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CATGGCCAG	1620
	TGAGGCTTGG	TCAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
15	GTGACCGGCT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTGCG	1740
	ACCAGTGCAA	AGCAGGCTAT	TTGGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTC	1800
	GAGCTTGCAA	CTGTAACCCC	ATGGGCTCAG	AGCCTGTAGG	ATGTGGAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTG	AGCTGTCCAG	1920
	CTTGCTATAA	TCAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
20	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCAG	2100
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAGGT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAG	AGTTCCGGGT	CTGGGAAGTC	2220
	AGTACCAGAA	CCGAGTTCGG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
25	CAGAAAGTGA	AGCTTCCCTG	GGAAACACTA	ACATTCTCTG	CTCAGACCAC	TACGTGGGGC	2340
	CAAAATGGCTT	TAAAGTCTTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAGT	2400
	CAGCCAGTAA	CATGGAGCAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACCTGGTGG	CAAGGCCCTG	CATGAAGGAG	TGGGAAGCGG	AAGCGGTAGC	CCGGAAGGTG	2520
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAACCAA	GTCCTGGGCC	CAGCAGTTGA	2580
30	CAAGGGAGGC	CACCTAAGCG	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGCTCTCG	CTTCAGGGAG	TCAGTGATCA	GTCCTTTCAG	GTGGAAGAAG	2700
	CAAAGAGGAT	CAAAACAAAA	GCGGATTTC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAAG	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAATGGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
35	AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTCG	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGAGGC	CCTGGAAATC	TCCAGTAGGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
40	AAGCCCAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAAG	3240
	GTGAGATGAG	GGAAGTGGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAGAAGC	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCTGTCAT	CTGATGGACC	3420
	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAAGCT	TCCCGAGCCA	3480
45	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCAGCTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAACTTGGA	GAACATTAGG	GACAACTTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AGCTGCGCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCTATG	TGAGTGGGTG	GGATGGGGAC	ATTGGAACAT	GTTTAATGGG	3780
50	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTTGTCTTAT	3840
	TGCACCATAC	TCTTGTCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCCT	CATAATAGTC	GTAAGTGGAG	TCTTGGAAAT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATTCCTTGA	GTAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCCAGGC	4080
55	ATGAAATCTT	TCTAATGTG	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
	ACTATTGCCT	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCCT	CCTACTTACA	4200
	ACCCAGGGTG	TGAACGATG	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCC	ATTGAGAGCT	ATGGTGCTTG	CTGGTGCCCTG	CCACCTTCAA	4320
	GTCTTGAGCC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
60	ATTTTATTAT	AAGCAATGTC	TACCAGCAAA	GCAAAATGTT	GGAAAGTATT	TACTTTTTCG	4440
	GTTTCAAAGT	GATAGAAAAG	TGTGGCTTGG	GCAATTGAAAG	AGGTAAATTT	CTCTAGATT	4500
	ATTAGTCTTA	ATTCAATCCT	ACTTTTCGAA	CACCAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTCTACT	4620
	CACACTTCAG	CTGGGTGACA	TCCATCCCTC	CATTTCATCT	TCCATCCATC	TTTCCATCCA	4680
65	TTACCTCCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
	GTGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTTAA	AAAAATAAAT	TAAACTTAC	AACTTTGTT	TGTCACAAGT	GGTGTATTAT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTG	CTCAACAGAA	CATATGTTGC	AAGACCCTCC	4920
	CATGGGGGCA	CTTGAGTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTGTGCA	CATTTCTTTG	4980
70	CATTCCAGCT	GTCACTCTGT	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
	TAACACCAGT	GGGAATTGCT	GGAGGAACCA	GAGGCACCTC	CACCTTGGCT	GGGAAGACTA	5100
	TGGTCTGCC	TGTCTCTGT	ATTTCTTGG	ATTTCTCTGA	AAGTGTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 591 Protein sequence
Protein Accession #: NP_005553.1

	1	11	21	31	41	51	
80	MPALWLGCC	LFSLLLPAAR	ATSRREVDCD	NGKSRCQIFD	RELHROQTGNG	FRCLNCNDNT	60
	DGHLCEKCKN	GFYRHRERDR	CLPCNCSKG	SLSARCDNSG	RCSCKPGVTG	ARCDRLPGF	120
	HMLTDAGCTQ	DQRLLDLSDKD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYYNLDGGN	180
	PBGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRDPVY	FVAPAKFLGN	QQVSYGQSL	FDYRVDGRGR	HPSAHDVILE	GAGLRITAPL	300
85	MPLGKTLPCG	LTKTYTFLRN	EHPSNNWSPQ	LSYFEYRRL	RNLTLALRIRA	TYGEYSTGYI	360
	DNVTILISAR	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY	KRDSARLGP	GTCIPCNQCY	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDRSCK	PCPCHNGFSC	SVMPEEEV	480

CWNCPPGVGTG	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPASAGN	CDRLTGRCLK	540
CIHNTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCNPMGS	EPVGCSDGT	CVCKPGFPGP	600
NCEHGAFSCP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAQAL	660
QDILRDAQIS	EGASRSLGLQ	LAKVRSQENS	VQSRLLDDLKM	TVERVRALGS	QYQNRVRDTH	720
RLITQMQLSL	AESEASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780
ETEDYSKQAL	SLVRKALHEG	VGSGSGSPDG	AVVQGLVEKL	EKTKSLAQQL	TREATQAEIE	840
ADRSYQHSRL	LLDSVSRLQG	VSDQSFOVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG	900
NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEALSM	GNATFYEVES	ILKNLREFDL	960
QVDNRKAEAE	EAAMKRLSYIS	QKVSADSDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
IEQEIGSLNL	EANVTADGAL	AMEKGLASLK	SEMRVEVEGEL	ERKELEFDTN	MDAVQMVITE	1080
AQKVDTRAKN	AGVTIQDTLN	TLDGLLHLM	QPLSVDEEGL	VILLEQKLSRA	KTQINSQLRP	1140
MMSELEERAR	QQRGHLHLE	TSIDGILADV	KNLENIRDNL	PPGCYNTQAL	EQQ	

Seq ID NO: 592 DNA sequence
Nucleic Acid Accession #: AF101051.1
Coding sequence: 221.856

1	11	21	31	41	51	
GAGCAACCTC	AGCTTCTAGT	ATCCAGACTC	CAGCGCGGCC	CCGGGCGCGG	ACCCCAACCC	60
CGACCCAGAG	CTTCTCCAGC	GGCGGCGCAG	CGAGCAGGGC	TCCCCGCCTT	AACCTTCTCC	120
CGCGGGCCCC	GCCACCTTCG	GGAGTCCGGG	TTGCCACCTC	GCAAACTCTC	CGCCTTCTGC	180
ACCTGCCACC	CCTGAGCCAG	CGCGGGCGCC	CGAGCGAGTC	ATGGCCAACG	CGGGGCTGCA	240
GCTGTTGGGC	TTTATCTCG	CCTTCTGGG	ATGGATCGGC	GCCATCGTCA	GCACTGCCTT	300
GCCCCAGTGG	AGGATTTACT	CCTATGCCGG	CGACAACATC	GTGACCGCCC	AGGCCATGTA	360
CGAGGGGCTG	TGGATGCTCT	GGGTGTCGCA	GAGCACCGGG	CAGATCCAGT	GCAAGTCTT	420
TGACTCCTTG	CTGAATCTGA	GCAGCACATT	GCAAGCAACC	CGTGCCTTGA	TGGTGGTGG	480
CATCCTCCTG	GGAGTGATAG	CAATCTTTGT	GGCCACCGTT	GGCATGAAGT	GTATGAAGTG	540
CTTGGAAAGAC	GATGAGGTGC	AGAAGATGAG	GATGGCTGTC	ATTGGGGGTG	CGATATTTCT	600
TCTTGCAAGT	CTGGCTATTT	TAGTTGCCAC	AGCATGGTAT	GGCAATAGAA	TCGTTCAAGA	660
ATTCTATGAC	CCTATGACCC	CAGTCAATGC	CAGGTACGAA	TTTGGTCAGG	CTCTCTTAC	720
TGGCTGGGCT	CTGCTTCTC	TCTGCCCTCT	GGGAGGTGCC	CTACTTTGCT	GTTCTGTGCC	780
CCGAAAAACA	ACCTCTTACC	CAACACCAAG	GCCCTATCCA	AAACCTGCAC	CTTCCAGCGG	840
GAAAGACTAC	GTGTGACACA	GAGGCAAAAG	GAGAAAATCA	TGTTGAAACA	AACCGAAAAT	900
GGACATTGAG	ATACTATGCT	TAACATTAGG	ACCTTAGAAT	TTTGGGTATT	GTAATCTGAA	960
GTATGGTATT	ACAAAACAAA	CAAAACAAACA	AAAAACCCAT	GTGTTAAAT	ACTCAGTGCT	1020
AAACATGGCT	TAATCTTATT	TTATCTTCTT	TCCTCAATAT	AGGAGGGAAG	ATTTTACCAT	1080
TTGTATTACT	GCTTCCCAAT	GAGTAATCAT	ACTCAAATGG	GGGAAGGGGT	GCTCCTTAAA	1140
TATATATAGA	TATGTATATA	TACATGTTTT	TCTATTAAAA	ATAGACAGTA	AAATACTATT	1200
CTCATATTGT	TGATACTAGC	ATACITAAAA	TATCTCTAAA	ATAGGTAAAT	GTATTTAATT	1260
CCATATTGAT	GAAGATGCTT	ATTGGTATAT	TTTCTTTTTC	GTCCTTATAT	ACATATGTAA	1320
CAGTCAAATA	TCATTTACTC	TTCTTCATTA	GCTTTGGGTG	CCTTTGCCAC	AAGACCTAGC	1380
CTAATTTACC	AAGGATGAAT	TCITTTCAAT	CTTCATGCGT	GCCCTTTTCA	TATACTTATT	1440
TTATTTTFTA	CCATAATCTT	ATAGCACTTG	CATCGTTATT	AAGCCCTTAT	TTGTTTGTG	1500
TTTCATTGGT	CTCTATCTCC	TGAATCTAAC	ACATTTTATA	GCCTACATTT	TAGTTTCTAA	1560
AGCCAAGAAG	AATTTATTAC	AAATCAGAAC	TTTGGAGGCA	AATCTTTCTG	CATGACCAAA	1620
TGATAAAAT	CTGTGTGACC	TTCCACACACA	ATCCCTGTAC	TCTGACCCAT	AGCACTCTTG	1680
TTTGCTTTGA	AAATATTTGT	CCAATTGAGT	AGCTGCATGC	TGTTCCCCCA	GGTGTGTAA	1740
CACAACCTTT	TTGATTGAAT	TTTTAAGCTA	CTTATTCATA	GTTTATATAT	CCCCTAAAT	1800
ACCTTTTGTG	TCCCAATCTC	TTAATTGTAT	TGTTTTCCTA	AGTGTAAATTA	TCATGCGTTT	1860
TATATCTTCC	TAATAAGGTG	TGGTCTGTTT	GTCTGAACAA	AGTGTAGTAC	TTTCTGGAGT	1920
GATAATCTGG	TGACAAATAT	TCTCTCTGTA	GCTGTAAGCA	AGTCACTTAA	TCTTTCTACC	1980
TCITTTTCTT	ATCTGCCAAA	TTGAGATAAT	GATACTTAA	CAGTTAGAAG	AGGTAGTGTG	2040
AATATTAATT	AGTTTATATT	ACTCTCATTC	TTTGAACATG	AACATAGCCT	ATGTAGTGTG	2100
TTTATTTGCT	CAGCTGGCTG	AGACACTGAA	GAAGTCACTG	AACAAAACCT	ACACACGTAC	2160
CTTCATGTGA	TTCACTGCCT	TCCTCTCTCT	ACCACTCTAT	TTCCACTGAA	CAAAAACCTAC	2220
ACACATACCT	TCATGTGGTT	CAGTGCCTTC	CTCTCTCTAC	CAGTCTATTT	CCACTGAACA	2280
AAACCTACGC	ACATACCTTC	ATGTGGCTCA	GTGCCTTCTC	CTCTCTACCA	GTCTATTTCC	2340
ATTCTTTTCA	CTGTGCTGTA	CATGTTTGTG	CTCTGTTCCT	TTTAAACAAC	TGCTCTTACT	2400
TTTCCAGTCT	GTACAGAATG	CTATTTCACT	TGAGCAAGAT	GATGTATGGA	AAGGGTGTG	2460
GCATCTGGT	CTGGAGACCT	GGATTGAGT	CTTGGTGCTA	TCAATCACCG	TCTGTGTTTG	2520
AGCAAGGCAT	TTGGCTGCTG	TAAGCTTATT	GCTTCATCTG	TAAGCGGTGG	TTGTGAATTC	2580
CTGATCTTCC	CACCTCACAG	TGATGTTGTG	GGGATCCAGT	GAGATAGAAT	ACATGTAAGT	2640
TGGGTTTGT	AATTTGAAAA	GTGCTATACT	AAGGGAAAGA	ATTGAGGAAT	TAAGTGCATA	2700
CGTTTGGGTG	TTGCTTTTCA	AATGTTTGAA	AATAAAAAAA	TGTTAAGAAA	TGGGTTTCTT	2760
GCCTTAACCA	GTCTCTCAAG	TGATGAGACA	GTGAAGTAAA	ATTGAGTGCA	CTAAACGAAT	2820
AAGATTCTGA	GGAGTCTTAA	TCTTCTGCAG	TGAGTATGGC	CCAATGCTTT	CTGTGGCTAA	2880
ACAGATGTAA	TGGGAAGAAA	TAAAGCCCTA	CGTGTGGTA	AATCCAACAG	CAAGGGAGAT	2940
TTTTGAATCA	TAATAACTCA	TAAGGTGCTA	TCTGTTTCA	GATGCCCTCA	GAGCTCTTGC	3000
TGTTAGCTGG	CAGCTGACGC	TGCTAGGATA	GTTAGTTTGG	AAATGGTACT	TCATAATAAA	3060
CTACACAAAG	AAAGTCAGCC	ACCGTGTCTT	ATGAGGAATT	GGACCTAATA	AATTTTAGTG	3120
TGCCTTCCAA	ACCTGAGAA	ATATGCTTTT	GGAAGTTAAA	ATTTAAATGG	CTTTTGCCAC	3180
ATACATAGAT	CTTCTAGATG	TGTGAGTGTA	ATTCCATGTG	GATATCAGTT	ACCAACATT	3240
ACAAAAAAT	TTTATGGCCC	AAAATGACCA	ACGAAATTGT	TACAAATAGAA	TTTATCCAA	3300
TTTGATCTTT	TTATATTCTT	CTACCACACC	TGGAACAGCA	CCAATAGACA	TTTGGGGTT	3360
TTATAATGGG	AATTTGTATA	AAGCATTACT	CTTTTCAAT	AAATGTTTTT	TTAATTTAAA	3420
AAAAGGAAAA	AAAAAATAAA	AAA				

Seq ID NO: 593 Protein sequence
Protein Accession #: AAD16433.1

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QIQCKVFDLS	LNLSSLTQAT	RALMVGIGLL	GVIAIFVATV	GMKCMKCLSD	DEVQKMRMAV	120
IGGAIFLLAG	LAILLVATAWY	GNRIVQEFYD	PMPVFNARYE	FGQALFTGWA	AASLCLLGGA	180
LLCCSCPRKT	TSYPTPRPYP	KPAESGKDY V				

Seq ID NO: 594 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

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CCCCCTGTAA	AGCGGTTGCG	TATGCGGGGA	CCACTGTGAA	CCCTGCCGCC	TGCCGGAACA	180
CTCTTCGCTC	CGGACCAAGT	CAGCCTCTGA	TAAGCTGGAC	TGGCAGCGCC	CGCAACAAGC	240
ACCGAGGAGT	TAAGAGAGCC	GCAAGCGCAG	GGAAGGCCTC	CCCCGACGGG	TGGGGGAAAG	300
CGGCCGGTGC	AGCGCGGGGA	CAGGCACTCG	GGCTGGCACT	GGCTGCTAGG	GATGTCGTCC	360
TGGATAAGGT	GGCATGGACC	CGCCATGGCG	CGGCTTTGGG	GCTTCTGCTG	GCTGGTTGTG	420
GGCTTCTGGA	GGGCCGCTTT	CGCCTGTCCC	ACGTCTCTGA	AATGCAGTGC	CTCTCGGATC	480
TGGTGCAGCG	ACCCTTCTCC	TGGCATCGTG	GCATTTCCGA	GATTGGAGCC	TAAACAGTGA	540
GATCCTGAGA	ACATCACCGA	AATTTTCATC	GCAAACCGA	AAAGGTTAGA	AATCATCAAC	600
GAAGATGATG	TTGAAGCTTA	TGTGGGACTG	AGAAATCTGA	CAATTGTGGA	TTCTGGATTA	660
AAATTTGTGG	CTCATAAAGC	ATTTCTGAAA	AACAGCAACC	TGCAGCACAT	CAATTTTACC	720
CGAAACAAAC	TGACGAGTTT	GTCTAGGAAA	CATTTCCGTC	ACCTTGACTT	GCTGAACTG	780
ATCCTGGTGG	GCAATCCATT	TACATGCTCC	TGTGACATTA	TGTGGATCAA	GACTCTCCAA	840
GAGGCTAAAT	CCAGTCCAGA	CACCTCAGGAT	TTGTACTGCC	TGAATGAAAG	CAGCAAGAAT	900
ATTCCCTCGG	CAAACCTGCA	GATACCCAAT	TGTGGTTTGC	CATCTGCAAA	TCTGGCCGCA	960
CCTAACCTCA	CTGTGGAGGA	AGGAAAGTCT	ATCACATTAT	CCTGTAGTGT	GGCAGGTGAT	1020
CCGGTTCTTA	ATATGTATTG	GGATGTTGGT	AACCTGGTTT	CCAAACATAT	GAATGAAACA	1080
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ATCTCCAATG	GGAGTAACAC	TCCATCTTCT	TGCGAAGGTG	GCCGAGATGC	TGTCATTATT	1860
GGAATGACCA	AGATCCCTGT	CATTGAAAAT	CCCCAGTACT	TTGGCATCAC	CAACAGTCAG	1920
CTCAAGCCAG	ACACATTGTT	TACAGCACATC	AAGCGACATA	ACATTTGTTCT	GAAAAGGGAG	1980
CTAGGCGAAG	GAGCCTTTGG	AAAAGTGTTC	CTAGCTGAAT	GCTATAACCT	GCTCTCTGAG	2040
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CCGCCACCGG	AACCTGACGA	GTCCGAGATG	CTGCATATAG	CCCAGCAGAT	CGCCGCGGGC	2340
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GTCCGGGAGA	ACTTGCTGGT	GAAAATCGGG	GACTTTGGGA	TGTCCCGGGA	CGTGTACAGC	2460
ACTGACTACT	ACAGGGTCCG	TGGCCACACA	ATGCTGCCCA	TTCGCTGGAT	GCCTCCAGAG	2520
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CATCTTTTAA	TCGCCGCTGG	AGGCCACCAA	GCTGCTCTCC	TTCACTCTGA	CAGTATTAAC	2940
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ACCCTTTTCT	TTGAATCAAT	CTGGCTTCTG	CATTACTATT	AACTCTGCAT	AGACAAAGGC	3180
CTTAACAAAC	GTAATTTGTT	ATATCAGCAG	ACACTCCAGT	TTGCCACCA	CAACTAACAA	3240
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ATTTATTATG	AACCGCAATA	TGGGAGGAAC	AAAGACAACC	ACTGGGATCA	GCTGGTGTCA	3540
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CCTGAGGACC	TTTCTGAGGA	GTAAAAAGAC	TACTGGCCTC	TGTGCCATGG	ATGATTCTTT	3660
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Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

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NFTRNKLTL	SRKHFRHL	SELILVGNPF	TCSCDIMWIK	TLQEAQKSPD	TQDLYCLNES	180
SKNPLANLQ	IPNCGLPAN	LAAPNLTV	GKSITLSCSV	AGDPVPMYV	DVGNLVSXHM	240
NETSHQSG	RITNISDD	GKQISCAEN	LVGEDQDSV	LTVHFAPTIT	FLESPTSDHH	300
WCIPFTVKGN	PKPALQWYFN	GAILNESKYI	CTKIHVTNHT	EYHGCLQLDN	PTHMNGDYT	360
LIAKNEYGKD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSENPST	420
DVTDKRGREH	LSVYAVVVIA	SVVGFCLLVM	LFLKLARHS	KFGMKGPASV	ISNDDDSASP	480
LHHISNGSNT	PSSSEGPD	VIIGMTKIPV	IENPQYFGIT	NSQLKPDFTV	QHIKRHNIVL	540
KRELGEAGFG	KVFLAECYNL	CPEQDKILVA	VKTLKADSDN	ARKDFHREAE	LLTNLQHEHI	600
VKFYGVCEVG	DPLIMVFYEM	KHGDNLKFLR	AHGPDAVLMA	BGNPTELTQ	SQMLHIAQOI	660
AAGMVYLASQ	HFVHRDLATR	NCLVGENLLV	KIGDFGMSRD	VYSTDYRVG	GHTMLPIRWM	720

PPESIMYRKF TTESDVWSLG VVLWEITYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ 780
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Coding sequence: 483..2999

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    CGCCCGGTCC GTGCCCGGCG CGCCGGGCCA TGCAGCGACG GCCCGCGCGG AGCTCCGAGC 240
15  AGCGGTAGCG CCCCTCTGTA AAGCGGTTTC CTATGCCGGG ACCACTGTGA ACCCTGCGCG 300
    CTGCCGGAAC ACTCTTCGCT CCGGACCAGC TCAGCCTCTG ATAAGCTGGA CTCCGACACG 360
    CCGCAACAAG CACCGAGGAG TTAAGAGAGC CGCAAGCGCA GGGAAAGGCCT CCCCGCACGG 420
    TGGGGGAGAA GCGGCGGGTG CAGCGCGGGG ACAGGCATCT GGGCTGGCAG TGGCTGCTAG 480
    GGATGTCGTC CTGGATAAAG TGGCATGGAC CCGCCATGGC GCGGCTCTGG GGCTTCTGCT 540
20  GGCTGGTTGT GGGCTTCTGG AGGGCCGCTT TCGCCTGTCC CACGTCTGTC AAATGCAGTG 600
    CCTCTCGGAT TCGGTCGAGC GACCCCTTCT CTGGCATCGT GGCATTTCCG AGATTGGAGC 660
    CTAACAGTGT AGATCTCTAG AACATCACCG AAATTTTCAT CGCAAACAG AAAAGGTTAG 720
    AAATCATCAA CGAAGATGAT GTTGAAGCTT ATGTGGGACT GAGAAATCTG ACAATTGTGG 780
    ATTCTGGATT AAAATTGTG GCTCATAAAG CATTCTGAA AAACAGCAAC CTCGAGCACA 840
    TCAATTTTAC CCGAAACAAA CTGACGAGTT TGTCTAGGAA ACATTTCCGT CACCTTGACT 900
25  TGCTTGAATC GATCCTGGTG GGCAATCCAT TTACATGCTC CTGTGACATT ATGTGGATCA 960
    AGACTCTCCA AGAGGCGGTG TCCAGTCCAG ACACCTCAGG TTTGTACTGC CTGAATGAAA 1020
    GCAGCAAGAA TATTCCTCTG GCAAACTGTC AGATACCCAA TTGTGGTTTG CCATCTGCAA 1080
    ATCTGGCCCG ACCTAACCTC ACTGTGGAGG AAGGAAAGTC TATCACATTA TCCTGTAGTG 1140
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30  TGAATGAAAC AAGCCACACA CAGGGCTCCT TAAGGATAAC TAACATTTC TCCGATGACA 1260
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    ACTGGTGCAT TCCATTCACT GTGAAAGGCA ACCCCAAACC AGCGCTTCAG TGGTCTTATA 1440
    ACGGGGCAAT ATTGAATGAG TCCAAATACA TCTGTACTAA AATACATGTT ACCAATCACA 1500
35  CGAGTACCA CTGCTGCTCT CAGCTGGATA ATCCCACTCA CATGAACAAT GGGGACTACA 1560
    CTCTAATAGC CAAGAATGAG TATGGGAAGG ATGAGAAACA GATTCTGCT CACTTCATGG 1620
    GCTGCGCTGG AATTGACGAT GGTGCAAAAC CAAATTATCC TGATGTAATT TATGAAGATT 1680
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    CAGACGTCAC TGATAAAACC GGTGCGGAAC ATCTCTCGGT CTATGCTGTG GTGGTGATTG 1800
40  CGTCTGTGGT GGGATTTTGC CTTTGTGTAA TGCTGTTTCT GCTTAAGTTG GCAAGACACT 1860
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45  TCAAGCCAGA CACATTGTGT CAGCACATCA AGCGACATAA CATTGTTCTG AAAAGGGAGC 2160
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65  CCCTTCTTTT TGAATCAAT TGGCTCTGC ATTACTATTA ACTCTGCATA GACAAAGGCC 3360
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75  ATGGCGCATA GTGTGCTCGG ACACAGTTT GTCTCTGTA GTTGTGATG TAGCACTGGT 3960
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Seq ID NO: 597 Protein sequence
Protein Accession #: AAL67965.1

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    NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSIDIMWIK TLQBAKSSPD TDLYCLNES 180
    SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSITLSCSV AGDPVPNNYW DVGNLVSKHM 240

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 FHREAEELLN LQHEHIVKFY GVCVEGDPLI MVFEYMKHGD LNKPLRAHGP DAVLMAEGNP 660
 PTELTSQSQL HIAQQAAGM VYLAHQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720
 DYYRVGGHTM LPIRWMPPE S IMYRKFTTES DVWSLGVVLW EIFTYKQFPW YQLSNNEVIE 780
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 Protein Accession #: BAB61048.1

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 Coding sequence: 57..482

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 ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA 420
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 CCACCCCTGG ACTGGTGGCC CCCACCCTGC GGGAGGCTC CCCATGTGCC TGCGCCAAGA 600
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Seq ID NO: 601 Protein sequence
 Protein Accession #: NP_001889.1

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Seq ID NO: 602 DNA sequence
 Nucleic Acid Accession #: NM_003976.2
 Coding sequence: 299..961

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 GGGTGGCAGG CCGGTCCCCC ACAAAGATA ACTCATCTCT TAAATTGCAA GCTGCTCAA 240
 CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT 300
 GGAACCTGGA CTCTGGAGGC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360
 TGCCCTGTGG CCTTCTCGGC CCGCTCTGGC TCTGCTGAGC AGCGTCGAG AGGCTCCCT 420
 GGGCTCGCGC CCGCGCAGCC CTGCCCCCGC CGAAGGCCCC CCGCTGTGCC TGGCGTCCCC 480
 CGCGGGCCAC CTGCCCCGGG GACGACGGC CCGCTGGTGC AGTGGAGAG CCCGGCGGCC 540
 GCGCGCGCAG CCTTCTCGGC CCGCGCCCCC GCGGCTGCA CCCCCTCTG CTCTTCCCG 600
 CGGGGGCCGC GCGGCGCGGC CTGGGGGCCC GGGCAGCCGC GCTCGGGCAG CGGGGGCGCG 660
 GGGGTGCGCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGC CTCGGCTGG GCCACCGCTC 720
 CGACGAGCTG GTGCGTTTCC GCTTCTGAGC CGGCTCCTGC GCGCGCGCGC GCTCTCCACA 780
 CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCG 840
 GCCCGTCAAG CAGCCCTGCT GCGGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
 CAACAGCACC TGGAGAACCG TGGACCGCCT CTCGCGCACC GCCTGCGGCT GCCTGGGCTG 960
 AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCTTACCCTG TGGCTCTTCC TGCTGGGAC 1020
 CCTCCGCGAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
 AGGCCCCTAC CGGTGGGTGA TGGATATCAT CCCGAACAG GTGAAGGGAC AACTGACTAG 1140
 CAGCCCCAGA GCCCTCAGCC TGGGATATCC AGCCTAAAAG ACACAGAGA CCTCAGCTAT 1200
 GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAC 1260
 CCCTCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGGCCAGG CCTGTAGGG 1320
 ACAGCATTTG AAGGACACAT ATTGCAGTTG CTGTGTTGAA AGTGCTGTG CTGGAACCTG 1380
 CCTGTACTCA CTATGGGAG CTGGCCCC

Seq ID NO: 603 Protein sequence
 Protein Accession #: NP_003967.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCRRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRARRSP HDLSLASLLG AGALRPPPGS 180
 RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 604 DNA sequence
 Nucleic Acid Accession #: NM_057091.1
 Coding sequence: 783..1445

1 11 21 31 41 51
 ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
 GGACCCCAAA ATCTGCACGT ACCAGCAGTC AGCCGCCCA CGCAGGGACC GGCTTACCCC 120
 TCGCTCCCCG CCTCTACTCA CTTTCTCCCG CCCTCGGCC GGCCTCCAG CTCTACTT 180
 CGCGTGTCTA CAACTCAAC TCCCGGTTTC CGTGCCTCTC CACGCTCGA GTTCTCTACT 240
 CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCTC CCAACCTCGG GGGACCTAGC 300
 CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG 360
 CGGGGCGAGG GCCTCCAG CCGCACCCCG GGATCTGGTG ACGCTGGGGC TGGAAATTGA 420
 CACCGGACGG CTGCGCGCGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC 480
 CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGCACCCAGC CTGCTGCCA 540
 CCGGGGCTG GAGCCCCACA CCGAGGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAGAGGCG ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGAGA 660
 GCCCAGCACT GGTCCCCCGA AAGGTGCCCTA GAAGAACAAG GTGCAGGACC CCGTCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCCTCCTG GTGTTGATAG 780
 AGATGGAACT TGGACTTGA GGCCTCTCCA CGCTGTCCCA CTGCCCTTGG CCTAGGCGGC 840
 AGCCTGCCCT GTGGCCCTCT CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCT 900
 CCCTGGGCTC CGCGCCCGC AGCCCTGCCC CCGCGGAAG CCCCCCGCT GTCTTGGCT 960
 CCCCCGCGG CCACCTGCGG GGGGAGCGCA CGGCCGCTG GTGAGTGA AGAGCCCGGC 1020
 GCGCGCGCGC CCGGGGGCTC CCGCCGCGC CCGCGCGCC TGACCCCA TCTGCTCTTC 1080
 CCGCGCGGG CCGCGCGCG CCGGCTGGGG GCGCGGCGC CCGCTCGG GCAGCGGGG 1140
 CGCGGGGCTG CCGCTTGGC TCGCAGCTGG TGCCGGTGGC CGCGCTCGC CTGGGCCACC 1200
 GCTCCGACGA GCTGGTGGCT TCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGGCTCTC 1260
 CACACGACCT CAGCTTGGCC AGCCTACTGG GCGCGGGGC CCTGCGACCG CCCCCGGCT 1320
 CCGCGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 ACGTCAACAG CAGCTGGAGA ACCGTGGACC GCCTCTCCG CACCGCTGCG GGCTGCCCTG 1440
 GCTGAGGGCT CGCTCAGGG CTTTGCAGAC TGGACCTTA CCGGTGGCTC TTCCTGCTG 1500
 GGACCCCTCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
 TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA 1620
 CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACCCA GAGACCTCAG 1680
 CTATGGAGCC CTTCGAGCCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
 GGAACCCCTC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGC CAGGCCCTGT 1800
 AGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
 CTGGCTGTGA CTCACTCATG GGAGCTGGCC CC

Seq ID NO: 605 Protein sequence
 Protein Accession #: NP_003967.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCRRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRARRSP HDLSLASLLG AGALRPPPGS 180
 RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 606 DNA sequence
 Nucleic Acid Accession #: NM_057160.1

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1      11      21      31      41      51
5      |      |      |      |      |
ATGCCGGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC 60
CAGCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
TGGCCCAACC TGGCGCTCTT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC 180
GCGCCCGCGA GCGCTGCCCC CGCGGAAGGC CCCCAGCTTG TCCTGGCGTC CCGCGCGGCG 240
CAGCTGCCGG GGGGACGCAC GGCCCGCTGG TGCAGTGGAA GAGCCCGCGG GCGCGCGCGG 300
10     CAGCCTTTCT GGGCCGCGCC CCGCGCGCCT GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
CGCGCGGCGC GGGCTGGGGG CCGGGGAGGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
CGCTGCGCTG CCGAGCTGGT GCGGTGCGCG GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
CTGGTGGGTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGG CGCGCTCTCC ACACGACCTC 540
AGCCTGGCCA GCTACTCTGG CCGCGGGGCC CTGCGACCGC CCGGGGCTC CCGGCCGCTC 600
15     AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
ACCTGGAGAA CCGTGGACCG CCTCTCCGCC ACCGCTGCGG GCTGCCTGGG CTGAGGGCTC 720
GCTCCAGGGC TTTCAGACTT GGACCTTAC CGGTGGCTCT TCCTGCGTGG GACCCCTCCG 780
CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC 840
TACCGGTGGG TGATGGATAT CATCCCGGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
20     AGAGCCCTCA CCGTGGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
TTGGGACCCA CTCTCAGAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT 1080
TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCTT GTGCTGGAAC TGGCCTGTAC 1140
25     TCACTCATGG GAGCTGGCCC C

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Seq ID NO: 607 Protein sequence
Protein Accession #: NP_476501.1

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1      11      21      31      41      51
30     |      |      |      |      |
MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSSVAEASLGS 60
APRSPAPREG PPPVLASPAH HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
RAARAGGPGS RARAAGARGC RLRSQLVFVR ALGLGHRSD LVRFRFCSGS CRRARSPHDL 180
35     SLASLLGAGA LRPFGSRPV SQPCRPRTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

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Seq ID NO: 608 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

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1      11      21      31      41      51
40     |      |      |      |      |
CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTTGGAGGCC TCTCCACGCT 60
GTCCCACTGC CCCTGGCCTA GCGCGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120
45     GTGGCCCAAC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC 180
CGGCGCCCGC AGCCCTGCCC CCGCGGAAGG CCCCCGCTG GTCTGGCGT CCGCGCGCGG 240
CCACTTGGCG GGGGACGCGA CCGCCCGCTG GTGCACTGGA AGAGCCCGGC GCGCGCGGCC 300
GCAGCCTTCT CCGCCCGCGC CCGCGCGGCC TGCACCCCA TCTGCTCTTC CCGCGGGGG 360
CCGCGCGGCG CCGGCTGGGG GCGCGGGCAG CCGCGCTCGG GCAGCGGGGG CCGGGGGCTG 420
CCGCTGCGCG TCGCAGCTGG TGCCGGTTCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
50     GCTGGTGGCT TTCCGCTTCT GCGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CCTGCGACCG CCGCGGGGCT CCGGGCCCGT 600
GAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG 660
CACCTGGAGA GTCGCTTCTT GCCTCTCCGC CACCGCCTGC GGCTGCGCTG GCTGAGGGCT 720
CGCTCCAGGG CTTTGCAGAC TGGACCCCTA CCGGTGGCTC TTCCTGCTTG GACCCCTCCC 780
55     GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGACGGAAG GCCTCAAAGC TGAGAGGCCC 840
CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
CTTCGAGACC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACTTG GACCCCTCC 1020
TCTGTGAAC ACATACAGTG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
60     TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140
CTCACTCATG GGAGCTGGCC CC

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Seq ID NO: 609 Protein sequence
Protein Accession #: NP_476431.1

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1      11      21      31      41      51
65     |      |      |      |      |
MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG 120
70     SRARAAGARG CRLRSQLVFV RALGLGHRSD ELVRFRFCSG SCRARSFPHD LSLASLLGAG 180
ALRPPGSRP VSQPCRPRTR YEAVSFMDVN STWRTVDRLS ATACGCLG

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Seq ID NO: 610 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

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1      11      21      31      41      51
80     |      |      |      |      |
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GCTTACCATG GCTGCCCTAG CGAGTGTACC TGCTCCAGGG CCTCCAGGT GGAGTGCACC 120
GGGGCACGCA TTGTGGCGGT GCGCCACCCCT CTGCCCTGGA ACGCCATGAG CCTGCAGATC 180
CTCAACACGC ACATCACTGA ACTCAATGAG TCCCCGTTCC TCAATATCTC AGCCCTCATC 240
GCGCTGAGGA TTGAGAAGAA TGAGCTGTGC GGCATCACGC CTGGGGCCTT CCGAAACCTG 300
85     GGCTCGTGC GCTATCTCAG CCTCGCCAAC AACAGCTGC AGGTTCTGCC CATCGGCTC 360
TTCCAGGGCC TGGACAGCCT TGAGTCTCTC CTCTGTCCA GTAACAGCT GTTGACAGATC 420
CAGCGGCCCC ACTTCTCCCA GTGCAGCAAC CTCAGGAGC TGCAGTTGCA CGGCAACCAT 480
CTGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG 540

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	GGCAAGAATA	GCCTCACCAC	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCTCGGC	TGTATGAGAA	CAGGCTCAGC	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660
	GTTAACCTGC	AGGAACCTGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
5	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCCAT	CTCCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTTCTCT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGTATTC	TTAGCCGCAA	TCAGATCAGC	TTTATCTCCC	CGGGTGCCTT	CAACGGGCTA	1020
10	ACGGAGCTTC	GGGAGCTGTG	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCATGT	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATGCTCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAAACCAG	1200
	CTGGAGAACT	TGCCCCCTCG	CATCTTCGAT	CACCTGGGGA	AACGTGTGTA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
15	AACCAGCCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCGAGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTCTGTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	TGTCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	TTAGCCCTGA	GCTAACACAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTGAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
20	ATTGCCGCCA	TTGTAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGG	1680
	TGTTGCTGCT	GCAAGAAAG	GAGCCAAAGT	GTCCCTGATG	AGATGAAGGC	ACCCAAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCTACG	CTTCTCTGTA	CTTGCCTGAT	TCTCCCGTAG	AGAAGCAGT	1920
25	CGTGCCGGAC	CTTCTCTACA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCCGA	TTTCATACCC	TGGGCTTCTT	TGAGAGGGG	TCTTCTCTCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCTCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
30	ACCCAGCATG	TCCCCTCAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCTT	GAAGGCAAGG	2280
	TGAGTTCTCT	CCTCAAGAA	GACTTCAAAC	CATTTAACTG	GTTTCTTAAG	AGCCGTCAAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAAG	GCGGTCTACT	GTGTCTCACT	TGTGATTTT	ATCTGGAATA	GGAGAAACAA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAACTGCA	AATTTGCTT	2520
	TGAAAGGTTT	AGCCCTTTAA	GGAAATGAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
35	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCCCTGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGGTGAC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCGAG	2820
40	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGA	GCCAGGACGG	2880
	TCCCCCCACA	CTCAGCCTGT	GCAAGGCCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCTCG	3000
	AGAGACCCTG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCTCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCT	3120
45	TCCGCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTAAATTT	TTTCTCTTCT	3180
	ACTTAGGGGA	AGTGAATTCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTCTTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAACTTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTAGTG	3360
	GTCTGGGGGC	TCCCTGGAGC	TCTCCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
50	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
	CTGCTATACA	CATATTACAA	TGGCGCTCAA	GAAATTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	CTGGCCCACT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTCACTGTAC	TTCCAGGGGA	TCTGGAAATC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCGCTGAC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
55	TCCGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGG	TTTTCCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC		3900
	TGTTTGCAAA	CACTAGTGCA	CTTTGTAGCT	TTTCACTCTC	TGTCCAGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCATTTCCAC	4020
60	ACTATTGGTG	GACCTGTGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCTT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGGCCAC	AGACCTGTCT	4200
	GGTGCTCCTG	TGAGTGGCCT	CAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGAGGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCTTA	4320
	GGTATTCTCT	GCAGTAGCCA	TGACATTGGA	GCACTTCTCT	CTCCAGCCAG	AGGCTGACCT	4380
65	GAGGGCCACT	GTCTCAGAT	GACACCACCC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCTTTTC	CAACAGGATG	ATGCATTGTC	TCAATTCTCA	4620
70	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGTACAGA	GTTTCACTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740
	GTGTTGGAGA	AGAAACAACA	AAAGCCAATT	AGAACCACCTA	TTTTTAAAAA	GTGCTTACTG	4800
	TGCACAGATA	CTCTTCAAGC	ACTGGACGTG	GATTCTCTCT	CTAGCCCTCA	GCACCCCTGC	4860
	GGTAGGAGTG	CCGCTCTTAC	CCACTTGTGA	TGGGGTACAG	AGGCACCTGC	TCTTCTGCAT	4920
75	GGTGTCAAT	AGGCTGGGAG	TTTTATTAT	CTCTTCAAAC	TTTGTACAAG	AGCTCATGGC	4980
	TTGTCTTGGG	CTTCTGTCAT	TAAACCAAAG	GAAATGGAAG	CCATTCCTCT	GTTGCTCTCC	5040
	TTAGTCTTGG	TCATCAGAAC	CTCACTTGGT	ACCATATAGA	TCAAAAGCTT	TGTAACCACA	5100
	GGAAAAAATA	AACCTCTCCA	TCCCTTAAAG	AATAGAAATG	TTTGTCCCTC	TCATGGGAAT	5160
	TGGGCTGTAT	GTATATTGTT	CTTCTCTCTT	AGAATTTAGA	GATACAAGAG	TTCTACTTAG	5220
80	AACCTTTTCA	GGACACAAAT	TCCACAACCT	TTCAGATGCT	GATGTAGAGC	TATTGGGAAA	5280
	GAACCTTCAA	ACTCAGGAGC	TTTGACAGAG	GCAGACAGCT	AGAGATAACT	CGGGACCCAG	5340
	AGTTGGTCTG	CAGATGTTAG	ATGTATCCTA	GCTTTTAGCC	ATAAACCACT	CAAAGATTCA	5400
	GCCCCAGAT	CCCCAGTCA	GAACCTGAAT	TGCGTTGTTG	GGAGGCCAGC	AGTGGCCCTG	5460
	GGAAAGGAGC	CATGGCTGTG	TTTGACAGAG	GGTGGGCTGG	CAAGCCACTT	CCGGGAAAAA	5520
	CTCCTTCCGC	CCCAGGTTTC	TTCTTCTCTT	AAGGAGAGAT	TGTTCTCACC	AACCCGCTGC	5580
85	CTTCATGCTG	CTTCTCAAAG	TAGATCATGT	TTGCCTTGTG	TAGAGAATTA	CTGCAATTCA	5640
	GCCCCAGTGC	CTTCTCAGAT	ATTTACAGAT	TTCTAGGCC	TCAGGGTTT	GTAGAGTGTG	5700
	AGCCCTGGTG	GGCAGGGTTG	GGGGTCTGCT	CTTCTGCTGG	ATGCTGCTTG	TAATCCATTT	5760

GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 611 Protein sequence

Protein Accession #: BAB84587.1

5

1	11	21	31	41	51	
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LNTHITELNE	SPFLNISALI	ALRIEKNELS	RITPGAFRNL	GSLRYLSLAN	NKLQVLPIGL	120
FQGLDSLES	LLSSNQLLQI	QPAHFSQCSN	LKELQLHGNH	LEYIPDGAFF	HLVGLTKLNL	180
GKNSLTHISP	RVFQHLGNLQ	VLRLYENRLT	DIPMGTFDGL	VNLQELALQQ	NQIGLLSPGL	240
FHNHNLQRL	YLSNNHISQL	PPSIFMQLPQ	LNRLTLFGNS	LKELSLGIFG	PMPNLRELWL	300
YDNHISLPD	NVFSNLRQLQ	VLILSRNQIS	FISPGAFNGL	TELRELSLHT	NALQDLGDNV	360
FRMLANLQNI	SLQNNRLRQL	PGNIFANVNG	LMALQLQNNQ	LENLPLGIFD	HLGKLCLELRL	420
YDNPWRCDS	ILPLRNWLLL	NQPRLGTDVT	PVCFSFANVR	QQSLIIINVN	VAVPSVHVPE	480
VPSYPETPWY	PDTPSPYDPT	SVSSTTELTS	PVEDYTDLT	IQVTDDRSVW	GMTQAQSGLA	540
IAAIVIGIVA	LACSLAACVG	CCCCKKRSQA	VLMQMKAPNE	C		

Seq ID NO: 612 DNA sequence

Nucleic Acid Accession #: XM_098151

Coding sequence: 1..447

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1	11	21	31	41	51	
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AGTGGGGTAC	AGAGTTTCAGT	TTTCTCTCT	GTTTACAGCT	CCTTGACAGT	CCCACGCCCA	120
TCTGGAGTGG	GAGCTGGGAG	TCAGTGTGG	AGAAGAAACA	ACAAAGCCA	ATTAGAACCA	180
CTATTTTAA	AAAGTGCTTA	CTGTGCACAG	ATACTCTTCA	AGCACTGGAC	GTGGATTCTC	240
TCCTAGCCC	TCAGCACCCC	TGCGGTAGGA	GTGCCGCCCTC	TACCCACTTG	TGATGGGGTA	300
CAGAGGCACT	TGCTCTTCTG	CATGGTGTCT	AATAGGCTGG	GAGTTTTATT	TATCTCTTCA	360
AACCTTTGAC	AAGAGCTCAT	GGCTTGTCTT	GGGCTTTCGT	CATTAAACCA	AAGGAAATGG	420
AAGCCATTCC	CCGTGTGCTC	TCCTTAG				

Seq ID NO: 613 Protein sequence

Protein Accession #: XP_098151

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LFLKSAYCAQ	ILFKHWTWIL	SLALSTPAVG	VPPLPTCDGV	QRHLDFCMVF	NRLGVLFISS	120
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Seq ID NO: 614 DNA sequence

Nucleic Acid Accession #: NM_002658.1

Coding sequence: 77..1372

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CCCCGACCTC	GCCACCATGA	GAGCCCTGCT	GGCGCGCCTG	CTTCTCTGCG	TCCTGGTCTG	120
GAGCGACTCC	AAAGCGAGCA	ATGAACCTCA	TCAAGTTCCA	TGGAAGCTGT	ACTGTCTAAA	180
TGGAGGAACA	TGTGTGTCCA	ACAAGTACTT	CTCCAACATT	CACTGGTGCA	ACTGCCCAAA	240
GAAATTCGGA	GGGACGCACT	GTGAAATAGA	TAAGTCAAAA	ACCTGCTATG	AGGGGAATGG	300
TCACCTTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	TGCCCTGGAA	360
CTCTGCCACT	GTCTTCAGC	AAACGTACCA	TGCCCCACAGA	TCTGATGCTC	TTCAGCTGGG	420
CCTGGGGAAA	CATAATTACT	GCAGGAACCC	AGACAACCGG	AGGCGACCCT	GGTGTATGTT	480
GCAGGTGGGC	CTAAAGCCGC	TTGTCCAAGA	GTGCATGGTG	CATGACTGCG	CAGATGGAAA	540
AAAGCCCTCC	TTCTCTCCAG	AAGAATTAAA	ATTTCACTGT	GGCCAAAAGA	CTCTGAGGCC	600
CCGCTTTAAG	ATTATTGGGG	GAGAAATCAC	CACCATCGAG	AACCAGCCCT	GGTTTGCAGC	660
CATCTACAGG	AGGCACCGGG	GGGGCTCTGT	CACCTACGTG	TGTGGAGGCA	GCCTCATCAG	720
CCCTTGCTGG	GTGATCAGCG	CCACACACTG	CTTCATTGAT	TACCCAAAAGA	AGGAGGACTA	780
CATCGTCTAC	CTGGGTCTGT	CAAGGCTTAA	CTCCAACACG	CAAGGGGAGA	TGAAGTTTGA	840
GGTGGAAAAC	CTCATCTTAC	ACRAGGACTA	CAGCGCTGAC	ACGCTTGCTC	ACCACAACGA	900
CATTCGCTTG	CTGAAGATCT	GTTCCAAGGA	GGGCAGGTGT	GCGCAGCCAT	CCCGGACTAT	960
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CACTGGCTTT	GGAAAAGAGA	ATTCTACCGA	CTATCTCTAT	CCGGAGCAGC	TGAAAATGAC	1080
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CACCACCAAA	ATGCTATGTG	CTGCTGACCC	CCAATGGAAA	ACAGATTCCCT	GCCAGGGAGA	1200
CTCAGGGGGA	CCCCTCGTCT	GTTCCCTCCA	AGGCCGCTAG	ACTTTGACTG	GAATTGTGAG	1260
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TCCATCAGCT	GTAAGAAGAG	ACTGGGAAGA	TAGGCTCTGC	ACAGATGGAT	TTGCCTGTGG	1500
CACCAACAGG	GTGAACGACA	ATAGCTTTAC	CCTCACGGAT	AGGCCCTGGT	GCTGGCTGCC	1560
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AATGTGGGAG	CAGCGGTTTG	GGGAGCAGAG	ACACTAACGA	CTTCAGGGCA	GGGCTCTGAT	1860
ATTCCATGAA	TGATCATGGA	AATATATATG	TGTGTGTATG	TTTGACACT	TGTTGTGTGG	1920
GCTGTGAGTG	TAAGTGTGAG	TAAGAGCTGG	TGTCTGATTG	TTAAGTCTAA	ATATTTCTCT	1980
AAACTGTGTG	GACTGTGATG	CCACACAGAG	TGGTCTTTCT	GGAGAGGTTA	TAGGTCACTC	2040
CTGGGGCTCT	TTGGGTCCCC	CACGTGACAG	TGCCTGGGAA	TGTACTTATT	CTGCAGCATG	2100
ACCTGTGACC	AGCACTGTCT	CAGTTTCACT	TTCACATAGA	TGTCCCTTTC	TTGGCCAGTT	2160
ATCCCTTCCT	TTTAGCTTAG	TTTATATTTT	TTTATATTTT	TGTAATTTTA	AATAAAGATG	2220
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Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

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YCRNFDNRRL PWCYVQVGLK PLVQECMVHD CADGKPKSSP PEELKFPCCG KTLRPRFKII 180
10    GGEFTTIENQ PWFAAIYRRH RGGSVTVVCG GSLISPCWVI SATHCPIDYP KKEDYIVYLG 240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNDIALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCBITGFGK ENSTDYLYPE QLKMTVVKLI SHRECCQPHY YGSEVTTKML 360
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Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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25    GACCTGCCCC GAGCCTCTC CATGGAGGCA GCCCGCCCTC CCGGCTCCTG GAACGGAGCC 240
CTCTGCGCGC GTCTCTGCTC GACCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA 300
AATGTGACAT TACATGTTCC CTCCAAATA GATGCCGAGA AACTTGTTGG TAGAGTTAAC 360
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30    TTTACCATAT TACTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540
GAGCATCAAA CAAAGGTCTT AAAGAAAAGA CATACTAAAG AAAAGTTCTT AAGGCGCGCC 600
AAGAGAAGAT GGGCTCCACT TCCTTGTTCC ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
CTTTTCTTTC AACAGTTTCA ATCTGACACG GCCCAAACCT ATACCATATA CTATTCCATA 720
AGAGGTCCTG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 780
35    AACTTGTAAT GTTCTGCTCT TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
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GAGGATGAAA ATGATACTTA CCCAATTTTT ACAGAAGAAA CTTATACTTT TACAATTTTT 960
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GACACGATGC ACACACGCTT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCACCC 1080
40    CTATTTTCTA TGCATCCAA TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
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GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
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CAAAATGGTG TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
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55    AGCCCATTC TACCTAAAA GACAGTGATC ATCTGCAAC CCACCATGTC ATCTGCGGAG 1980
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GTCCTGACAT ATAAGTATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT 2820
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Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

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 TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDVDND HLPFTTTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTNEGVLCVV 420
 KPLNYEKKQ MLQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
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 VTSLDVTLCD CITENDCTHR VDPRIGGGV QLGKWLAI LGLIALLFCI LFTLVCGASG 720
 TSQPKVIPD DLAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAGVCG TVGSGIKNGG 780
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Seq ID NO: 618 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
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Seq ID NO: 619 Protein sequence
 Protein Accession #: NP_004940.1

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 TSKQPKVIPD DLAAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAGQVCG TVGSGIKNGG 780
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Seq ID NO: 620 DNA sequence
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 Protein Accession #: NP_115934.1

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 GAACCATGGC TGTGCCAGGC GGCAACCAGG TGTGGAGACA AGATCTACAA CCCCTGGAG 180
 CAGTGCTGTT ACAATGAGCG CATCGTGTCC CTGAGCGAGA CCGGCCAATG TGGTCCCCC 240
 TGACCTTCT GGCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300
 TTTGTTGTA AGCTGAAGGT TCAGGGTGTG AATCCCACT GCCACTCATC TCCCATCTCC 360
 AGTAAATGTG AAAGAGGCCG GATATGTTAG

Seq ID NO: 623 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLCQPAPR CGDKIYNPLE 60
 QCCYNDAIVS LSETRQCGRP CTFWPCFELC CLDSFGLTND FVVKLVQGV NSQCHSSPIS 120
 SKCERGRIC

Seq ID NO: 624 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 51..1085

1 11 21 31 41 51
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 GGAGCTCAAG CTCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTCGAGAG GGGGAAGGAG GTTCTTCTAC TCGCCACAAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGTACC CCAAGGGCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTATCCAG AACGTACCCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCCGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCATCTCC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACTCG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660

	GCCTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACC	GCGAGTGCCA	720
	ACCGCAGTGA	CCCAGTACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCC	780
	CCTCAAAAGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
5	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCATAACT	960
	CAGCCACTGG	CCTCAATAGG	ACCAAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCCTG	1020
	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGATTT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCC	1140
10	GAATTCCTCT	AGCTCCTCCA	ATCCCATTTT	ATCCCATGGA	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAATC	AATGAAAATT	TAAAGGGAAA	1260
	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACATATGGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCTT	TGCTTATGCC	1440
	TGCTCTTTTC	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
15	GGGTAACTTA	ACAGAGTGTG	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAACACAG	CCGTGTGTTC	1620
	AAATGTACAG	TGGTCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
	TTTAATTCAA	CCCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
	GGAGGAGTCT	GTGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
20	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAATAGG	CTACACTCAT	1860
	CTGACTCATT	CTTTATTCTA	TTTGTATGTT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920
	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAAGC	TTTAAATGTC	TGCATGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
25	GGCTGGAATT	ACAAAACCTCA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGTGGTG	TAAGTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160
	TCTCACCTAG	GTGAGCGCAT	TGAGCCAGTG	GTGCTAAATG	CTACATACTC	CAACTGAAAT	2220
	GTTAAGGAAG	AAGATAGATC	CAATTAAAAA	AAATTAATAA	CAATTTAAAA	AAAAAAAGA	2280
	ACACAGGAGA	TTCAGTCTA	CTTGAGTTAG	CATAATACAG	AAGTCCCTTC	TACTTTAACT	2340
30	TTTACAAAAA	AGTAACCTGA	ACTAATCTGA	TGTTAAACAA	TGTATTATT	TCTGTGGTTC	2400
	TGTTTCTCTG	TTCCAATTG	ACAAACCCCA	CTGTTCTGT	ATTGTATTGC	CCAGGGGGAG	2460
	CTATCACTGT	ACTGTAGAG	TGGTGCTGCT	TTAATTGATA	AATCACAAT	AAAAGCCAAT	2520
	TAGCTCTATA	ACT					

Seq ID NO: 625 Protein sequence
Protein Accession #: AAA59907.1

	1	11	21	31	41	51	
40	MGPPSAPPCR	LHVPWKEVLL	TASLLTFWNP	PTTAKLTIES	TPPNVAEGKE	VLLLAHNLPO	60
	NRIGVSWYK	ERVDGNSLIV	GYVIGTQAT	PGPAYSGRET	IYPNASLLIQ	NVTQNDTGFI	120
	TLQVIKSLV	NEEATGQFHV	YPELPKPSIS	SNNPNPVEDK	DAVAFTCEPE	VQNTTYLWVW	180
	NGQSLPVSPR	LQLSNGNMTL	TLLSVKRND	GSYECEIQNP	ASANRSDPVT	LNVLPGPDVP	240
	TISSPKANYR	PGENLNLSCH	AASNPPAQYS	WFINGTFQOS	TQELFIPNIT	VNNSGSSYMCQ	300
45	AHNSATGLNR	TTVTMITVSG	SAPVLSAVAT	VGITIGVLAR	VALI		

Seq ID NO: 626 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

50	1	11	21	31	41	51	
	GGAGCTCAAG	CTCCTCTACA	AAGAGGTGGA	CAGAGAAGAC	AGCAGAGACC	ATGGGACCCC	60
	CCTCAGCCCC	TCCCTGCAGA	TGTCATGTCC	CCTGGAAGGA	GGTCTGTCTC	ACAGCCTCAC	120
55	TTCTAACCTT	CTGGAACCCA	CCCACCACCTG	CCAAGCTCAC	TATTGAATCC	ACGCCATTCA	180
	ATGTCGCAGA	GGGGAAGGAG	GTTCTTCTAC	TCGCCCACAA	CCTGCCCCAG	AATCGTATTG	240
	GTTACAGCTG	GTACAAAGGC	GAAAGAGTGG	ATGGCAACAG	TCTAATTGTA	GGATATGTAA	300
	TAGGAACTCA	ACAAGCTACC	CCAGGGCCCG	CATACAGTGG	TCGAGAGACA	ATATACCCCA	360
	ATGCATCCCT	GCTGATCCAG	AACGTCACCC	AGAATGACAC	AGGATTCTAT	ACCCTACAG	420
60	TCATAAGTCA	AGATCTTGTG	AATGAAGAAG	CAACCGGACA	GTTCCATGTA	TACCCGGAGC	480
	TGCCCCAGCC	CTCCATCTCC	AGCAACAAC	CCAACCCCGT	GGAGGACAAG	GATGCTGTGG	540
	CCTTACCTGT	TGAACCTGAG	GTTCAGAACA	CAACCTACCT	GTGGTGGGTA	AATGTCAGAA	600
	GCCTCCCGGT	CAGTCCAGG	CTGCAGCTGT	CCAATGGCAA	CATGACCCCTC	ACTCTACTCA	660
	GGCTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACC	GCGAGTGCCA	720
65	ACCGCAGTGA	CCCAGTACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCC	780
	CCTCAAAGGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCATAACT	960
	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCCTG	1020
	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
70	TATAGCAGCC	CTGGTGATTT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCC	1140
	GAATTCCTCT	AGCTCCTCTA	ATCCCATTTT	ATCCCATGGA	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAATC	AATGAAAATT	TAAAGGGAAA	1260
	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACATATGGAC	AGCTTTTCCC	AAGATGTCAA	1380
75	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCTT	TGCTTATGCC	1440
	TGCTCTTTTC	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	GGGTAACTTA	ACAGAGTGTG	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAACACAG	CCGTGTGTTC	1620
	AAATGTACAG	TGGTCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
80	TTTAATTCAA	CCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
	GGAGGAGTCT	GTGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAATAGG	CTACACTCAT	1860
	CTGACTCATT	CTTTATTCTA	TTTGTATGTT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920
	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
85	CTCTAAAAGC	TTTAAATGTC	TGCATGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
	GGCTGGAATT	ACAAAACCTCA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGTGGTG	TAAGTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160

TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAAC CAATTTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 627 Protein sequence
 Protein Accession #: AAA59908.1

1 11 21 31 41 51
 | | | | |
 MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SPAWQDDAVI SISQEVASEG NLTECQIYLV 60
 NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

Seq ID NO: 628 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 2370..2501

1 11 21 31 41 51
 | | | | |
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATACTAGTG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTACCTG TGAACCTGAG GTTCAGAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCTC ACTCTACTCA 660
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGAGTGA CCCGCTCAG CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
 ACCCACTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGTCTCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC TGGGTGTATT TTCGATATT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAATC AATGAAATTT TAAAGGGAAA 1260
 ACCCTCAGCG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACCTAGAGA CAGTCAAACT 1320
 GCAAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAAAGACT CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
 TGCTCTCTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAATG 1560
 AGATCCTTTA GTGACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTT 1620
 AAATGTACAG TGTGCTTTT CAGAGTTGGA CTTCTAGACT CACTGTCTCT CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCACTTTC TGACACTTGT TGTGTAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
 CTGACTCAT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTGGTAT TACCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCATAAAGC TTTAAATGTC TGCATGCAG CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAAGCCC CAAATGGTGG TAACGTGATA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACCTAG GTGAGCGCAT CAATTAAAAA AAATTAAAAAC CAATTTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 629 Protein sequence
 Protein Accession #: AAA59909.1

1 11 21 31 41 51
 | | | | |
 MLTNVPIVSV LPPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 630 DNA sequence
 Nucleic Acid Accession #: NM_016639.1
 Coding sequence: 40..429

1 11 21 31 41 51
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 GCGGCGGGCG CAGACAGCGG CGGGGCGCAGG ACGTGCACTA TGGCTCGGGG CTCGCTGCGC 60
 CGGTTGCTGC GGCTCCTCGT GCTGGGGCTC TGGCTGGCGT TGTGCGCTC CGTGGCCGGG 120
 GAGCAAGCGC CAGGACCGCG CCCCTGCTCC CGCGGCGAGT CCTGGAGCGG GGACCTGGAC 180
 AAGTGCATGG ACTGCGCTGC TTGCAAGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
 CTGTCAGCAC CTCCTGCCCT CTTCCGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
 CTGACCTTGC TGTGGGGGCT GCTTCTGGC TTTTGGTCT GGAGACGATG CCGCAGGAGA 360
 GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGGAGAGG GCTGCCAGC TGTGGGCTG 420

ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTTCATCCA 480
 TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GCGGGGAGCC AAGCTCCTCC AACCAACAAGG 540
 GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
 AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
 ACAAACAGC TGACACTGAC TAAGGAACTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
 CCTTCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
 TCACTCAGAT GTCTGAAAT TCCACCAGG GGGTCACCT GGGGGTTAG GGACCTATT 840
 TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCAATC 900
 CCCAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT 960
 AATAAAGAA TCTTTAATTT TAAAAAATA AAAAAAATA

Seq ID NO: 631 Protein sequence
 Protein Accession #: NP_057723.1

1 11 21 31 41 51
 MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
 SDFCLGCAAA PPAPFRLWLP ILGGALSLTF VLGLLSGLFLV WRRRERRREKF TPIETETGGE 120
 GCPAVALIQ

Seq ID NO: 632 DNA sequence
 Nucleic Acid Accession #: NM_003816.1
 Coding sequence: 79..2538

1 11 21 31 41 51
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTGC TGTGTCTTGG CCTGGTGGGC CCAGTCTCTG GTGCGGCGCG GCCAGGCTTT 180
 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATACTC CTGAGGAGAT AACTAGAGAA 240
 AGAAGAGAAG CCCCTAGGCT CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TTAATCAGTT GGAAGGAAC AAAGACCTTT TGCTTGAAGA TTTTGTGGTT 360
 TATACTTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420
 CATTATCGGG GCTATGTGGA GGGAGTTTAT AATTATCTCA TTGCTCTTAG CGACTGTTTT 480
 GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CTGCAGAAC 540
 AGCTCTCATT TTGAGCACAT CATTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG 720
 GAGCTGTTC TGTGCTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAAG AGATGATTTT CCTGGCAAC TACTTGGATA GTATGTATAT TATGTTAAAT 840
 ATTGGAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGGTGTCT GTGATGTGCT GGGGAACCTC GTGCACTGGC GGGAAAAGTT TCTTATACA 960
 CTGCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAGAAAG GTTTTGGTGG AACTGCAGGA 1020
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 CAAATCACTG TGGAGACATT TGCTTCCATT GTTCTCATG AATTGGGTCA TAATCTTGA 1140
 ATGAATCAGC ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA 1200
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 TTAAATAAAG GAGGAAACTG CCTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320
 CCTCTCTGTG GTAATAAGTT GGTGGAGGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380
 GAATGTGAAT TGACCTCTTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCATATG GTGACTGTG TAAAGACTGT CGGTTCTTTC CAGGAGGTAC TTTATGCCGA 1500
 GGAAAAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTCTAG 1560
 CCAGATGTTT TTATTACAG TGGATATCCT TGCCAGATA ACAAGCCTA TTGTACAAAC 1620
 GGCATGTGCC AGTATTATGA TGCTCAATG CAAGTCACTT TTGGCTCAA AGCCAAGGCT 1680
 GCCCCCAAAG ATTGTTTCTA TGAAGTGAAT TCTAAAGGTG ACAGATTGG CAATTGTGGT 1740
 TTCTCTGGCA ATGAATACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAATG TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCT 1860
 AGTCGAGGCA CCAATGTTG GGGTGTGGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 GGGATGTTA TGCAGGCTCA AAAATGTGGT GCTGGAAGA TCTGTAGAAA CTTCAGTGT 1980
 GTAGATGCTT CTGTTCTGAA TTATGACTGT GATGTTTACA AAAAGTGTCA TGGACATGGG 2040
 GTATGTAAAT GCAATAAGAA TTGTCACTGT GAAATATGGT GGGCTCCCCC AAATTGTGAG 2100
 ACTAAAGGAT ACGAGGGAAG TGTGACAGT GGACCTACAT ACAATGAAAT GAATACTGCA 2160
 TTGAGGGACG GACTTCTGGT CTCTCTCTTC CTAATTGTTT CCCTTATTGT CTGTGCTATT 2220
 TTATCTTCA TCAAGAGGGA TCACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACAA 2280
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTTCCT 2340
 CGACATGTTT CTCCAGTGAC ACCTCCAGCA GAAGTTCTTA TATATGCAA CAGATTGCA 2400
 TTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCCAT CAAGGCCACC TCCACCACAA 2460
 CCGAAAGTAT CATCTCAGGG AAACCTTAAT CTGCTCCTGC CTGCTCCTGC ACCTCCTTTA 2520
 TATAGTTCCC TCACTTGATT TTTTAACTT TCTTTTGA AATGCTTCA GGGAACTGAG 2580
 CTAATCTTT TTTTCTTCT TGATGTTTC TTGAAAAGCC TTTCTGTTGC AACTATGAAT 2640
 GAAAAACAAA CACCACAAA CAGACTTCAC TAACACAGAA AAACAGAAAC TGAGTGTGAG 2700
 AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTCCGTTTTC 2760
 CATCATGAA TAAGTCTTAT TCAGTCACTG GTGAGGTTAA TGCACTAATC ATGGATTTT 2820
 TGAACATGTT ATTGAGTGA TTCTCAAAAT AACTGTATTG TGTAAAGATT TTTGTCTA 2880
 AGTGTAAAG TGTATTCTG AATTTTCTAC CTTAGTTATC ATTAATGTAG TTCCTCATTG 2940
 AACATGTAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000
 TTTTTCATCA TGTCAAGATT AATAATCAT ATACTCTAGA ATCTTGTCTG TCACTCACTA 3060
 CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA 3120
 TTATTTTGA AGTACAAAAT ATACTAAAAG AGTGTGTGTG TATTACGCA GTTACTCGCT 3180
 TCCATTTTGA TGACCTTTCA ACTATAGGTA ATAACCTTGA GAGAAATTA TTAATATTA 3240
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA 3300
 TAAATATATA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAATAT GTTGATTAT 3360
 GGCATAATA AGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTTGAGAATT TCATGAGCAC TTTAAATCT GAACCTTCAA AGCTTGTCTAT TAAATCATTT 3480
 AGAATGTTA CATTTACTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540
 CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTT CTTAATATACC TACAAAAAAG 3600
 TTAATGTGGT ATCTATGAGT TATCATCTTA GCTGTGTAA AAATGAATTT TTAATATGCG 3660

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAATT TTTTCATAAC CTTTCATAAT 3720
 AAAGTTTAAT AATAGGTTTA TTAAGTGAAT TTCATTAGTT TTTTAAAGT GTTTTGGTT 3780
 TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAATACTT GAAATCTCA 3840
 AAAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 633 Protein sequence
 Protein Accession #: NP_003807.1

1 11 21 31 41 51
 | | | | |
 MGSARFPSPG TLRVRWLLLL GLVGPVLGAA RPFQQTSHL SSYEIITPWR LTRERREAPR 60
 PYSKQVSYVI QAEGKEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHYRGYV 120
 EGVHNSIAL SDCFGRLGLL HLENASYGIE PLQNSSHFEH IYRMDVYK EPLKCGVSNK 180
 DIEKETAKDE EEEPPSMTQL LRRRAVLPO TRYVELFIVV DKERYDMMGR NQTAVREEMI 240
 LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGQITVET FASIVAHELG HNLGMNHDDG 360
 RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTLNKGNN CLLNIPKPDE AYSAPSCGNK 420
 LVDAGEECDC GTPKECELDP CCEGSTCKLK SFAECAYGDC CKDCRFLPGG TLCRGKTSEC 480
 DVEPYCNGSS QFCQPDVFIQ NGYPCQNNKA YCYNMGCMQYY DAQCQVIFGS KAKAAPKDCF 540
 IEVNSKGRDF GNCGPSGNEY KKCATGNALC GKLCENVQE IPVFGIVPAI IQTPSRGTC 600
 WGVDFQLGSD VPDPMVNEG TKCGAGKICR NFQCVDAVL NYDCDVQKKC HGHGVCNSNK 660
 NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
 DQLWRSYPRK KRSQTYESDG KNQANPSRQP GSVPRHVSFV TPPREVPIYA NRFAPVPTAA 780
 KQPQQPPSRP PPPQPKVSSQ GNLPARPAP APPLYSSLT

Seq ID NO: 634 DNA sequence
 Nucleic Acid Accession #: NM_002091.1
 Coding sequence: 56..503

1 11 21 31 41 51
 | | | | |
 AGTCTCTGCT CTTCCAGCCG TCTCCGCGCG GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
 CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCCTC TGCCTAGCGC CCCGGGGGCG 120
 AGCGGTCCCG CTGCTCGCGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
 CCACTGGGCG GTGGGGCACT TAATGGGGAA AAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
 TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
 GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
 GGCTTGGGCG AATCAGCAGC CTTCTGGGGA TTCAGAGGAT AGCAGCAACT TCAAAGATGT 420
 AGGTTCAAAA GGCAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
 CCCCCAGCTG AACCAAGCAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
 TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA 600
 AAATATTTGA CTATTCTGTA TCTTTTCATC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
 CTTCTGGTTT AAACCTGTTT GCTGTGAACA ATTGTCGAAA AGAGTCTTCC AATTAATGCT 720
 TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAGGCCCC CGAGCTGTGA CCATTACACA 780
 TAAAGCTTA AACACAT

Seq ID NO: 635 Protein sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 | | | | |
 MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKKSTGESSS 60
 VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPS WDSSESSNFK 120
 DVGSKGKQVR LSAPGSQREG RNPQLNQ

Seq ID NO: 636 DNA sequence
 Nucleic Acid Accession #: NM_016522.1
 Coding sequence: 265..1299

1 11 21 31 41 51
 | | | | |
 GCGGAAGCAG CGAGGAGGGA GCCCCTTTG GCCGTCCTCC GTGGAACCGG TTTTCCGAGG 60
 CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
 TTTTCTCCTC CCCGCGCCTC CCGGTGCGCG CGGGTTCAAC GCTCAGTCCC CGCGCTCGCT 180
 CCGCACCCCA CCCACTTCCT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCGGAGT 240
 TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
 TGCTCTGTGG TCGTGTCTCT CAGGCTGCTG TTCCTTGATC CCACAGGAGT GCCCGTGGCG 360
 AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACGTGA CGGTCCGGA GGGGAGAGC 420
 GCCACCTCA GGTGCACTAT TGACAACCGG GTCAACCGGG TGGCTGGCT AAACCGCAGC 480
 ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTTGATC CTGCGTGGT CCTTCTGAGC 540
 AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
 TACACCTGCT CGGTGACAGC AGACAACAC CCAAAGACCT CTAGGGTCCA CCTCATTTGT 660
 CAAGTATCTC CCAAATTTGT AGAGATTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
 ATTAGCTCA CTGCTAGC AACTGGTAGA CCAGAGCCTA CGTTACTTG GAGACATC 780
 TCTCCCAAAG CGGTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
 CGGGAACAGT CAGGGGACTA CGAGTGAGT GCCTCCAATG ACCTGGCCCG GCCCGTGGTA 900
 CGGAGAGTAA AGGTCAACCGT GACATATCCA CCATACATT CAGAAGCCAA GGTACAGT 960
 GTCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGGT ACAAGGATGA CAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCCTCTCAA ACTCATCTT TCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGGC TGGCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CCAGGCGCGG TCAGCGAGGT GAGCAACGGC ACCTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
 CTGCTCTTC TGCTCTTGA CCTGCTTCTC AAATTTTGT GTGAGTGCCA CTTCCCAACC 1320
 CGGGAAGGCG TCCCGCCACC ACCACCACA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
 GGGAGGGGAA CAAAGAATAT TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAAATTG 1500
 CCTTGAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCA AACGGGAAGA ACACAGCACA 1560

CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CAGTGGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTCATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCCAAG CGTGGCGCTG CCGGCACTTT GGTAGACTGT GCCACCACGG CGTGTGTTGT 1800
 GAAACGTGAA ATAAAAAGAG CAAAAAATAA AAAAAAATAA

Seq ID NO: 637 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 | | | | |
 MGVCGLFLP WKCLVVSRLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTTRVAVLN RSTILYAGND KWCLDPRVVL LSNTQTQYSI EIQNVVDVYDE GPYTCSVQTD 120
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCTAT GRPEPTVTWR HISPRAVGFV 180
 SEDEYLEIQG ITRQSGDYE CSAANDVAAP VVRVRKVTVN YPPYISEAKG TGVFVQKGT 240
 LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VENRPFLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FPGAVSEVS NGTSRRAGCV WLLPLLVLHL LLLKF

Seq ID NO: 638 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 | | | | |
 GATTTGCTCT GCGCAGCAGT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGAATACG CGCTCCCTCC CTCGCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCACCTGCA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCGAGTT CTCCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAAAGAAT 300
 GGAAATCTCT TCAGGCTTTT CCACTAACCC TGAAGAGAT ATATTGTGG TCGGGGAAAA 360
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TACGTGATC TGATCACAGA ACAGGCCGAT ATCGCATGA CCGGGGAGC 480
 TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAGGCCAC AACATGTCCA AGGGACCTGA 600
 GCGGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACGCA GTCAGTGTCT GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT 720
 CACCCCGCTT GGGAGTCTCT ATGATGTGCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
 TGATCCGACG AAGACGCTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTGACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCTTGA TTTTGGGGCT CATCTTGGGC CTGTCATCA TGGTAACACT 960
 CGCATTTTAC CAGTCCACC ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
 ATCCCACTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTTCATC TTGTACACGA GATACACCAA 1140
 CATAGCTACA ATCAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
 ATGCTGGGGA GGAGGGGAGG AGGCTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCAA AGTTTAGGGA 1380
 TTGAAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGTCT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500
 TCATGCTCCC TGACGCAAGA CCCCTGAAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AACACACTA 1740
 TTCTCTGGC

Seq ID NO: 639 Protein sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 | | | | |
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELVQFW VDRAYALKML 120
 FVKESHNMKS GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDPQKTVT MILSAVHIQF FDIISDFVFS EEHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM

Seq ID NO: 640 DNA sequence
 Nucleic Acid Accession #: NM_002993.1
 Coding sequence: 64..408

1 11 21 31 41 51
 | | | | |
 GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC 60
 ACTATGAGCC TCCGCTCAG CCGCGCGGCC CGTGTCCGG GTCTTCGGG CTCCCTGTGC 120
 GCGCTGCTCG CGCTGCTGCT CCTGCTGACG CCGCGGGGCG CCCTCGCCAG CGCTGGTCCT 180
 GCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTTTAC CGGTACGCT GAGAGTAAAC 240
 CCCAAAACGA TTGGTAAACT GCAGGTGTTT CCGCAGGCC CGCAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
 AAGAAAGTCA TCCAGAAAT TTTGGACAGT GGAACAAGA AAAACTGAGT AACAAAAAAG 420
 ACCATGCATC ATAAATATGC CCACTCTTCA GCGGAGCAGT TTTCTGGAGA TCCTTGAGC 480
 CAGTAAGAAT AAGAAGGAAG GGTGGTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAAGTT ACAGCTCAGC TAATGAAGTA 600
 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCITTGG 660
 CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG 780
 ATTTGATATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTCTTCT 840
 ACTCACTCTT CTCATAAAT AGGAAATATT TTAGTTCTGT TTTCTTGGGG AATATGTTAC 900

TCTTTACCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTCATACCG 960
 TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
 CTAATATATT CTCTTCCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
 CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA 1140
 ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGCTAA TTTACATAGA AATGTATTCT CTGGTGTGTT TAAATAAAG CAAATTAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT 1320
 CATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTAGCATT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCACT TTTATTTT CCTGTGTGTC ATGTTGGTTT TTGTACTTGT TATTGTCAAT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAAAA

Seq ID NO: 641 Protein sequence
 Protein Accession #: NP_002984.1

1 11 21 31 41 51
 | | | | |
 MSLPSSRAAR VPGPSGSLCA LLALLLLTLP PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60
 KTIGKLQVFP AGPQCSKVEV VASLRNGKQV CLDPEAPPLK KVIQKILDSG NKKN

Seq ID NO: 642 DNA sequence
 Nucleic Acid Accession #: NM_013271.1
 Coding sequence: 27..809

1 11 21 31 41 51
 | | | | |
 TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
 CCGGGGGCGT CGGCCCTTTG GTGCTGTCTGC TGCTCGGCCT GTTTCGGCCG CCCCCGCGCG 120
 TCTGCGCGCG GCGCGTAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
 AGACTGGCGC TCCTCGCGCG TTCGCGCGGT CAGTGCCTCG AGGTGAGGCG GCGGGGGCGG 240
 TGCAGGAGCT GCGCGGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCTG GAGCGGGCGC 300
 GGGCGGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGGCGAG CTGCTGCGCG 360
 TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCGACGCGC 420
 CTGCAGCGCA GCTCGCTCGC GCTCTGTCTC GCGCCCGCCT TGACCTTGCC GCCCTAGCAG 480
 CCCAGCTTGT CCCCCTGCGC GTCCCCGCGC CGGCGCTCCG ACCCCGCGCC CCGGTCTACG 540
 ACGACGGCCC CGCGGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
 CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
 TGGCAGCCCC GCGCGCGCTC CGCGGTGCGC CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
 CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAAACGCCT AGAGACCCCG GCGCCCGCAG 780
 TGCTGACGCG CGGCTCTTGG CCACCTGAG CACTGCGCGG ATCCCGTGCA CCTTGGGACC 840
 CAGAAGTGCC CCGCCCATCC CGCCACGAG ACTTCTCCCC CGCAGCACGT CCAGAGCAAC 900
 TTACCCCGGC CAGCCAGCCC TCTACCCGGA GGATCCCTAC CCCCTGCCCC ACAATAACAT 960
 GATCTGAGC

Seq ID NO: 643 Protein sequence
 Protein Accession #: NP_037403.1

1 11 21 31 41 51
 | | | | |
 MAGSPLLWGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
 RSVPRGEAAG AVQELARALA HLEAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD 120
 PALGLDDDDP APAQQLARAL LRARLDPAAL AAQLVPAPVP AAALRPRPPV YDDGPAGPDA 180
 EEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSSEL PPEGVLGALL 240
 RVKRLPTAP QVPARRLLFP

Seq ID NO: 644 DNA sequence
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 681..2990

1 11 21 31 41 51
 | | | | |
 CCCAGAGCCG CCTCCCCCTG TTGTGGCAT CCCGAGCTTC CTCCTTGCC AGCCAGGACG 60
 CTGCCGACTT GTCTTTGGCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
 GTTGGCTCC CTGCCCACT GTGGAAGCAA CTGCGTGAT TGATGCGCCA CAGACTTTTT 180
 TCCCTCGAC CTCGCCGCG TACCCTCCA CAGATCCAGC ATCACCCAGT GAATGTACAT 240
 TAGGGTGGTT TCCCCCAG CTTGGGGCTT TGTTGGGTT TGATTGRTT TGGCTCTCG 300
 CTAAGCTGAT TTATGCGACA GAAGCCAC CCGCTGGAGA GAAACAAAAG CTCTTTTCTT 360
 TGTCCCGGAG CAGGTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCCGC GCCGGGCCCT 420
 TGGCCGTCGA AGGAGGTGCT TCTGCGGAG ACCGCGGGAC CCGCGTGCC GAGCCGGGAG 480
 GGCCTGAGG GCCCTGAGT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540
 CCGAGCCGCG GGGTCCGCT GCTAGGCTG CGGAAAACGT CCTAGCGACA CTCGCCGCG 600
 GGCCTGAGG TCGCCCGGGA GGCAGGCCC GCGTCCGGA GGCAGCCAGG CCGCGGGCGC 660
 GGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITACC GCTGCATTG 720
 TCTGCTGCA AAACGACCGG CGAGGTCCCG CCTGTTCTT CTGGGCGAGC TTGGGTGTTT 780
 CACTTGTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCCCTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900
 TTTAGGTGAG ATCAAGAAGT GAAAGTTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAATGAAA 1020
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT CGGTCCAGGA GCCGAAGCTA 1080
 ATTTATGCT CCAAGTTTCT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAAATTA TCCGTTGGA AACGATTTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCGTGACT TTCGTCTTGG ATTTGGCTCA TACGTTGATA 1260
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA 1380
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440
 AAGGAGGTTT TGACGCCATG CTTAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560

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GCAAATTGGC AGGCATAGTG GTGCCAATG ACGGAACTG TCATCTGAAA AACACGCTCT 1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
ACAACAACAT TAAATGTCATC TTGTCAGTTC AAGGAAAACA ATTTCAATTG TATAAGGATC 1740
TTCTACCCCT CTGTGCCAGG ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800
ATAATTGGT AGTGGAAAGC TATCAGAAGC TCATTTTACA AGTGAAAGTT CAGGTGGAAA 1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
TTACAATGAA AAAATGTGAT GTACACAGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040
GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCTG TGTGAGGACA 2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAATTTTCT AGATTCCAAG TGTTTCCAGT 2160
GTGATGAGAA TAAATGTGAT TTTGATGAAG ATCAGTTTTT TTCTGAGAGT TGCAAGTCAC 2220
ACAAGGATCA GCCGTGTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340
CATATCACCA TGGAAATCTG TGTGCTGGG ATGGAGAGTG TGAAGCAGG AGATGCCAAT 2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
TCAATTCAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
GCACGCATCC CAGGAGCATC GGCCTCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTGTCT CAGGCTATAC 2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACA CAATTATGTC GACCAAACTT 2700
CAGAATGTT CTCCAGCCCA AGTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
ATAAAATTAA GTCTCTATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATT 2880
TGCAAGTGT TTGCACAAGA GCAGTCACTT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
TGGATATCAG CAAATTAAT GCTCATGAAA CTTCAGGTG CAATCTCTAA AAAAAAGATT 3000
TTAAACACTT AATGGGAAAC TGGAAATGTT AATAATTGCT CCTAAGATT ATAATTTTAA 3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC 3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
AAAAATGTGT TTACTACTGT TTGAGACTAG TGTGCTGTGA GCATTTTACT GTAATATATA 3240
ACTTATTTAG ATTCAGTATC AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
TACCTGTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTTGTG 3360
CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
TATATTTCTA GGTGCGAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
ATGAATAAAT GATTCTGTGT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
AAGATTATT GCTTTTAAAA GTGTGTAGTT TTATGATGAT GTGTTTATGG TTTGCTTATT 3600
TTTGCAAGAT GGATCTAAT TCCAGCATT CTTCTCTTT GCCTTTATGT TTTGTTTCT 3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAGT GCTAAGTTAC 3720
TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTAAAAAGCT 3780
GAATGTAA

Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

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55
60

1 11 21 31 41 51
MCGSALAFFT AAFVCLQND RGPASFLWAA WVFLVLGLG QGEDNRCASS NAASCARCLA 60
LGPECGWCVQ EDFISGGERS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASM NNIKELNSVG NDLSRKMAFF 180
SRDFRLGFGS YVDKTVSPYI SIHPERIHQ CSDYNLDMP PHGYIHVLSL TENITEPEKA 240
VHRQKISGNI DTPEGGFDM LQAACVSHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
VPNDGNCHLK NNVVYKSTTM EHPSLGQLE KLIDNNINVI FAVQKGQFHW YKDLLPLLP 360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420
NVTSNDEVLV NVTVTMKKCD VTGKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
CVDETFLDSK FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV 540
VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV 600
CSGRGTVCVG RCECTDPRSI GRFCEHPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660
CALMEQQHYV DQTSCEPSSP SYLRIFFIIF IVTFLIGLLK VLIRQVILQ WNSNLIKSSS 720
DYRVSASKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

65
70
75
80
85

1 11 21 31 41 51
ATGGAATCCG AGGATTTAAG TGGCAGAGAA TTGACAATTG ATTCCATAAT GAACAAAGTG 60
AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACCTAG CTGGAATAAA 120
ATTTCTGCTG ATACTACAGA TAACCTCGGA ACTGTTAACC AAATTATGAT GATGGCAAA 180
AACCAGAGG ACTGGTTGAG TTTGTTGCTC AAACCTAGAGA AAAACAGTGT TCCGCTAAGT 240
GATGCTCTTT TAAATAAAT GATTGGTCTG TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300
GATAAATATG GCCAAATGA GAGTTTGTCT AGAATTCAG TGAGATTTGC TGAATTAATA 360
GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAACCTGCAAG 420
AAATTGCTTT TTGTTTATAT ATCTTTTGCA CAATTGGAAC TGTCACAAGG TAATGTCAAA 480
AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCCT AGAAATGCTG 540
GAAATGCCCC TGCGGAATTT AAACCTCCAA AAAAGCAGC TGCTTTTACA GGAGGAAAG 600
AAGAATTTAT CAGCATCTAC GGTATTAACT GCCCAAGAT CATTTTCCGG TTCCTTGGG 660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT 720
TTATATGGAG AGAATCATGCC ACCACAAGT GCAGAAATAG GTTACCGGAA TTCATTGAGA 780
CAAACTAACA AAACTAACA GTCATGCCCA TTTGGAAGAG TCCAGTTAA CCTTCTAAAT 840
AGCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTGTTTAT TGAAGAACA 900
ACCTCTAGAT CAGAATGCCG AGATTGGTT GTGCCCTGGAT CTAACCAAG TGGAAATGAT 960
TCCTGTGAAT TAAGAAATTT AAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG 1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCTGAA GAATAAAACG 1080
GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGTTTCCA 1140
GAGAGTAACC AGAAGACAGT GCAATCTAAG AGAAAGTCAG AGTGATTAA CCAGAATCCT 1200
GCTGCATCTT CAATCACTG GCAGATTCCG GAGTTAGCCC GAAAGTTAA TACAGAGCAG 1260
AAACATACCA CTTTGTAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA 1320
ACATCTAAAT GGTTTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT 1380

	GATTACATGA	GCTGTTTATG	AACTCCAGTT	GTAAGAATG	ACTTTCACC	TGCTTGTGAG	1440
	TTGTCAACAC	CTTATGGCCA	ACCTGCCTGT	TTCCAGCAGC	AACAGCATCA	AATACTTGCC	1500
	ACTCCACTTC	AAAATTTCAC	GGTTTTAGCA	TCTTCTTCAG	CAAATGAATG	CATTTGCGTT	1560
5	AAAGGAAGAA	TTTATTCAT	TTTAAAGCAG	ATAGGAAGTG	GAGGTTCAAG	CAAGGTATTT	1620
	CAGGTGTTAA	ATGAAAAGAA	ACAGATATAT	GCTATAAAAT	ATGTGAACCT	AGAAGAAGCA	1680
	GATAACCAAA	CTCTTGATAG	TTACCGGAAC	GAAATAGCTT	ATTGGAATAA	ACTACAACAA	1740
	CACAGTGATA	AGATCATCCG	ACTTTATGAT	TATGAAATCA	CGGACCAGTA	CATCTACATG	1800
	GTAATGGAGT	GTGGAATAT	TGATCTTAAT	AGTTGGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
10	CCATGGGAAC	GCAAGAGTTA	CTGGAAAAAT	ATGTTAGAGG	CAGTTCACAC	AATCCATCAA	1920
	CATGGCATTG	TTACAGATGA	TCTTAAACCA	GCTAACTTTC	TGATAGTTGA	TGGAATGCTA	1980
	AAGCTAATTG	ATTTTGGGAT	TGCAAAACCA	ATGCAACCAG	ATACAACAAG	TGTTGTTAAA	2040
	GATTCTCAGG	TTGGCACAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGCTCTCC	2100
	TCCAGAGAGA	ATGGGAAATC	TAAGTCAAAG	ATAAGCCCCA	AAAGTGATGT	TTGGTCCTTA	2160
	GGATGTATTT	TGTACTATAT	GACTTACGGG	AAAACACCAT	TTACAGCAGT	AATTAATCAG	2220
15	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TGTAATTTC	CGATATTCCA	2280
	GAGAAAGATC	TTCAAGATGT	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
	TCCATTCTCG	AGCTCTCTGG	TCATCCCTAT	GTTCAAATTC	AAACTCATCC	AGTTAACCAA	2400
	ATGGCCAAGG	GAACCACTGA	AGAAATGAAA	TATGTTCTGG	GCCAACTTGT	TGGTCTGAAT	2460
20	TCTCCTAACT	CCATTTTGAA	AGTGCTGAAA	ACTTTATATG	AACACTATAG	TGGTGGTGAA	2520
	AGTCATAAAT	CTTCATCCTC	CAAGACTTTT	GAAAAAATAA	GGGGAATAAA	ATGA	

Seq ID NO: 647 Protein sequence
Protein Accession #: NP_003309.1

25	1	11	21	31	41	51	
	MESEDLSGRE	LTIDSIMNKV	RDINKPKPNE	DLTDELSLNK	ISADTTDMSG	TVNQIMMMAN	60
	NPEDWLSLLL	KLEKNSVPLS	DALLNKLIGR	YSQAIELAPP	DKYQGNESFA	RIQVRFELK	120
	AIQEPDDARD	YFQMARANCK	KPAFVHISFA	QFELSQQNVK	KSKQLLQKAV	ERGAVPLEML	180
30	EIALRNLNLQ	KKQLLSEEEK	KNLSASTVLT	AQESFSGSLG	HLQNRNNSCD	SRGQTTKARF	240
	LYGENMPPQD	ABIGYRNLRL	QTNKTKQSCP	FGRVFNLLN	SPDCDVKTDD	SVVPCFMKQ	300
	TSRSECRDLV	VPGSKPSGND	SCELRNLKSV	QNSHFKEPLV	SEKSSSELI	ITDSITLKNKT	360
	ESSLLAKLEE	TKEYQEPEVP	ESNQKQWQSK	RKSECINQNP	AASSNHWQIP	ELARKVNTEQ	420
	KHTTFEQPVF	SVSKQSPPI	TSKNFDPKSI	CKTPSSNTLD	DYMSCFRTPV	VKNDFPPACQ	480
35	LSTPYGQAPC	FQQQHQHILA	TPLQNLQVLA	SSSANECISV	KGRIYSILKQ	IGSGGSSKVF	540
	QVLNEKKQIY	AIKYVNLBEE	DNQTLDSYRN	EIAYLNKLQ	HSDKIIRLYD	YEITDQYIYM	600
	VMCEGNIDLN	SWLKKKKSID	PWERKSYWKN	MLEAVHTIHQ	HGIVHSDLKP	ANFLIVDGLM	660
	KLIDFGIANQ	MQPDFTSVVK	DSQVGTVNYM	PPEAIKDMSS	SRENGKSKSK	ISPKSDVWSL	720
40	GCILYMYTYG	KTFPQQIINQ	ISKLHAIIDP	NHEIEFPDIP	EKDLQDVLKC	CLKRDPKQRI	780
	SIPPELLAHFY	VQIQTHPVNQ	MAKGTTTEEMK	YVLQQLVGLN	SPNSILKAAR	TLYEHYSGGE	840
	SHNSSSSKTF	EKKRGK					

Seq ID NO: 648 DNA sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241..1902

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50	CGCCCCTGCC	CGCGTGCCCTG	GCCTCCCCCTC	CCAGACTGCA	GGGACAGCAC	CCGGTAACCTG	120
	CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
	ATGCCTCTGC	CTGTGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGCTTTC	300
	GGGAACGCGG	CCAGTGCAAG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
55	TGTCACTATG	GAACTAAACT	GGCCTGCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
	TGTGAAGCTA	CATGCGAAC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
	AGATGCTTTC	CAGGATACAC	CGGGAACACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
	AAACCCCGGC	CATGCCAAC	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
60	CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
	ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
	TCAGGACTCC	GCCTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCCTCT	780
	GGTAAAGTCA	CTCTGCTGCA	CAATCGAAGA	TGTGTGAACA	CATTTGGAAG	CTACTACTGC	840
	AAATGTCACA	TTGGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
65	GGGTCTCTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
	ATCCCTGAAA	ATTCTGTGAA	GGAAGTCCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
	AAGAAGTTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAAAG	CAAAAATTAA	AAATGTTACC	1140
	CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
70	ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAAATGAAA	1260
	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
	AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCCTGATT	1380
	CTGGTCCAAA	GGAAAGCGCT	AACTTCCAAA	CTGGAACATA	AAGATTAAA	TATCTCGGTT	1440
	GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
75	TGGAATCTCG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGCA	1560
	GGTCACAAGA	AAGACATTGG	CCGATTGAAA	CTTCTCTTAC	CTGACCTGCA	ACCCCAAAGC	1620
	AACTTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
	TGGAAGACAG	GGAAATTC	GTTGTATCAA	GGAAGTATG	CTACCAAAAG	CATCATTTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
80	TCAGGCTTAT	GTCAGATGAT	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
	TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
	TAGAATTATC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040
	TCTTGATATA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCACGTATC	TCTCAGTCA	2100
	TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAAT	GTCAGTTTAT	CTCCCCCTCT	2160
85	CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
	TAGAAAAAAA	AGCACAGAGA	AATGTTTAAC	TGTTTGACTC	TTATGATACT	TCTTGGAAAC	2280
	TATGACATCA	AAGATAGACT	TTTGCCCTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340

TGTATATTAA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

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MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	FGECVGNPKC	RCFPGYTGKT	CSQDVNECGM	KPRPCQHRVC	NTHGSYKCF	120
LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYYC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
GSFKCKCKG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
PEPTRTPTEK	VNLQPFNYEE	IVSRGGNSHG	GKKGNBEEKM	EGLEDEKREE	KALKNDIEER	360
SLRGDVFFPK	VNEAGEFLGI	LVQRKALTSK	LEHKDLNISV	DCSFNHGICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPAAL	GHKKDIGRLK	LLLPDLQPQS	NFCLLFYRL	AGDKVGKLRV	480
FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERKGKGTG	EIAVDGVLLV	540
SGLCPDSSL	VDD					

Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

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CTCATTTTCA	GGAAAGCCTG	AAAATGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
ATCAGGAATT	TGAAGAAAAT	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
CTCCTAAGAG	GGCAGCTCT	CTTCACCTGT	GAACCAATTA	CTGTTCCCAG	ATGTATGAAA	360
ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
GCGGTGGAAA	TGGAGCATTT	TCTTCTCTCT	GCAAACTCTG	AATGTTCAAC	AAACATTGAA	480
ACTTTCCTCT	GCAAAAGCATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GTTTCCACCT	540
TGTCTGTAAC	TTCGTGAGAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACTTTGGGG	600
ATCCGATGCG	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTTCTT	660
GTAACCTTTG	ATCCACACAC	AGAATTTCTT	GGTCTCAGA	AGAAAACAGA	ACAAGTCCAA	720
AGAGACATTG	GATTTTGGTG	TCCAAGGCTT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
TTTCTGGGAA	TTGACCAGTG	TGCGCCTCCA	TGCCCAACA	TGTATTTTAA	AAGTGATGAG	840
CTAGAGTTTG	CAAAAAGTTT	TATTGGAACA	GTTTCAATAT	TTTGTCTTTG	TGCAACTCTG	900
TTACATTCTT	TACTTTTGT	AATTGATGTT	AGAAGATTCA	GATACCCAGA	GAGACCAATT	960
ATATATTACT	CTGTCTGTTA	CAGCATTGTA	TCTCTTATGT	ACTTCATTGG	ATTTTGTCTG	1020
GGCGATAGCA	CAGCCTGCAA	TAAGGCAGAT	GAGAAGCTAG	AACTTGGTGA	CACCTGTTGT	1080
CTAGGCTCTC	AAAATAAGGC	TTGCACCGTT	TTGTTCATGC	TTTGTGATTT	TTTCACAATG	1140
GCTGGCAGTG	TGTGTGGGT	GATTCTTACC	ATTACTTGGT	TCTTAGCTGC	AGGAAGAAAA	1200
TGGAGTTGTG	AAGCCATCGA	GCAAAAAGCA	GTGTGGTTTC	ATGCTGTTGC	ATGGGGAACA	1260
CCAGGTTTCC	TGACTTTGGT	GCTTCTTGCT	CTGAACAAAG	TTGAAGGAGA	CAACATTAGT	1320
GGAGTTTGCT	TGTGTGGCT	TTATGACCTG	GATGCTTCTC	GCTACTTGT	ACTCTTGCCA	1380
CTGTGCCTTT	GTGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTTAAAT	1440
CATGTTTCGAC	AAGTATGAGC	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAAATTTATG	1500
ATTTCGAATTG	GAGTCTTCAG	CGGCTTGAT	CTTGTGCCAT	TAGTGACACT	TCTCGGATGT	1560
TACGTCTATG	AGCAAGTGAA	CAGGATTACC	TGGGAGATAA	CTTGGGTCTC	TGATCATTGT	1620
CGTCAGTACC	ATATCCCATG	TCCTTATCAG	GCAAAAAGCAA	AAGCTCGACC	AGAAATTGAT	1680
TTATTATGTA	TAAATACCT	GATGACATTA	ATTGTTGGCA	TCTCTGCTGT	CTTCTGGGTT	1740
GGAGCAAAA	AGACATGCAC	AGAATGGGCT	GGGTTTTTAA	AACGAAATCG	CAAGAGAGAT	1800
CCAATCAGTG	AAAGTCGAG	AGTACTACAG	GAATCATGTG	AGTTTTCTT	AAAGCACAAT	1860
TCTAAAGTTA	AACACAAAAA	GAAGCACTAT	AAACCAAGTT	CACACAAGCT	GAAGGTCATT	1920
TCCAAATCCA	TGGGAACCGC	CACAGGAGCT	ACAGCAAAATC	ATGGCACTTC	TGCAGTAGCA	1980
ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAAC	CTCACCAGAA	2040
ACATCAATGA	GAGAGGTGAA	AGCGGACGGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
TGTGGTGAAC	CTGCCTCGCC	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTCGAC	2160
GGGAAGGGCC	AGGCAGGCGA	TGTATCTGAA	AGTGCAGGGA	GTGAAGGAGG	GATTAGTCCA	2220
AAGAGTGATA	TACTGACAC	TGGCCTGGCA	CAGAGCAACA	ATTGACAGGT	CCCCAGTTCT	2280
TCAGAACCAA	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTCAACCCAGT	TTCAGGAGTG	2340
AGAAAAGAGC	AGGGAGGTGG	TTGTCAATTC	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
CAGAAGCAAA	TTTGTGTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
TACGTTCTTC	TTTTGCACTT	AAAGTTGCAT	TGCCTACTGT	TATACTGGAA	AAAATAGAGT	2520
TCAAGAATAA	TATGACTCAT	TTCAACAAA	GGTTAATGAC	AACAATATAC	CTGAAAACAG	2580
AAATGTGCAG	GTTAATAATA	TTTTTTTAA	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCCTT	2760
GTATCTTTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACTTTT	TTGAAATCCT	2820
ATTCAAGTAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTACACTGA	2880
ATTCTAAGA	AAATGTGAAA	ATAGTCTTCT	TTTATACTGT	AAAAAAGAT	ATACCAAAAA	2940
GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTTATTG	ATACCTTACC	ATCTAAAAATG	3000
TGTGATTTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTATGTA	ACTGAAATAA	3060
GGTGTCTACT	CAAGAGTGTA	CCACTATTGA	TTGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
ATATTAAAAA	TAAATGTGCC	TAAAGGGTTA	GTAGACAAAA	TGTTAGTCTT	TTGTATATTA	3180
GGCCAAGTGC	AATTGACTTC	CCTTTTTTAA	TGTTTCATGA	CCACCCATTG	ATTGTATTAT	3240
AACCACTTAC	AGTTGCTTAT	ATTTTTTGT	TTAAGTTTGT	TTTCTTAAAC	TTTAGAATAT	3300
TACATTTTGT	ATTATACAGT	ACCTTTCTCA	GACATTTTGT	AG		

Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

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 FLPLANLECS PNIETFLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRNPEE 120
 LECDRLOQYD ETVPVTFDPH TEFLGPQKKT EQVQRDIGPW CPRHLKTSBG QGYKFLGIDQ 180
 CAPPFCNMYF KSDLELEFAKS FIGTVSIFCL CATLFTFLT F LIDVRRFRYP ERPIIYYSVC 240
 5 YSIVSLMYPI GFLLDGSTAC NKADEKLELG DTVVLGSONK ACTVLFMLLY FFTMAGTVWW 300
 VILTTITWFLA AGRKNSCEAI EQKAVWPHAV AWGTGPGFLTV MLLALNKEVG DNISGVCVFP 360
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKI KKFMRIGVF 420
 SGLYLVLPLVT LLGCVYVEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALPMIKY 480
 10 LMTLIVGISA VEWVSGSKTTC TEWAGFPKRN RKRDPISER RVLQESCEFF LKHNSKVKHK 540
 KKHYPSSSHK LKVISKSMGT STGTANHGT SAVAITSHDY LGQETLLEIQ TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNLQ VPSSEPSL KGSTSLVHP VSGVRKEGG GCHSDT

Seq ID NO: 652 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

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 20 TTGGCGGGCG GAAGCGGCCA CAACCCGGCG ATCGAAAAGA TTCTTAGGAA CGCCGTACCA 60
 GCCGGTCTCT TCAGGACAGC AGGCCCTGT CCTTCTGTCT GGGCCGCTC AGCCGTGCCC 120
 TCCGCCCTCT AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAC TCTCAAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA 240
 25 AGGTCAAAC TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360
 TGAGACATCA GCATATATGT CAACCTTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTCTTGA GTACTGCCCT GGAGGAGAGC TGTCTGACTA TATAATTCC CAGGATCGCC 480
 TGTCAGAAGA GGAGACCCGG GTTGCTCTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTT GATGAATATC 600
 30 ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC 660
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 CATATCTTGG ATCAGAGGCA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780
 GTGGATTCTT ACCATTGTAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 35 GAAAATATGA TGTTCCTAAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900
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 40 AGGCTCGGG AAAACCAAGT CGTTTAAGGC TTTCTTCTTT CTCCTGTGGA CAAGCCAGTG 1200
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 AATCTAAATC ATTAATCTCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAAG 1440
 45 AAAATGTATA TACTCTAAG TCTGCTGTA AGAATGAAGA GTACTTTATG TTTCTGAGC 1500
 CAAAGACTCC AGTTAATAAG AACCAGCATA AGAGAGAAAT ACTCACTACG CCAATCGTT 1560
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 TAAATCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCTT TAGCCCTGAG AGGCGGTGCC 1680
 GCTCAGTGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAA AGAAAGGGAG 1740
 50 CCAAAGTGT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGTA 1800
 GCAAAAGGAA GGTGCTCTGC AGAGACGGGC CCAAGAGACT AAAGCTTAC TATAATGTGA 1860
 CTACAAC TAG ATTAGTGAAT CCAGATCAAC TGTGAATGA AATAATGTCT ATTCTTCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT 1980
 TTTGGAAAGT GACAAATGAA TTTGAATTAG AAGTGTGCCA GCTTCAAAA CCGATGTGG 2040
 55 TGGGTATCAG GAGGCAGCG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGAAG 2100
 ACATCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCTGCGG GATGAGTGTG 2160
 GGTGTGATAC AGCTACGATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCAATGGAA 2220
 CTACCAACTT GTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280
 GATATATTAT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGCTTTTT 2340
 60 TAATCATGTG GTTTGTGATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTAACTATG TCTCTTTGTA ATGTGTAATT TCTTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 653 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 65 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELFDYIIS QDRLSEETR VVFRQIVSAV 120
 70 AYVHSQGYAH RDLKPENLLF DEYHKLKID FGLCAKPKGN KDYHLQTCG SLAYAAPELI 180
 QGKSYLGSEA DVWSMGILLY VLMCGFLFFD DDNVMALYKK IMRGKYDVPK WLSPPSILL 240
 QQMLQVDPKK RISMKNLNLH PWIMQDYNYP VEWQSKNFFI HLDDDCVTEL SVHHRNRRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSPSCG QASATPFTDI KSNNWSLEDV 360
 75 TASDRNYVAG LIDVDWCEDD LSTGAATPRT SQFTKYNTES NGVESKSLTP ALCRTPANKL 420
 KNKENVYTPK SAVKNEEYFM FPEKTPVKN NQHKREILT PNRYYTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
 LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKKHVDFV QXGYTLKQCT 600
 QSDFGKVTMQ FELEVCLQK PDVVGIRRR LKGDWVYKR LVEDILSSCK V

Seq ID NO: 654 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
 85 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AACGCCGACC AAGGAAACT CACTACCATG AGAATTGCAG TGATTGTGCT TTGCTCTCTA 120

	GGCATCACCT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAAGCAG	180
	CTTTACAACA	AATACCCAGA	TGCTGTGGCC	ACATGGCTAA	ACCCTGACCC	ATCTCAGAAG	240
	CAGAACTCTC	TAGCCCCACA	GACCTTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCCATG	300
5	GATGATATGG	ATGATGAAGA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
	AACGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
	TCTGATGAAT	CTGATGAAT	GGTCACTGAT	TTTCCCACGG	ACCTGCCAGC	AAACGGAAGTT	480
	TTCACTCCAG	TGTCTCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTTAT	540
	GGACTGAGGT	CAAAATCTAA	GAAGTTTCGC	AGACCTGACA	TCCAGTACCC	TGATGCTACA	600
10	GACGAGGACA	TACACCTACA	CATGGAAAGC	GAGGAGTTGA	ATGGTGCATA	CAAGGCCATC	660
	CCCGTTGCC	AGGACCTGAA	CGCGCTTCT	GATTGGGACA	GCCGTGGGAA	GGACAGTTAT	720
	GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
	TATAAGCGGA	AAGCCAAATGA	TGAGAGCAAT	GAGCATTCCG	ATGTGATTGA	TAGTCAGGAA	840
	CTTTCCAAAG	TGAGCCGCTGA	ATCCACAGC	CATGAATTTT	ACAGCCATGA	AGATATGCTG	900
15	GTTGTAGACC	CCAAAAGTAA	GGAAGAAGAT	AAACACCTGA	AATTTCTGAT	TTCTCATGAA	960
	TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAGGAGAAAA	AATACAAATTT	CTCACTTTGC	1020
	ATTTAGTCAA	AAGAAAAAAT	GCTTTATAGC	AAAATGAAAG	AGAACATGAA	ATGCTTCTTT	1080
	CTCAGTTTAT	TGGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	TGTTTGTATA	1140
	ATTAGTTTAG	TTTGTGGCTT	CATGGAAACT	CCCTGTAAAC	TAAAAGCTTC	AGGGTTATGT	1200
20	CTATGTTTAT	TCTATAGAAG	AAATGCAAA	TATCACTGTA	TTTTAATATT	TGTTATTCTC	1260
	TCTAGTAATG	AAATTTATGT	AGAAGCAAA	AAAATACTTT	TACCCACTTA	AAAAGAGAA	1320
	ATAACATTTT	ATGTCACAT	AATCTTTTGT	TTTTTAAGTT	AGTGTATATT	TTGTTGTGAT	1380
	TATCTTTTGT	TGGTGTGAAT	AAATCTTTTA	TCTTGAATGT	AATAAGAATT	TGGTGGTGT	1440
	AATTGCTTAT	TGTTTTCCT	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTCTACT	1500
25	GCCTAAAAAA	AAAAAATAAA	AAAA				

Seq ID NO: 655 Protein sequence
Protein Accession #: NP_000573

	1	11	21	31	41	51	
30	MRIAVICFCL	LGITCAIPVK	QADSGSSEK	QLYNKYPDV	ATWLNPDPSQ	KQNLLAPQTL	60
	PSKSNESHDH	MDDMDEDDDD	DHVDSDSID	SNDSDVDVDT	DDSHQSDSH	HSDEDELVT	120
	DFPTDLPLATE	VTPVPTVD	TYDGRGDSV	YGLRSKSKKF	RRPDIQVPA	TDEDITSHME	180
35	SEELNGAYKA	IPVAQDLNAP	SDWDSRGKDS	YETSQLDDQS	AETHSHKQSR	LYKRKANDES	240
	NEHSDVIDSQ	ELSKVSREEF	SHEFHSHEM	LVDVPSKEE	DKHLKFRISH	ELDSASSEVN	

Seq ID NO: 656 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

	1	11	21	31	41	51	
45	GGGGTGGGAG	GGGGAGGGGG	ACCTCCGCAC	GAGACCCAGC	GGCCCGGGTT	GGAGCGTCCA	60
	GCCCTGCAAC	GGATCATGTT	GCAGCAGCG	GAGAGCTTGG	AAGCGGAGAG	CAACCTGCCC	120
	CGGGAGGGCG	TGGACACGGA	GGAGGGCGAA	TTCATGGCTT	GCAGCCCGGT	GGCCCTGGAC	180
	GAGAGCGACC	CAGACTGGTG	CAAGACGGCG	TCCGGCCACA	TCAAGCGGCC	GATGAACGCG	240
	TTGATGTTAT	GGTCCAGAT	CGAACGCGAG	AAGATCATGG	AGCAGTCTCC	GGACATGCAC	300
50	AACGCCGAGA	TCTCCAAGAG	GCTGGGCAAG	CGCTGGAAGA	TGCTGAAGGA	CAGCGAGAAG	360
	ATCCCGTTCA	TCCGGGAGCG	GGAGCGGCTG	CGGCTCAAGC	ACATGGCCGA	CTACCCCGAC	420
	TACAAGTACC	GGCCCGGAA	AAAGCCCAA	ATGGAACCCCT	CGGCCAAGCC	CAGCGCCAGC	480
	CAGAGCCAG	AGAAAGAGCG	GGCCGGCGGC	GGCGGCGGGA	GCGCGGCGG	AGGCGCGGGC	540
	GGTGCCCAAGA	CTCCCAAGGG	CTCCAGCAAG	AAATGCGGCA	AGCTCAAGGC	CCCGCGGGCC	600
55	GCGGGCGCCA	AGGCGGGCGC	GGGCAAGCG	GCCAGTCCG	GGGACTACGG	GGGCGCGGGC	660
	GACGACTACG	TGCTGGGAG	CCTGCGCTG	AGCGGCTCGG	GCGGCGGCGG	CGCGGGCAAG	720
	ACGGTCAAGT	GGGTGTTTCT	GGATGAGGAC	GACGACGACG	ACGACGACGA	CGACGAGCTG	780
	CAGCTGCAGA	TCAAACAGGA	GCCGACGAG	GAGGACGAGG	AACCAACCGCA	CCAGCAGCTC	840
	CTGCAGCGCG	CGGGGACGCA	GCCGTGCGAG	CTGCTGAGAC	GCTACAACGT	CGCCAAAGTG	900
60	CCGCGCAGCC	CTGCTGTAG	CAGCTCGGCG	GAGTCCCGCG	AGGGAGCGAG	CCTCTACGAC	960
	GAGGTGCGGG	CGGCGCGAC	CTCGGCGGCC	GGGGGCGGCA	GCCGCTCTTA	CTACAGCTTC	1020
	AAGAAACATCA	CCAAGCAGCA	CCCGCCGCGG	CTCGGCGAGC	CCGCGCTGTC	GCCCGCGTCC	1080
	TGCGGCTCGG	TGTCTACCTC	CTCGTCCAGC	AGCAGCGGCA	GCAGCAGCGG	CAGCAGCGGC	1140
	GAGGACGCGG	ACGACCTGAT	GTTGACCTG	AGCTTGAATT	TCTCTCAAAG	CGGCGACAGC	1200
65	GCCAGCGAGC	AGCAGCTGGG	GGGCGGCGCG	GCGGCGGGGA	ACCTGTCCCT	GTGCTGGTGG	1260
	GATAAGGATT	TGGATTCTGT	CAGCGAGGGC	AGCCTGGGCT	CCCACTTCGA	GTTCGCCGAC	1320
	TACTGCACGC	CGGAGCTGAG	CGAGATGATC	GCGGGGAGCT	GGCTGGAGGC	GAACTTCTCC	1380
	GACCTGGTGT	TCACATATTG	AAAGGCGCCC	GCTGCTCGCT	CTTTCTCTCG	GAGGGTGCAG	1440
	AGCTGGGTTT	CTTGGGAGGA	AGTTGTAGTG	GTGATGATGA	TGATGATGAT	AATGATGATG	1500
70	ATGATGGTGG	TGTTGATGTT	GGCGGTGGTA	GGGTGGAGGG	GAGAGAAGAA	GATGCTGATG	1560
	ATATTGATAA	GATGTGCTGA	CGCAAAGAAA	TTGGAAAACA	TGATGAAAAT	TTTGGTGGAG	1620
	TTAAAGTGAA	ATGAGTAGTT	TTTAAACATT	TTTCTGTCTC	TTTTTTTGTG	CCCCCTCCCT	1680
	TCCTTTATCG	TGTCTCAAGG	TAGTTGCATA	CCTAGTCTGG	AGTTGTGATT	ATTTTCCCAA	1740
	AAAATGTGTT	TTTGTAATTA	CTATTCTTTT	TTCTGAAAT	TCGTGATTGC	AACAAAGGCA	1800
75	GAGGGGGCGG	CGCGGCGGAG	GGGAGGTAGG	ACCGGCTCCG	GAAGGCGCTG	TTTGAAGCTT	1860
	GTCGGTCTTT	GAAGTCTGGA	AGACGTCTGC	AGAGGACCCT	TTTGGCAGCA	CAACTGTTAC	1920
	TCTAGGGAGT	TGGTGGAGAT	ATTTTCTTTT	CTTAAGAGAA	CTTAAAGAAC	TGTTGATTTT	1980
	TTTTTAACAA	AAAAAGGG					

Seq ID NO: 657 Protein sequence
Protein Accession #: NP_003099.1

	1	11	21	31	41	51	
85	MVQQAESLEA	ESNLPREALD	TEEGEFMACS	PVALDESDPD	WCKTASGHIK	RPMNAFMVWS	60
	KIERRKIMEQ	SPDMHNAEIS	KRLGKRWKML	KDSEKIPFIR	EAERLRLKHM	ADYPDYKYRP	120
	RKKPKMDPSA	KPSASQSPK	SAAGGGGGSA	GGGAGGAKTS	KGSSKKCKGL	KAPAAAGAKA	180
	GAGKAAQSGD	YGGAGDDYVL	GSLRVSGSGG	GGAGKTVKCV	FLDEDDDDDD	DDDELQLQIK	240

QEPDEEDEEP PHQQLLPFGP QPQSLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG 300
 ATSGAGGGR LYYSFKNITK QHPPLAQA LSPASSRSVS TSSSSSGSS SGSSGEDADD 360
 LMFDSLNLFS QSAHSASEQQ LGGGAAGNL SLSLVDKDL SFSEGLSGSH FEFPDYCTPE 420
 LSEMIAGDWL EANFSDLVFT Y

Seq ID NO: 658 DNA sequence
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123..1418

10 1 11 21 31 41 51
 | | | | | |
 GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
 CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
 CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
 15 CCTCTTCTCT GCTGCGCTCC GCCTTGCGCG ACTTCAGCCT GGACAAACGAG GTGCACTCGA 240
 GCTTCATCCA CCGGCGCTCT CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
 CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTTTAT GCTGAGCTCG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
 20 GCCAGGGCTT TCCTACCCC TACAAGGCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
 GCCTGCAAGA TGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
 TGAACATGA CAAGGAATTC TTCCACCACG GCTACCACTA TCGAGAGTTC CGGTTTGATC 600
 TTTCAAGAT CCCAGAAGG GAACTGTCA CGCAGCCGA ATTCCGGATC TACAAGGACT 660
 ACATCCGGGA AGCTTCCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCGCTCG 780
 25 AGGAGGGCTG GCTGGTGTG GACATCACAG CCACGACCAA CCACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGCTTCGAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACA GCAGCCCTTC ATGGTGGCTT 960
 TCTTCAAGC CACGGAGTGC CACTTCGCA GCATCCGCTC CACGGGAGC AAACAGCGCA 1020
 30 GCCAGAACCG CTCGAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 AGAACAGCAG CAGCGACCAG AGGCAAGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
 AGGGGAGTGT TGCCTTCCTT CTGAACCTCT ACATGAACGC CACCAACCA GGCATCGTGC 1260
 AGACGCTGCT CCATTCATC AACCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCAAGC 1320
 35 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTCTGG ATCTCTCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
 CTGCCTTTTG TGAGACCTTC CCTCTCCCTAT CCCCACTTT AAAGGTGTGA GAGTATTAGG 1560
 AAACATGAGC RISVYQLVQE TTTTGTACAG TTTTGTACAG GCAGCATCCA ATGAACAAGA 1620
 40 TCTTACAAGC TGTGCAGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
 GCCGGGCCAG GTCATTGGCT GGGAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTATGAGCGC CTACCAAGCA GGCACCCGAG CCGTGGGAGG AAGGGGGCGT GCAAGGGGT 1800
 GGGCACATTG GTGTCGTGTC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
 CAATAAACG AATGAATG

Seq ID NO: 659 Protein sequence
 Protein Accession #: NP_001710

1 11 21 31 41 51
 | | | | | |
 50 MHVRSRLAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQRE REMQREILS 60
 ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGSYPYKAV FSTQGPPLAS 120
 LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREPRFDL SKIPEGEAVT AAEFRYKYD 180
 IRERFDNETF RISVYQLVQE HLGRESLFL LDRSLWASE EGWLVDITA TSNHVVNPR 240
 55 HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
 QNRSTPKNQ BALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAAYCE 360
 GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
 RNMVVRACGC H

Seq ID NO: 660 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 211..1895

1 11 21 31 41 51
 | | | | | |
 65 GGATCTGAGG GGCGCCAGT CACTTCTCC ACCTTCTCGT GCTGGGCGGG AGGAGCGGAT 60
 GGGGCTTGGG AGGAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTT TTGGGTGCGA 120
 GAGGAATTAT CTGATAAAT TCCTGGGTTA ATATTTTAA AAACGAGAG TTTTAAAAA 180
 TGATTTTTT CCCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGT CACAGCATA 240
 70 GTGCTTTTC TTTTCTTTC TTTTCTACG ATAAATGAAA GCATTCTTC AAGAAAAAG 300
 CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
 CTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCAACATCA CAGCTCAACT CCAGGAGGGA 420
 GAAGTAATT GTTCCCTGA ATGGGATGGA CTCATTGTG GGGCCAGAG AACAGTGGG 480
 AAAATATCGG CTGTTCCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
 75 TTCCGACACT GTAACCCAA TGGAAACATG GATTTTATGC ACAGCTTAAA TAAACATGG 600
 GCCAATTATT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
 TTCTTTGAAC GCCTCATGT AATGTATACC GTTGGCTACT CCATCTCTT TGGTTCTT 720
 GCTGTGGCTA TTCTCATCAT TGTGTACTTC AGACGATTGC ATTGCACTAG GAACTATATC 780
 CACATGCACT TATTTGTGTC TTTTATGCTG AGAGCTACAA GCATCTTGT CAAAGACAGA 840
 GTAGTCCATG CTCACATAG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
 80 CAAAATCCA TTGAGGCAAC TTCTGTGAC AAATCAAAAT ATATCGGGT CAAGATTGCT 960
 GTTGTGATGT TTATTACTT CCTGGCTACA AATTATTATT GGATCTGGT GGAAGGTCTC 1020
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTGGGACA CCAATACCT GTGGGGCTTC 1080
 ATCTTGATAG GTCGGGGTTC TCCAGCAGCA TTTGTTGCG CATGGCTGT GGCACGAGCA 1140
 85 ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGTGGAG ACATCAAGTG GATTTATCAA 1200
 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATTCTGT TTCTGAATAC GGTAGAGTT 1260
 CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAGGAA GCAATACAGG 1320
 AAATGGCCA AATCGACACT GGTCTGGTC CTAGTCTTTG GAGTGATTA CATCTGTTT 1380

GTATGCCTGC CTCCTCTCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAGAGG 1560
 ACACCCCAT GTGGCAGCCG CAGATGCGGC TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCCTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 CAGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCTTA TGGATCTAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 661 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MLRSSLSTSI VLFLPSSPST INESSISRRK HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
 LNIITAQLEGE EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120
 DPMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMTY VGSISFGLS AVAILLIIGYF 180
 RRLHCTRNYY VMHFLVFSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSV 240
 KSOYIGCKIA VMPFIYFLAT NYWILVEGL YLHNLIFVAF FSDTKYLWGP ILIGWGFPA 300
 FVAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILFLNTVRV LATKIWETNA 360
 VGHDTRKQYR KLAKESTLVLV LVFVGHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFGGFFV 420
 SIIYCYCNGE VQAEEVKKWS RWNLSVDWKR TPPCGSRRCG SVLTTVTHST SSQSQVAAST 480
 RMLVLSGKAA KIASRQPDHS ITLPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
 SRPMESNPDT EGCGGETEDV L

Seq ID NO: 662 DNA sequence
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143..1795

1 11 21 31 41 51
 GGCCGGTGGC CGGGGCCCGA CCACCCAGC TGCGCGTCTG TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTTACA GCGGTTCGGG GCATGGCCGG GCTGGGGCGG TCGCTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTAC 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTT 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGTC CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTACTTCTA GAGGATTGCA 660
 TTGCACTAGG AACTATATGC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGACG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGTCT TTGTGATGTT TATTACTTTC CTGGCTACAA ATTATTATTG 900
 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCTT TTTCCGACAC 960
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTGTCAGC 1020
 ATGGGCTGTG CACACAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACCTA GTGCTGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
 CACAAGGAAG CAATACAGCA AACTGGCCAA ATCGACACTG GTCTGGTCTC TAGTCTTTGG 1260
 AGTGCAATTAC ATCGTGTTCC TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCAC TGTGAGCTCT TCTTCAATC CTTCAGGGT TTCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGAGAGAG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCGCG AGATGCGGCT CAGTGTCTAC 1500
 CACCGTGACG CACAGCACC ACGAGCCATC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620
 TGGCTATGTC TGGAGTAAT CAGAGCAGGA CTGCTTGCCA CACTCTTTCC ACGAGGAGAC 1680
 CAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980
 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCAATTT TTTCTGTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGATC 2160
 ATTTTCTTTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTTAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 TTCTTTGTAA ACCATGTGAT GTGGAAAAGT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTCTCTTG 2580
 TTTGAGCTGT TACTACATG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640
 T

Seq ID NO: 663 Protein sequence
 Protein Accession #: NP_005039

1 11 21 31 41 51
 MAGLGASLHV WGNWLMGSLC LARAQLSDSG TITIEEQIVL VLKAKVQCEL NITAEQLQGE 60
 EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW FMHSLNKTWA 120
 NYSDCLRLFL QPDISIGKQE FFERLYVMTY VGSISFGLS AVAILLIIGYF RRLHCTRNYYH 180
 MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240

VMPIYFLATN YYWILVEGLY LHNLIQVAFV SDTKYLWGFPI LIGWGPPAFAF VAANAVARAT 300
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTRVRL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLVVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVFS ILYCYCNGEV 420
 QAEVKKMWSR WNLSDWKRTP PCGSRRCGS VLTIVTHSTS SQSQVAASR MVLISGKAAK 480
 IASRQPDSEI TLPQVVSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPMESNPDE 540
 GCQGETEDVL

Seq ID NO: 664 DNA sequence
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43..1104

1 11 21 31 41 51
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 CTCTTTTAA TTTCTTTCTA GGATGTTTCC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTT TTATAATAGG AGCAACACTG ATACTGTGGA TGACTGGACA 120
 GGAAACAAAG TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
 TCTAATTTCT TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240
 TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTGCTG GAATTGCCTA TGTATCTCTG 300
 ATGTTTAAAC CAGGCCCACT TTCAAAAAC TTGACTGTCA ACCGCTGGTT TCTCCGTGAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
 AGGCACATGT CAATCATGAG GATCGGGTCC CATAGCAACC TGACCAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTTGTCTG GGCATCGGCC ATTTTATAGG GGGCGGTCCC CACACTGGGC 540
 TGGAAATGCC TCTGCAACAT CTCTGCCCTG TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600
 TACCTTGTCT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC 660
 CTGCGGATCT ACGTGTAGCT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC CGCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
 GCGTTTGTGG TATGCTGGAC CCCGGGCTG GTGGTCTGTC TCCTCGACGG CCTGAAGTGC 840
 AGGCAGTGTG CGCTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
 GTCGTGAACC CAGTACTCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
 GTCTCAGCA GAGGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
 GTCTGCAATA AAAGCACTTC CTAACCTCTG GATGCCTCTC GGCCCAACCA GGTGATGACT 1140
 GTCTTAGG

Seq ID NO: 665 Protein sequence
 Protein Accession #: NP_036284

1 11 21 31 41 51
 | | | | |
 MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60
 FHFFFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
 LVIAVERHMS IMRMVHNSL TKKRVTLIL LVWAIAPFMG AVPTLGNWCL CNISACSSLA 180
 PYRSYLVF WTVSNLMAPL IMVVYLRIV VYVKRKTNL SPHTSGSISR RRTPMKLMKT 240
 VMTVLGAPVV CMTPLVLVLL LDGLNCRQCG VQHVKNWFL LALLNSVNP IYYSKDEDM 300
 YGTMKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

Seq ID NO: 666 DNA sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150..3362

1 11 21 31 41 51
 | | | | |
 AACTCCCGCC TCGGGACGCC TCGGGGTCCG GCTCCGGCTG CGGCTGCTGC TCGCGCGCCC 60
 GCGCTCCGGT GCGTCCGCTT CCTGTGCCCG CCGCGGAGCA GTCTGCCGCC CGCGTGCGC 120
 CCTCAGCTCC TTTTCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC 180
 CCGCGCGGTT GCTCTGCTC AGCTCTCTGC TGCTGCCGCT GCTGGGCGGT ACCCAGACAG 240
 CCATTGTCTT CATCAAGCAG CCGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
 TTCGTGTGA GGTGAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
 CTGTCCAGGA CACGAGGCGG CGTTTCGCC AGGGCAGCAG CCTGAGCTTT CGAGCTGTGG 420
 ACCGGCTGCA GGAATCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480
 AAGCCCGCAG TGCCACCGCC TCCTTCAACA TCAATGGAT TGAGGCAGGT CCTGTGGTCC 540
 TGAAGCATCC AGCCCTGGAA GCTGAGATCC AGCCACAGAC CCAGGTACA CTTCGTGTGC 600
 ACATTGATGG GCACCTCGG CCCACCTACC AATGGTCCG AGATGGGACC CCCCTTCTG 660
 ATGGTCAGAG CAACACACA GTACGAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG 720
 GTCTGAGCA TAGTGGCTG TATTCTGCT GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780
 GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840
 CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
 AGCCACCCCG GAGCCTGCAG TGGCTCTTTG AGGATGAGAC TCCATCACT AACCGCAGTC 960
 GCGCCCCACA CCTCCGAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
 TCCGGCCACG CAATGACGGG ATCTACCGCT GCATTGGCCA GGGGCAGAGG GGCCCAACCA 1080
 TCATCTGGA AGCCACACT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTGAGCCAC 1140
 GGGTGTTTAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCAAG GGTCTGCCAG 1200
 AGCCAGCGT GTGGTGGGAG CACGCGGAG TCCGGCTGCC CACCATGGC AGGGTCTACC 1260
 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACT 1320
 GCCACGCGCG CAACCTGGCT GGTACGCGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
 TTCCCTCCTG GCTGAAGAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440
 TGGATTGCTT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGTACAGA AACCATGTC 1500
 TCATCTCAGA GGAATCACGG TTCGAGGTCT TCAAGATGG GACCTTGCCT ATCAACAGCG 1560
 TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGCC GGCAGCATCG 1620
 AGGCGCAAGC CGGTGTCAA GTGCTGGAAG AGCTCAAGTT CACACCAACA CCGCAGCCAC 1680
 AGCAGTGCAT GGAGTTTAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GGCCGAGAGA 1740
 AGCCCACTAT TAAGTGGGAA CGGCAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA 1800
 ACGCTGGGAC CTGCACTTTT GCGCGGGTGA CTCGAGATGA CGTGGCAAC TACACTTGCA 1860
 TTGCTTCAA CGGGCCGAG GGCCAGATTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT 1920
 TTATCACCTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
 TGCAGTGCAG GGCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAGGC AAGGACCGCA 2040
 TCCTGAGACC CACCAAGCTG GGACCCAGGA TGCACATCTT CCAGAAATGGC TCCCTGGTGA 2100

	TCCATGACGT	GGCCCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
	ACATCAAGCA	CACGGAGGCC	CCCCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
	AGGGCCCTTG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTG	2280
5	CGCTGTGGC	CTACATCAT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
	AAGCCAAGCG	GCTGCAGAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCCCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCCACGGTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
10	TCCTGGCAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCCTGTA	CTTGTAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAGCTGAA	CCACGCCAAC	GTGCTGCGGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCCT	2820
	AGAGCAAGGA	TGAAAAATTT	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
15	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACTGCCTG	GTGAGTGGCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCG	3000
	TCAGCAAGGA	TGCTGACAA	AGTGAGTACT	ACCACTTCCG	CCAGGCCTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTCGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
20	CAGATGATGA	AGTACTGGCA	GATTTCAGG	CTGGGAAGGC	TAGACTTCTC	CAGCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGAAGCTCA	3420
	CAGCATGATG	GGCAAGATCC	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
25	GGCTGACTTG	GACCCAAATG	GGGGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCTGCCAC	3600
	CTCTCTCTCT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTCT	GGCCTTCAAC	3660
	TTCTCCCTCT	GACCGGGTCC	AACTCTGCCA	CTCATCTGCC	AACTTTGCCT	GGGGAGGGCT	3720
	AGGCTTGGGA	TAGGTCTGGT	TTGTGGGGAG	TTCTTAAATA	TTCTCAAGTT	CTGGGCACAC	3780
30	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	GKAGTCCCTC	CCACTCTGGG	CTTGTGCACA	CTGACCAGA	CCCACGTCTT	3900
	CCCCACCTTT	CTCTCCTTTC	CTCATCTTAA	GTGCTTGCCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GCCCTTTTTC	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
35	GCCATCCTTA	CCCCACACTT	TTATTTGTGT	CGTTTTTTGT	TTGTTTTGTT	TTTTTGTITT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTTA		

Seq ID NO: 667 Protein sequence

Protein Accession #: NP_002812

40	1	11	21	31	41	51	
	MGAARGSPAR	PRRLPLLSVL	LLPLLGTTQT	AIVFIKQPSS	QDALQGRRAL	LRCEVEAPGP	60
	VHVVWLLDGA	PVQDTERRFA	QGSLSFAAV	DRLQDSGTFQ	CVARDDVTGE	EARSANASFN	120
45	IKWIEAGPVV	LKHPASEAEI	QPQTQVTLRC	HIDGHPRTY	QWFRDGTPLS	DGQSNHTVSS	180
	KERNLTLRPA	GPEHSGLYSC	CAHSAFGQAC	SSQNFTLSIA	DESFAFVFLA	PQDVVVARYE	240
	EAMFHCQFSA	QPPPSLQWLF	EDETPITNRS	RPHLRRAATV	FANGSLLLTQ	VRPRNAGIYR	300
	CIGQGQRGPP	IILEATLHLA	EIEDMPLFEP	RVFTAGSEER	VTCLPPKGLP	EPSVWWEHAG	360
	VRLPHTHGRVY	QKQHELVLAN	IAESDAGVYT	CHAANLAGQR	RQDVNITVAT	VPSWLKKPQD	420
50	SQLLEGKPGY	LDCLTQATPK	PTVVVYRNQM	LISEDSRFEV	FKNGTLRINS	VEVYDGTWYR	480
	CMSSTPAGSI	EAQARVQVLE	KLKFTPPPPQ	QQCMFEDKEA	TVPCSATGRE	KPTIKWERAD	540
	GSSLPWVTD	NAGTLHFARV	TRDDAGNYTC	IASNGPQQOI	RAHVQLTVAV	FITPKVEPER	600
	TTVYQGHATL	LQCEAQGDPK	PLIQWKGKDR	ILDPTKLGP	MHIFQNGSLV	IHDVAPEDSG	660
	RYTCIAGNSC	NIKHTEAPLY	VVDKPVPEES	EGPGSPPPYK	MIQTIGLSVG	AAVAYIIAVL	720
55	KLMFYCKKRC	KAKRLQKQPE	GEEPEMECLN	GGPLQNGQPS	AEIQEEVALT	SLGSGPAATN	780
	KRHSTSDKMH	PPRSLLQPI	TLGSEFGEV	FLAKAQGLEE	GVAETLVLVK	SLQTKDEQQQ	840
	LDFFRELEMF	GKLNHANVVR	LLGLCREAEP	HYMVLEYVDL	GDLKQFLRIS	KSKDEKLKSQ	900
	PLSTKQKVAL	CTQVALGMEH	LSNRPVHKD	LAARNCLVSA	QRQVKVSALG	LSKDVIYNSEY	960
	YHFRQAWVPL	RWMSPEAILE	GDFSTKSDVW	AFGLVMNEVF	THGEMPHGGQ	ADDEVLDLQ	1020
60	AGKARLPQPE	GCPSKLYRLM	QRWALSFPK	RPSFSEIASA	LGDSTVDSKP		

Seq ID NO: 668 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1389

65	1	11	21	31	41	51	
	ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGAGA	GAGATTAGA	TGACAGAGAA	60
	ACCCTTGTTT	CTGAACATGA	GTATAAAGAG	AAAACCTGTC	AGTCTGCTGC	TCTTTTAAAT	120
70	GTGTGCAACT	CGATTATAGG	ATCTGGTATA	ATAGGATTGC	CTTATTCAAT	GAAGCAAGCT	180
	GGGTTTCCTT	TGGGAATATT	GCTTTTATTC	TGGGTTTCAT	ATGTTACGGA	CTTTCCCTT	240
	GTTTTATTGA	TAAAAGGAGG	GGCCCTCTCT	GGAACAGATA	CCTACCAGTC	TTTGGTCAAT	300
	AAAACTTTTC	GCTTTCCAGG	GTATCTGCTC	CTCTCTGTTT	TTCAGTTTTT	GTATCCTTTT	360
	ATAGCAATGA	TAAGTTACAA	TATAATAGCT	GGAGATACTT	TGAGCAAAGT	TTTTCAAAGA	420
75	ATCCCAGGAG	TTGATCTCTG	AAACGTGTTT	ATTGGTGGCC	ACTTCATTAT	TGGACTTTCC	480
	ACAGTTACCT	TTACTCTGCC	TTTATCCTTG	TACCGAAATA	TAGCAAAGCT	TGGAAAGGTC	540
	TCCCTCATCT	CTACAGGTTT	AACAACCTCG	ATTCTTGGAA	TTGTAATGGC	AAGGGCAATT	600
	TCACTGGGTC	CACACATACC	AAAAACAGAA	GACGCTTGGG	TATTTGCAAA	GCCCAATGCC	660
	ATTCAAGCGG	TGGGGTTTAT	GTCTTTTGCA	TTTATTGGCC	ACCATAACTC	CTTCTTAGTT	720
80	TACAGTTCTC	TAGAAGAACC	CACAGTAGCT	AAGTGGTCCC	GCCTTATCCA	TATGTCCATC	780
	GTGATTCTCT	TATTTATCTG	TATATTCTTT	GCTACATGTG	GATACTTGAC	ATTACTGGC	840
	TTACCCCAAG	GGGACTTATT	TGAAAATTAC	TGCAGAAATG	ATGACCTGGT	AACATTGGGA	900
	AGATTTTGTT	ATGGTGTCTC	TGTCAATTTG	ACATACCCTA	TGGAATGCTT	TGTGACAAGA	960
	GAGGTAATTG	CCAATGTGTT	TTTTGGTGGG	AATCTTTTCAT	CGGTTTTCCA	CATTGTTGTA	1020
	ACAGTGATGG	TCATCACTGT	AGCCACGCTT	GTGTCTATGC	TGATTGATTG	CCTCGGGATA	1080
85	GTTCTAGAAC	TCAAATGGGT	GCTCTGTGCA	ACTCCCTCA	TTTTTATCAT	TCCATCAGCC	1140
	TGTTATCTGA	AACTGTCTGA	AGAACCAAGG	ACACACTCCG	ATAAGATTAT	GTCTTGTGTC	1200
	ATGCTTCCCA	TTGGTGTGTT	GGTGATGTTT	TTTGGATTCT	TCATGGCTAT	TACAAATACT	1260

CAAGACTGCA CCCATGGGCA GGAAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACITTT CTACTTTAAA TATTAGTATC 1380
 TTTCATGA

5 Seq ID NO: 669 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 10 MG YQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60
 GFPLGILLLF WVS YVTFDSL VLLIKGGALS GTDTYQSLVN KTFGPPGYLL LSVLQFLYPF 120
 IAMISYNIIA GDTLSKVQFR IPGVDPENVF IGRHFIIGLS TVTPTLPLSL YRNI AKLGKV 180
 SLISTGLTTL LGIVMARAI SLGPHIPKTE DAWVFAKPN IAQAVGVMSEA FICHNSFLV 240
 15 YSSLEPTVA KWSRLIHMSI VISVFICIFP ATCGYLTFTG FTQGDLPENY CRNDDLVTFG 300
 RPYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVPHIVV TVMVITVATL VSLIDCLGI 360
 VLELNGVICA TPLIPIISA CYLKLSEEP THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
 QDCTHGQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

20 Seq ID NO: 670 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1284

1 11 21 31 41 51
 25 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCGCAGAG GAGGATTGCC TTATTCAATG 60
 AAGCAAGCTG GGTTCCTTT GGAATATTG CTTTATTCT GGGTTTCATA TGTACAGAC 120
 TTTCCCTTG TTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AAACITTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCT TCAGTTTGTG 240
 30 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300
 TTTCAGAGAA TCCCAGGAGT TGATCCTGAA AACGTGTTA TTGGTCGCCA CTTCATTATT 360
 GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT 420
 GGAAAGGTCT CCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGAAT TGAATGGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTGCAAAAG 540
 35 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTGCCA CCATAACTCC 600
 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
 ATGTCCATCG TGATTCTGT ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCAAGG GGAATTATT GAAATTACT GCAGAAATGA TGACCTGGTA 780
 ACATTTGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCTAT GGAATGCTTT 840
 40 GTGACAAGAG AGGTAATTGC CAATGTGTT TTTGGTGGGA ATCTTTCATC GGTTTCCAC 900
 ATTGTTGTA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCAATGCT GATTGATTGC 960
 CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
 TCTGTGTCA TGCTTCCCAT TGGTGTGTG GTGATGGTTT TTGGATTGCT CATGGCTATT 1140
 45 ACAAATAC TCAAGTGCAC CATGGGCAG GAAATGTTCT ACTGCTTTC TGACAAATTC 1200
 TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACITTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

50 Seq ID NO: 671 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 55 MG YQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVS YVTD FSLVLLIKGG ALSGTDYQS 60
 LVNKTGFPFG YLLLSVLQPL YPFIAMISYN IAGDTLSKV FORIPGVDP NVPIGRHFII 120
 GLSTVTFTLP LSLYRNIAKL KVSLSITGL TTLILGI VMA RAISLPHIP KTEDAWVFAK 180
 PNAIQAVGVM SFAPICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFATCGYLT 240
 FTGFTQGDLE ENYCRNDLIV TFGRCYGVV VILTYPMCF VTREIVANVF FGNLSSVFH 300
 IVVTVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
 60 SCVMLPIGAV VMVFGFVMAI TMTQDCTHGQ EMFYCFPDNF SLTNTSESHV QQTQLSTLN 420
 ISIFQLE

65 Seq ID NO: 672 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1203

1 11 21 31 41 51
 70 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCGCAGT TTTCCCTTGT TTTATTGATA 60
 AAAGGAGGGG CCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC 120
 TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTGTG ATCCTTTTAT AGCAATGATA 180
 AGTTACAATA TAATAGCTGG AGATACCTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240
 GATCCTGAAA ACGTGTAT TGGTCGCCAC TTCATTATTG GACTTTCAC AGTTACCTTT 300
 ACTCTGCCTT TATCCTTGT CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
 75 ACAGGTTTAA CAACTGTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTC ACTGGGTCCA 420
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480
 GGGGTTATGT CTTTGTCAAT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
 GAAGAACCCA CAGTAGCTAA GTGGTCCGCG CTTATCCATA TGTCCATCGT GATTTCTGTA 600
 TTTATCTGTA TATTCTTTCG TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAGGG 660
 80 GACTTATTG AAAATTA CTGAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTTGTAT 720
 GGTGTCACTG TCATTGTGAC ATACCTATG GAATGCTTTG TGACAAGAGA GGAATTTGCC 780
 AATGTGTTT TGGTGGGAA TCTTTCATCG GTTTCCACA TTGTTGTAAC AGTGATGGTC 840
 ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGATAGT TCTAGAACTC 900
 AATGGTGTGC TCTGTGCAAC TCCCTCAT TTTATCATTC CATCAGCTG TTAATCTGAA 960
 85 CTGTCTGAAG AACCAAGGAC AACTCCGAT AAGATTATGT CTGTGTGCT GCTTCCCAT 1020
 CATGGGCAGG AAATGTTCTA CTGCTTCTCT GACAATTTCT CTCTACAAA TACCTCAGAG 1140
 TCTCATGTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QPLYPFIAMI 60
SYNIIAGDTL SKVFQRIPIV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLSIS 120
TGLTTLILGI VMARAIISLG HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180
EEPTVAKWSR LIHMSIVISV PICIFFATCG YLTFTGTQG DLFENYCRND DLVTPGRFCY 240
GVTVILTYPM ECFVTREIV NVPFPGNLSS VFHIVVTVMV ITVATLVSLD IDCLGIVLEL 300
NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HQQEMFYCFP DNFSLTNTSE SHVQQTQLS TLNISIFQLE

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Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGG TCAATAAAAC TTTCGGCTTT 60
CCAGGGTATC TGCTCCTCTC TGTTCCTCAG TTTTGTATC CTTTTATAGC AATGATAAGT 120
TACAAATATA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240
CTGCCCTTAT CCTGTACCG AAATATAGCA AAGCTTGGA AGGTCTCCCT CATCTCTACA 300
GGTTTAAACA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATT GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420
GTTATGTCCT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATT 540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTGAAAA ACTTATGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACGTGTA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTGG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTGTGTGC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAAGGACACT CTCGATAAG ATTATGTCTT GTGTCATGCT TCCCATGGT 960
GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTCTACTG CTTTCCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTCAGC AGACAACACA ACTTCTACT TAAATATTA GTATCTTTCA ACTCGAGTAA

```

Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQVNKTGFP PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIVD 60
PENVFIRRH IIGLSTVFT LPLSLYRNI KLKVSLSIT GLTTLILGIV MARAISLGH 120
IPKTEDAWVF AKPNAIQAV VMSFAFICH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
ICIFFATCGY LTFTGFTQGD LFENYCRNDD LVTFGFRFCY VTVILTYPME CFVTREIVAN 240
VFPFPGNLSSV FHVIVVTMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
SEEPRTSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLNTSES 360
HVQQTQLST LNISIFQLE

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Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

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1      11      21      31      41      51
|      |      |      |      |      |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60
ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCTCCAGGC 120
CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCAG CCCTGGCAGG CAGCCTGTT 240
CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300
AGCCCACTGC CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA 360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCG GCTTCAACAA 420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
CAGCTGCCTC ATTTCCGGCT GGGCGAGCAC GTCCAGCCCC CAGTTACGCC TGCTCACAC 600
CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAAGC CCTACCCCGG 660
CAACATACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAG ACTCTGGCA 720
GGGTGACTCC GGGGGCCTTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCTGGGG 780
CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
ACCCCTCCAT TCCACTTGGT GTTTGGTTC TGTCACTCT GTTAATAAGA AACCTAAGC 960
CAAGACCCTC TACGAACATT CTTTGGGCCT CCTGGACTAC AGGAGATGCT GTCACCTAAT 1020
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
GACTCTGGGA ATGACAACAC CTGTTTGTG TCTGTTGTA TCCCCAGCCC CAAAGACAGC 1140
TCTTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

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Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

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1      11      21      31      41      51
|      |      |      |      |      |
MRILQLILLA LATGLVGGET RIIGFCECKP HSQFPQAALF EKTRLLCGAT LIAPRWLLTA 60

```

AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV 120
 SITWAVRPLT LSSRCVTAQT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCENAYPG 180
 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVVTKVCKYV 240
 DWIQETMKNN

Seq ID NO: 678 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..933

1	11	21	31	41	51	
ATGTGCAGCA	ATGGACGGTG	CATCCCGGGC	GCCTGGCAGT	GTGACGGGCT	GCCTGACTGC	60
TTCGACAAGA	GTGATGAGAA	GGAGTGCCCC	AAGGCTAAGT	CGAAATGTGG	CCCACCTTC	120
TTCCCGCTGT	CCAGCGGCAT	CCATTGCATC	ATTGGTCGCT	TCCGGTGCAA	TGGGTTTGAG	180
GACTGTCCCG	ATGGCAGCGA	TGAAGAGAAC	TGCACAGCAA	ACCCTCTGCT	TGCTCCACC	240
GCCCGCTACC	ACTGCAAGAA	CGGCCTCTGT	ATTGACAAGA	GCTTCATCTG	CGATGGACAG	300
AATAACTGTC	AAGACAAACG	TGATGAGGAA	AGCTGTGAAA	GTTCTCAAGA	ACCCGGCAGT	360
GGGCAGGTGT	TTGTGACTTC	AGAGAACCAA	CTTGTGTATT	ACCCACAGCAT	CACCTATGCC	420
ATCATCGGCA	GCTCCGTCAT	TTTTGTGCTG	GTGGTGGCCC	TGCTGGCACT	GGTCTGCAC	480
CACCAGCGGA	AGCGGAACAA	CCTCATGACG	CTGCCCGTGC	ACCGGCTGCA	GCACCCTGTG	540
CTGCTGTCCC	GCCCTGGTGT	CCTGGACCAC	CCCCACCACT	GCAACGTCAC	CTACAAACGTC	600
AATAATGGCA	TCCAGTAGTG	GGCCAGCCAG	GCGGAGCAGA	ATGCGTCGGA	AGTAGGCTCC	660
CCACCCTCCT	ACTCCGAGGC	CTTGCTGGAC	CAGAGGCCTG	CGTGGTATGA	CCTTCCTCCA	720
CGGCCCTACT	CTTCTGCACG	GGAATCTCTG	AACCAAGCCG	ACCTGCCCCC	CTACCGCTCC	780
CGGTCCGGGA	GTGCCAACAG	TGCCAGCTCC	CAGGCAGCCA	GCAGCCTCCT	GAGCGTGGAA	840
GACACCAGCC	ACAGCCCGGG	GCAGCCTGGC	CCCCAGGAGG	GCACTGCTGA	GCCCAGGGAC	900
TCTGAGCCCA	GCCAGGGCAC	TGAAGAAGTA	TAA			

Seq ID NO: 679 Protein sequence
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MCSNGRCIPG	AWQCDGLPDC	FDKSDEKECP	KAKSKCGPTF	FPCASGIHCI	IGRFRNGFGE	60
DCPDGSDSEN	CTANPLLCST	ARYHCKNGLC	IDKSFICDQG	NNQDNDSEDE	SCESSQEPGS	120
GQVFTVSENQ	LVVYPSITYA	IIGSSVIFVL	VVALLALVLH	HQRKRNNLMT	LPVHRLQHPV	180
LLSRLVLDH	PHHCNVTVNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPAYWDLPP	240
PPYSSDTBSL	NQADLPYRS	RSGSANSASS	QAASSLLSVE	DTSHSPGPQG	PQEGTAEPRD	300
SEPSQGTVEV						

Seq ID NO: 680 DNA sequence
 Nucleic Acid Accession #: S78203.1
 Coding sequence: 1..2190

1	11	21	31	41	51	
ATGAATCCTT	TCCAGAAAAA	TGAGTCCAAG	GAAACTCTTT	TTTCACCTGT	CTCCATTGAA	60
GAGGTACCAC	CTCGACCACC	TAGCCCTCCA	AAGAAGCCAT	CTCCGACAAT	CTGTGGCTCC	120
AACATATCCAC	TGAGCATTGC	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTTCTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCCTGTATT	TCCTGCAGTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCTTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCTGGGA	300
GCAGCCATTG	CTGACTCGTG	GTTGGGAAAA	TTCAAGACAA	TCATCTATCT	CTCCTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAAGTCCTTG	GGTGCCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCCTATCATT	GATCGGCCTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCCTGTG	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGGAGTTC	CAGGACTGCT	CATGGTAATT	GCACCTGTGT	TGTTTGCAT	GGGAAGCAAA	720
ATATACAATA	AACCAACCCC	TGAAGGAAAC	ATAGTGGCTC	AAGTTTTCAA	ATGTATCTGG	780
TTTGCTATTT	CCAATCGTTT	CAAGAACCGT	TCTGGAGACA	TTCCAAAGCG	ACAGCACTGG	840
CTAGACTGGG	CAGCTGAGAA	ATATCCAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTAT	TCCTTTATAT	CCCATGTCCC	ATGTTCTGGG	CTCTTTTGA	TCAGCAGGGT	960
TCACGATGGA	CTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGTTTITT	TGTGCTTCAG	1020
CCGGACCAGA	TGCAGTTTCT	AAATCCCTTT	CTGGTTCTTA	TCTTCATCCC	GTTGTTTGAC	1080
TTTGTCAATT	ATCGTCTGGT	CTCCAAGTGT	GGAAATTAAT	TCTCATCACT	TAGGAAAAATG	1140
GCTGTTGGTA	TGATCCTAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCTTACA	AGTCTTGAAT	1200
ATAAATGAAA	TGGCCCCAGC	CTGGCAGATG	GTGGGAAATG	AAAACAATTC	TCTGTTGATA	1260
CTGGCAGATG	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAAACAATTC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAAAACCCA	CACTATTCCA	AACCTGCACCT	GAAAAACAAA	1380
AGCCAGGATT	TTCACTTCCA	CCTGAAATAT	CACAATTTGT	CTCTCTACAC	TGAGCATTCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTTGTC	ATTCGTGAAG	ATGGGAACAG	TATCTCCAGC	1500
ATGATGGTAA	AGGATACAGA	AAGCAAAACA	ACCAATGGGA	TGACAACCGT	GAGGTTTGTT	1560
AACACTTTGC	ATAAAGATGT	CAACATCTCC	CTGAGTACAG	ATACCTCTCT	CAATGTTGGT	1620
GAAGACTATG	GTGTGTCTGC	TTATAGAACT	GTGCAAGAG	GAGAATACCC	TGCAGTGCAC	1680
TGTAGAACAG	AAGATAAGAA	CTTTTCTCTG	AATTGGGGTC	TCTAGACTTT	TGGTGCAGCA	1740
TATCTGTTTG	TTATTACTAA	TAACACCAAT	CAGGGTCTTC	AGGCCCTGGA	GATTGAAGAC	1800
ATTCACGCCA	ACAAAATGTC	CATTGCGTGG	CAGCTACCAC	AATATGCCCT	GGTTACAGCT	1860
GGGGAGGTCA	TGTTCTCTGT	CACAGGTCCT	GAGTTTCTTT	ATTCTCAGGC	TCCCTCTAGC	1920
ATGAAATCTG	TGCTCCAGGC	AGCTTGGCTA	TTGACAATTG	CAGTTGGGAA	TATCATCGTG	1980
CTTGTGTGGG	CACAGTTCAG	TGGCCTGGTA	CAGTGGGCGG	AATTCATTTT	GTTTTCTCTG	2040
CTCCTGCTGG	TGATCTGCCT	GATCTTCTCC	ATCATGGGCT	ACTACTATGT	TCCTGTAAAG	2100
ACAGAGGATA	TGGGGGTCC	AGCAGATAAG	CACATTCCTC	ACATCCAGGG	GAACATGATC	2160
AAACTAGAGA	CCAAGAAGAC	AAAACCTCTGA				

Seq ID NO: 681 Protein sequence
 Protein Accession #: AAB34388.1

1 11 21 31 41 51
| | | | |
MNPFQKNESEK ETLFSPVSIE EVPPRPSPSP KKPSPITICGS NYPLSIAPIV VNEFCERFSY 60
YGMKAVLILY FLYFLHWNED TSTSIYHAFS SLCYPTPILG AAIADSWLKG FKTIYLSLV 120
5 YVLGHVILKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFQGD QFEKHAEER 180
TRYFSVPYLS INAGSLISTP ITPLMRGDVQ CFGECDYALA FGVPGLLMVI ALVVFAMGSK 240
IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYKP QLIMDVKALT 300
RVLFYIPLP MFWALLDQGG SRWTLQAI RM NRNLGPFVLQ PDQMQLNPF LVLIFIPFLD 360
10 FVIYRLVSKC GINFSSLRKM AVGMILACLA FAVAAVEIK INEMAPAQSG PQEVFLQVLN 420
LADDEVKVTV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDPHFHLKY HNLSLYTEHS 480
VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540
EDYGVSAIRT VQGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN OGLQAWKIED 600
IPANKMSIAW QLPQYALVTA GEVMSVTGL EFSYSQAPSS MKSVLQAAWL LTIAGVNIIV 660
15 LVVAQFSGLV QWAEFILFSC LLLVICLIFS IMGYIYVPVK TEDMRGPADK HIPHIQGNMI 720
KLETKTKTL

Seq ID NO: 682 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

1 11 21 31 41 51
| | | | |
TCGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCGGAAG AGGTAGCTCA 60
CGCGATAGAA ACCTGTTCCG TGTCCAGAA GAAGGGAAG CGCGAGTGAG GAAAGGAGGT 120
25 ACTGTAGATG CCCTCCAAAT CCTTGGTTAT GGAATATTTG GCTCATCCCA GTACACTCGG 180
CTTGGCTGTT GGAAGTTGCT GTGGCATGTG CCTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
CTTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGGT CGAAATGACT TAAAGATGGG 360
30 AAAAGGGAAG ATGGCTGCC AGTGCTCTCA TGCTGCTGTT TCAGCCTACA AGCAGATTCA 420
AAGAAGAAAT CCTGAAATGC TCAACAATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT 480
CAAAGCTCCT GATGAAGAAA CCCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT 540
GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAGGCT CTCAACTGT 600
CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCAGTGGTC ACCTAAACT 660
35 TTACTAGGTG GACTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTGTTG AAGCCTGTCA 720
GATTCTAACA ACAAAAGCTG AATTCTTCA CCAACTTAA ATGTCTCTGA GATGAAATA 780
AAACCTATTC CCATGTTCTA AAAAAA

Seq ID NO: 683 Protein sequence
Protein Accession #: NP_057161.1

1 11 21 31 41 51
| | | | |
MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHY DTESEASILG 60
DSGEYKMLV VRNDLKMKGK KVAAQCASHA VSAYKQIQR NPMLKQWEY CGQPKVVVKA 120
45 PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPSPADLID KVTGHLKLY

Seq ID NO: 684 DNA sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26..952

1 11 21 31 41 51
| | | | |
CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC 60
TCAGATGCTC CTGGTGTTCG TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT 120
55 GGCCGAGGCG AGCCGCGCAA GTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
ATTCCGAGAG TTGCGGAAAC GTTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG 240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCTGCA GTCCGGATAC TCACGCCAGA 300
AGTGCGGCTG GGATCCGCGC GCACCTGCA CCTGCGTATC TCTCGGGCG CCCTTCCCGA 360
60 GGGGCTCCCC GAGGCTCCCC GCCTTACCG GGCTCTGTTT CGGCTGTCCC CGACGGCGTC 420
AAGGTGCTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480
GCCCGCGCTG CACTCGGAC TGTCGCGGCC GCCGTGCGAG TCGGACCAAC TGCTGGCAGA 540
ATCTTCTGCC GCACGGCCCC AGCTGGAGTT GCACTTGGC CGCAAGCCG CCAGGGGGCG 600
CGCAGAGCG CGTGCGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG 660
TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCGGATGGG TGCTGTGCC 720
65 ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA 780
CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACG AGCCAGCGCC 840
CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT 900
GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT 960
70 GGTCCCTCCA CTGTGCACCT GCGCGGGGGA GCGGACCTCA GTTGCTCTGC CCTGTGGAAT 1020
GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAACA GCTGTATTTA TATAAGTCTG 1080
TTATTATTA TTAATTTATT GCGGTGACCT TCTTGGGGAC TCGGGGCTG GTCTGATGGA 1140
ACTGTGTATT TATTAAAC TCTGGTGATA AAAATAAAGC TGTCTGAAC GTTAAAAAAA 1200
AAAA

Seq ID NO: 685 Protein sequence
Protein Accession #: NP_004855.1

1 11 21 31 41 51
| | | | |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRAS PGPSELHSED SRPRELRKRY 60
80 EDLLTRLRAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAL PEGLPASRL 120
HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPFSQSDQLL AESSSARPL 180
ELHLRPQAR GRRRARANG DDCLPGRC CRLHTRASL EDLGWADWVL SPREVQVTCM 240
85 IGACPSQFRA ANMHAQIKTS LHLRKPDEP APCCVPASYN PMVLIQKTDV GVSQTYDDL 300
LAKDCHCI

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
      ACCAAATCAA CCATAGGTCC AAGAACAAAT GTCTCTGGAC GGCAGCTATG CGACTCACCG 60
      TGCTGTGTGC TGTGTGCCCT CTGCCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG 120
      GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
      ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAAT 240
      TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCCGCGT CATAGAAATA ATGCAGAAGC 300
      CCAGATGTGG AGTGCCAGAT GTTGCAGAAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
      CTTCCAAAGT GGTACCTTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
      TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTCA 480
      GGAAAGTTGT ATGGGGAACT GCTGACATCA TGATTGGCTT TCGCGAGGA GCTCATGGGG 540
      15 ACTCTACCCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCTGGGACAG 600
      GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660
      GGATTAACCT CTGTATGCT GCAACTCATG AACTTGGCCA TTCTTGGGT ATGGGACATT 720
      CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
      20 AACTTTCCCA GGATGATATT AAAGGCATTG AGAAACTATA TGGAAAGAGA AGTAATTCAA 840
      GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCAATCA TTCATTGGAT TGATATCAT 900
      TGTTCACAA TCAGAATTGA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCACC 960
      CTTTTTATT GCAGTTGGTT TTGAATGTC TTCACTCCT TTTATTGGTT AAACCTCTTT 1020
      ATGGTGTGAC TGTGCTTAT TCCATCTATG AGCTTTGTCA GTGCGGTAG ATGTCAATAA 1080
      25 ATGTTACATA CACAATAAA TAAATGTTT ATTCCATGST AAATTTA
```

Seq ID NO: 687 Protein sequence
Protein Accession #: NP_002414.1

```
30      1      11      21      31      41      51
      |      |      |      |      |      |
      MRLTVLCAVC LLPGLALPL PQEAGGMSSEL QWEQAQDYLK RPYLYDSETK NANSLEAKLK 60
      EMQKFFGLPI TGMNLSRVIE IMQKPRGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120
      PHITVDRLVK KALNMWGKEI PLHFRKVVWG TADIMIGFAR GAHGDSPYFD GPNTLAHAF 180
      35 APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND 240
      PQNFKLSQDD IKGIQKLYGK RSNRKK
```

Seq ID NO: 688 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

```
40      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60
      45 TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACCTT GCCCGAGTCT 120
      TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCACGG CTACTGCTCT 180
      CCTACCTCGG CTTCCTATGG CAAAGCTCTC AACCCTACC AGTATCAGTA TCACGGCGTG 240
      AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300
      TACCACCACT ACGGCGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
      50 GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC 420
      AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
      TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCCTCGC TGGGATTGAC ACAAAACAG 540
      GTGAAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AACCGGGAG 600
      ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCCGAGTCT 660
      CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720
      55 CCTCCGACCT CCAACCAATC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780
      ACAAGTGCAG CCAGCTCAAT CAATTCCCAC CTGCCGCCGC CGGGCTCCTT ACAGCACCCG 840
      CTGGCGCTGG CCTCCGGGAC ACTCTATTAG
```

Seq ID NO: 689 Protein sequence
Protein Accession #: NP_005212.1

```
60      1      11      21      31      41      51
      |      |      |      |      |      |
      MTGVFDRRVP SIRSGDFQAP FQTSAMHHP SQESPTLPES SATDSDYSP TGGAPHGYCS 60
      65 PTSASYGKAL NPYQYQYHGV NGSAGSYPK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
      EVTEPEVRMV NGKPKKVRKP RTIYSSFLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180
      VKIWFQNKRS KIKKIMNGE MPPEHSPSSS DPMACNSPOS PAVWEPQSSS RSLSHHPHAH 240
      PPTSNQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTYL
```

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung
2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a lung cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated antibody in the biological
6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9 antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 18. The method of claim 16, wherein the patient is a human.

1 19. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby
9 monitoring the efficacy of the therapy.

1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated
3 polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 21. The method of claim 19, wherein the patient is a human.

1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1A-16.

1 23. The nucleic acid molecule of claim 22, which is labeled.

1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label

1 25. An expression vector comprising the nucleic acid of claim 22.

1 26. A host cell comprising the expression vector of claim 25.

1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1A-16.

1 28. An antibody that specifically binds a polypeptide of claim 27.

1 29. The antibody of claim 28, further conjugated to an effector component.

1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.

1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.

1 32. The antibody of claim 29, which is an antibody fragment.

- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a lung cancer cell in a biological sample from a
2 patient, the method comprising contacting the biological sample with an antibody of claim
3 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to lung cancer in a patient,
2 the method comprising contacting a biological sample from the patient with a polypeptide
3 encoded by a nucleic acid comprises a sequence from Tables 1A-16.
- 1 38. A method for identifying a compound that modulates a lung cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a lung cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1A-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.
- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.

1 44. A method of inhibiting proliferation of a lung cancer-associated cell to
2 treat lung cancer in a patient, the method comprising the step of administering to the subject a
3 therapeutically effective amount of a compound identified using the method of claim 38.

1 45. The method of claim 44, wherein the compound is an antibody.

1 46. The method of claim 45, wherein the patient is a human.

1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having lung cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of lung cancer.

1 48. The assay of claim 47, wherein the control is a mammal with lung
2 cancer or a cell therefrom that has not been treated with the test compound.

1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having lung cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having lung
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.